Evolution und historische Biogeographie von *Senecio* L. mit Fokus auf die Alte Welt

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“It has been shown … that the migration of most of the
Compositae, and of *Senecio* in particular,
took place along the mountain ranges.”
Small 1919:135

Vorwort

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Abstract

Senecio L. is one of the largest genera of angiosperms with a nearly cosmopolitan distribution. The evolution and biogeography of *Senecio* was investigated with the help of molecular phylogenies that are based on nuclear ribosomal and chloroplast data.

The genus evolved during the Mid Miocene in dry or winter rainfall regions of southern Africa and colonized the other continents several times independently (with the exception of Antarctica). The diversification rate of *Senecio* is higher compared to the tribe and comparable to other young radiations. It seems likely that the good dispersability, the high seed set and a preference for open or disturbed habitats facilitated the diversification of the group. The large number of species, the young age and the nearly cosmopolitan distribution set *Senecio* apart from several other recent radiations. Most other recent and rapid radiations are confined to limited geographic extents. The only radiation investigated so far next to *Senecio,* that is young, has a high diversification rate and is widely distributed is the radiation of *Poa* L. and closely related genera.

The Palaearctic was colonized twice independently. Both lineages occur in approximately the same region, but they differ in their habitat preference and life cycle. The Palaearctic vulgaris-clade most likely originated from an annual lowland species from dry or winter rainfall regions of southern Africa and the Palaearctic species are mostly confined to the area around the Mediterranean Basin. The other lineage, the doria-clade, most likely originated from the Drakensberg region and the species prefer mountainous regions in the Palaearctic.

The high altitude areas of the East African high mountains were colonized several times independently during the Pliocene or Pleistocene. In the so-called tropical afroalpine region, *Senecio* is the largest group of angiosperms. This is the result of several independent colonizations events, *in situ* speciation played only a minor role. Comparisons with other tropical alpine-like habitats suggest that the low diversification rate is an effect of area size.

Lineages either adapted to mountainous habitats or evolved an annual life cycle before the Palaearctic and tropical Afroalpine regions were colonized respectively. This shows the importance of niche evolution followed by niche stability for the evolution and range expansion of the genus.

Zusammenfassung

Die Gattung *Senecio* L. ist eine der größten Angiospermengattungen und ist nahezu kosmopolitisch verbreitet. Die Evolution und Biogeographie von *Senecio* wurde mit Hilfe von molekularen Phylogenien, die auf nukleär ribosomalen und plastidären Daten beruhen, nachvollzogen.

Die Gattung entstand Mitte des Miozäns in trockenen oder Winterregengebieten des südlichen Afrikas und die mehrmalige unabhängige Besiedelung der anderen Regionen ging von dort aus. Die hohe Artenzahl und die fast weltweite Verbreitung in Verbindung mit dem jungen Alter stellt eine Besonderheit der Gattung *Senecio* dar. Die meisten bisher untersuchten Radiationen sind entweder artenärmer, nicht nahezu weltweit verbreitet oder deutlich älter, mit Ausnahme der Gattung *Poa* L. und nahverwandten Gattungen. Die Diversifizierungsrate von *Senecio* ist höher im Vergleich zur Tribus und vergleichbar mit anderen schnellen Radiation. Die Ergebnisse dieser Arbeit lassen vermuten, dass eine gute Ausbreitungsfähigkeit, ein hoher Samenansatz sowie eine Präferenz von offenen oder gestörten Standorten für die weite Verbreitung und die hohe Artenanzahl mitverantwortlich sind.

Es kam zu zwei unabhängigen Kolonisierungsereignissen der Paläarktis, wobei die beiden Linien zwar ähnliche Regionen besiedelten, sich aber in ihrer Habitatpräferenz und Lebensdauer unterscheiden. Die Vulgaris-Klade stammt wahrscheinlich von einjährigen Tiefland-Arten aus trockenen oder Winterregengebieten des südlichen Afrikas ab und die paläarktischen Arten kommen hauptsächlich entlang des Mittelmeers vor. Die Arten der Doria-Klade sind mehrjährig, ihr Vorfahr stammt am wahrscheinlichsten aus der bergigen Drakensbergregion und die paläarktischen Arten kommen auch eher in bergigen Regionen vor.

Die alpin-ähnlichen Regionen der ostafrikanischen Hochgebirge wurden mehrfach unabhängig voneinander während des Pliozäns oder Pleistozäns besiedelt, am wahrscheinlichsten ausgehend von den Drakensbergen. Innerhalb der sogenannten tropisch afroalpinen Region stellt *Senecio* die größte Gattung dar. Dies ist das Ergebnis vielfacher unabhängiger Kolonisierungsereignisse, *in situ* Artbildung spielte nur eine untergeordnete Bedeutung. Vergleiche mit anderen tropisch alpin-ähnlichen Regionen lassen vermuten, dass die niedrige Artbildungsrate ein Effekt der Arealgröße ist.

Die untersuchten Linien passten sich an die ökologischen Bedingungen in bergigen Regionen an bevor die tropisch afroalpine Region besiedelt wurde beziehungsweise

entwickelten sie eine einjährige Lebensweise bevor die trockenen und Winterregengebiete der Paläarktis besiedelt wurden. Dies zeigt, dass Nischenevolution mit anschließender Stabilität ein wichtiger Aspekt bei der Evolution und Ausbreitung der Gattung war.

Inhaltsverzeichnis

1. Einleitung

Angewendete Konzepte der Evolutionsbiologie und -ökologie

Phylogeographie

Die Phylogeographie verbindet die Forschungsgebiete der Phylogenetik und der Biogeographie (Storch *et al*., 2013). Während die Phylogenetik die Rekonstruktion der Evolution von Organismen beinhaltet und der Erforschung von Verwandtschaftsverhältnissen dient, beinhaltet die Biogeographie die Rekonstruktion von Ausbreitungsmustern.

Die Evolution kann mit Hilfe von molekularen Phylogenien rekonstruiert werden, durch die Verwendung von sogenannten molekularen Uhren können Stammbäume zeitlich eingeordnet werden. Die Idee der molekularen Uhr war geboren als entdeckt wurde, dass sich die Proteinsequenz von Hämoglobin über die Zeit und über unterschiedliche evolutionäre Linien hinweg ähnlich schnell veränderte (Zuckerkandl & Pauling, 1962, 1965). Es wurde daher davon ausgegangen, dass sich die Substitutionsrate eines Gens nicht verändert und es eine globale molekulare Uhr gibt („*strict clock*“). Heutzutage ist bekannt, dass Substitutionsraten variieren und nicht einer strikten molekularen Uhr folgen (Storch *et al*., 2013; eine der ersten Publikationen, die dies für Pflanzen feststellte, ist Bousquet *et al*., 1992). Substitutionsraten variieren zwischen verschiedenen Bereichen des Genoms (z. B. zwischen dem Kern- und Plastidgenomen, zwischen kodierenden und nicht kodierenden Bereichen und abhängig von der Position im Basentriplet) und sind teilweise von linienspezifischen und/oder ökologischen Eigenschaften abhängig (z. B. Generationszeit und Populationsgrößen; Storch *et al*., 2013). Um diesen Unterschieden Rechnung zu tragen, wurden Methoden entwickelt die unterschiedliche Substitutionsraten für verschiedene Bereiche der Phylogenie annehmen können, sogenannte „*relaxed clocks*“ (vgl. Rutschmann [2006] für einen guten Überblick). Die Verwendung von molekularen Uhren ermöglicht, die relative zeitliche Einordnung der Aufspaltungsereignisse innerhalb eines Stammbaums. Mit Hilfe von Fossilien oder anderen Kalibrierungspunkten, wie z. B. einem Inselalter bei Inselendemiten, können den Aufspaltungsereignissen tatsächliche Altersangaben hinzugefügt werden (Storch *et al*., 2013). Dadurch kann die Evolution in den Zusammenhang erdgeschichtlicher Veränderungsprozesse gebracht und historische biogeographische Zusammenhänge aufgedeckt werden.

Biogeographie beschreibt räumliche Muster von biologischer Vielfalt. Mit Hilfe von biogeographischen Analysen wird versucht Fragen wie „Wo hat eine bestimmte Linie oder Art ihren Ursprung und wie hat sie verschiedene Orte besiedelt?“, „Warum unterscheidet sich die

Artenzusammensetzung in verschiedenen Regionen, obwohl die ökologischen Bedingungen sehr ähnlich sind?“ oder auch „Wie haben historische Ereignisse die Artenzusammensetzung in einer Region verändert?“ zu beantworten. Das heißt, biogeographische Untersuchungen dienen der Erforschung von Lebewesen in Raum und Zeit. Mit Hilfe der gewonnenen Ergebnisse wird versucht, sowohl die Evolution und Ausbreitung von Arten und Linien, als auch die Evolution in bestimmten Regionen besser nachzuvollziehen (Lomolino *et al.*, 2010).

Insgesamt werden verschiedenste Disziplinen der Biologie, wie auch anderer Naturwissenschaften (z. B. Morphologie, Karyologie, Histologie, Genetik, Ökologie, Geographie, Geologie, Paläontologie, historische Klimatologie oder Chemie) herangezogen, um die Entstehungs- und Ausbreitungsgeschichte, sowie die dazugehörigen Prozesse und Ursachen, von Arten und Linien zu untersuchen und zu verstehen (Lomolino *et al.*, 2010). Die gewonnenen Erkenntnisse können wiederum als Indizien für geologische oder klimatische Veränderungen dienen (Lomolino *et al.*, 2010).

Ausbreitung und Nischenkonservatismus

Die Verbreitung von Arten ist durch ihre ökologische Nische bestimmt und somit von den vorgefundenen biotischen und abiotischen Bedingungen abhängig (Hutchinson, 1957). Dies bedeutet, dass Arten nur an Standorten überleben und reproduktiv erfolgreich sein können, an denen sie passende Bedingungen finden. Geeignete Lebensräume einer Art existieren häufig in verschiedenen Regionen der Erde, die aber nicht immer alle besiedelt wurden. Besiedelung („*colonization*“) meint hier das Ausbreitungsereignis und die erfolgreiche Etablierung, letzteres ist häufig der ausschlaggebende Faktor für eine erfolgreiche Besiedelung und nicht das Ausbreitungsereignis selbst (Alsos *et al.*, 2007).

Die Besiedelung neuer Regionen geschieht entweder durch Migration oder Fernausbreitung, abhängig davon ob die Region dazwischen passende Habitate bereitstellt. Migration meint hier, die Erweiterung des Verbreitungsgebiets ohne dass dazwischen nicht besiedelte Regionen vorkommen (dies schließt nicht aus, dass die Art/Linie in einigen Region auch wieder ausstirbt), wobei Fernausbreitung eine Vergrößerung des Verbreitungsgebietes meint, in der dazwischen nicht besiedelte Regionen vorkommen können. Fernausbreitung beruht entweder auf externen, zufälligen Ereignissen (z. B. Wirbelstürme) oder auf externen, gerichteten Ereignissen (z. B. durch Zugvögel; Lomolino *et al.*, 2010). Häufig weisen Arten und Gattungen disjunkte, also nicht zusammenhängende, Verbreitungsgebiete auf, die entweder das Resultat von Vikarianzereignissen oder von Fernausbreitung sind. Vikarianzereignisse stellen die Unterbrechung eines ehemals zusammenhängenden Gebiets dar, wodurch sich in beiden

Regionen Populationen/Arten unabhängig voneinander entwickeln können. Seit der Akzeptanz der Theorie der Plattentektonik und der Kontinentaldrift dominieren Vikarianzhypothesen bei der Erklärung von disjunkten Verbreitungsmustern (Wiley, 1988; Lomolino *et al.*, 2010). Jedoch wird mittlerweile Fernausbreitungsereignissen wieder ein höherer Stellenwert zugesprochen, vor allem in der südlichen Hemisphäre (Muñoz *et al.*, 2004; Renner, 2004; Sanmartín & Ronquist, 2004; Queiroz, 2005).

Insgesamt scheint es für Arten leichter zu sein, sich in neuen Regionen mit ähnlichen ökologischen Bedingungen zu etablieren, als ihre ökologische Nische zu verändern (Donoghue, 2008). Die Tendenz, dass Arten ihre anzestrale ökologische Nische nicht verändern, ist unter dem Phänomen des Nischenkonservatismus bekannt (Wiens, 2004). Dabei wird angenommen, dass es für Organismen schwierig ist, sich an mehrere neue ökologische Bedingungen gleichzeitig anzupassen, insbesondere wenn sie im Verlaufe ihrer evolutionären Geschichte nie mit diesen neuen Bedingungen in Berührung kamen und keine dafür relevante genetische Variation aufweisen (Wiens *et al.*, 2010; Edwards & Donoghue, 2013; Donoghue & Edwards, 2014). Anpassungen an neue ökologische Bedingungen werden zusätzlich dadurch erschwert, dass durch Selektion und Genfluss Präadaptationen an Umweltfaktoren, für die sie momentan noch nicht optimal angepasst sind, wieder verloren gehen können. Allerdings gibt es in der Fachliteratur genügend Beispiele, in denen es zur Veränderung einer oder mehrerer Dimensionen der Nische kam und nicht zur Besiedelung neuer Regionen mit ähnlichen ökologischen Bedingungen (vgl. Beispiele in Donoghue & Edwards, 2014).

Diversifizierung und Radiation

Mit einer räumlichen Ausbreitung findet häufig auch eine Diversifizierung einer Art statt, da der Genfluss unterbrochen wird. Durch Isolation, Drift und anderen, selektiven Faktoren kommt es zur unabhängigen Evolution in den unterschiedlichen Regionen (Lomolino *et al.*, 2010). Als Maß der Diversifizierung werden häufig Diversifizierungsraten berechnet, die angeben, wie viele Arten in einem bestimmten Zeitintervall entstanden sind (Artbildungsereignisse minus Aussterbeereignisse). Es ist allerdings anzumerken, dass es schwierig ist Extinktionsraten anhand von Phylogenien zu bestimmen (Quental & Marshall, 2010; Rabosky, 2010). Innerhalb der Angiospermen gibt es große Unterschiede in den Diversifizierungsraten, nicht nur zwischen Kladen, sondern auch im Verlaufe der Zeit und in unterschiedlichen geographischen Regionen (Magallón & Sanderson, 2001; Magallón & Castillo, 2009; Hughes *et al.*, 2015).

Radiation beschreibt die Auffächerung einer Art in mehrere Arten (Artdiversifizierung; Schluter, 2000; Abbott *et al.*, 2008; Givnish, 2010) und ist das Ergebnis von Diversifizierungsprozessen.

Das bekannteste Beispiel ist die Radiation der Galapagos-Finken (Darwin, 1859), aber auch innerhalb der Angiospermen sind viele bekannt, wie z. B. in *Lupinus* L. oder den Mittagsblumengewächsen (Klak *et al.*, 2004; Drummond *et al.*, 2012). Bei Radiationen wird häufig zwischen adaptiver (ökologische oder phänotypische) und nicht adaptiver Diversifizierung unterschieden (Ricklefs, 2006; Moore & Donoghue, 2007; Linder, 2008; Rabosky, 2009; Givnish, 2010, 2015; Hughes *et al.*, 2015). Wobei adaptive und nicht adaptive Radiationen eher die beiden gegensätzlichen Pole eines Spektrums darstellen als zwei klar voneinander abgrenzbare Mechanismen (Donoghue & Sanderson, 2015). Bei adaptiven Radiationen kommt es zur Koexistenz von nahverwandten Arten durch Evolution in manchen Dimensionen ihrer ökologischen Nische. Dabei wird davon ausgegangen, dass dies meist durch disruptive Selektion aufgrund von intraspezifischer Konkurrenz (wegen ihrer ökologischen Ähnlichkeiten) vorangetrieben wird (Givnish, 1997, 2015; Schluter, 2000). Eine nicht adaptive Radiation beschreibt die Auffächerung einer Art in mehrere Arten („*lineage diversification*“) ohne bedeutende Veränderungen der ökologischen Nische (Gittenberger, 1991; Rundell & Price, 2009).

Allerdings wird diskutiert, welche Bedingungen wirklich gegeben sein müssen, um von einer Radiation sprechen zu können und wodurch Radiation am meisten beeinflusst wird (Givnish, 1997, 2010, 2015; Schluter, 2009). Häufig wird z. B. die Bedeutung von Diversifizierung durch Ausbreitung oder Nischendivergenz oder von hohen bzw. ansteigenden Diversifizierungsraten hervorgehoben (Sato *et al.*, 2001; Klak *et al.*, 2004; Hughes & Eastwood, 2006). Dies sind jedoch keine unabdingbaren Bedingungen, manche Radiationen sind langsam und bringen wenige Arten hervor, die sich aber an eine Vielzahl verschiedener Habitate angepasst haben. Andere sind sehr schnell, zeigen aber trotzdem keinen Anstieg der Diversifizierungsrate im Vergleich zur Schwestergruppe (Givnish, 2015). Viele untersuchte Radiationen sind relativ jung („*recent radiations*“) und gehen häufig mit einem Anstieg der Diversifizierungsrate einher, jedoch sind auch ältere Radiationen bekannt („*mature radiations*“; Linder, 2008), bei denen ein Rückgang der Diversifizierungsrate nach einiger Zeit zu beobachten war. Rückgänge in der Diversifizierungsrate sind häufig durch steigende Konkurrenz zwischen Arten der gleichen Linie oder durch sich verändernde ökologische Bedingungen erklärbar (Donoghue & Sanderson, 2015).

Die Evolution von morphologischen oder ökologischen Merkmalen, die es einer Art oder Linie erlaubt neue Nischen zu besetzen oder Ressourcen auf eine neue Weise zu nutzen, stellen häufig sogenannte Schlüsselinnovationen dar (Donoghue & Sanderson, 2015). Schlüsselinnovationen beeinflussen die Diversifizierung einer Linie, da sie einen positiven Effekt auf

Diversifizierungsraten haben (Erhöhung der Artbildungsrate oder Verringerung der Extinktionsrate), indem die Schlüsselinnovation erlaubt neue Nischendimensionen auszunutzen (z. B. Evans *et al.*, 2005; Ackerly *et al.*, 2006; Drummond *et al.*, 2012). Dabei wird heute davon ausgegangen, dass es sich meist nicht um eine einzige, sondern um eine Kombination von Schlüsselinnovationen handelt. Allerdings wird derEvolution mancher ökologischer und/oder morphologischer Merkmale nur in bestimmten Kontexten die Funktion einer Schlüsselinnovation zugewiesen (Bouchenak-Khelladi *et al.*, 2015; Donoghue & Sanderson, 2015). So wird etwa der Entwicklung von Mehrjährigkeit in einer überwiegend einjährigen Linie als Schlüsselinnovation bei der Besiedelung alpiner Regionen betrachtet (Datson *et al.*, 2008; Drummond, 2008). Genauso ist die Entwicklung eines neuen Bestäubungssyndroms erst evolutiv bedeutsam, wenn die Linie solche Regionen besiedelt in denen es genügend passende Bestäuber gibt (Kadereit & von Hagen, 2003).

Senecio L. – Tribus Senecioneae – Familie der Asteraceae

Die phylogenetische Stellung von Senecio *L.*

Die Gattung *Senecio* L., auch Greiskraut genannt, gehört zu der Familie der Korbblütler/Asteraceae und in die Tribus Senecioneae. Die Gattung ist eine der größten Pflanzengattungen der Welt (Frodin, 2004), wie auch innerhalb der Familie der Asteraceae (Stevens, 2001).

Die Asteraceae sind eine der artenreichsten Angiospermenfamilien mit mehr als 23000 Arten (Stevens, 2001; Funk *et al.*, 2009b; Barreda *et al.*, 2015) und wurden in 13 Unterfamilien aufgeteilt. Das Verwandtschaftsverhälltnis der Unterfamilien zueinander wurde in den letzten Jahren fast vollständig aufgelöst und eine weitere Unterfamilie beschrieben (Panero *et al.*, 2014). Smith *et al*. (2011) haben einen Anstieg der Diversifizierungsrate innerhalb der Asteraceae gefunden. Mutmaßungen über Schlüsselentwicklungen der Familie, die ihren Artenreichtum erklären würden, gibt es einige, z. B. anzestrale Genomverdopplung, Evolution des Köpfchens, hoher Samenansatz oder auch eine gute Ausbreitungsfähigkeit (Funk *et al.*, 2009a; Schranz *et al.*, 2012). Außerdem wurden zwei neue Fossilien der Familie beschrieben, die älter sind als alle bisher gefundenen, wodurch ein deutlich höheres Kronenalter, von etwa 80 Millionen Jahren, angenommen wird (Barreda *et al.*, 2010; Barreda *et al.*, 2015). Zuvor wurde das Alter der Asteraceae auf das Eozän geschätzt (z. B. Kim *et al.*, 2005; Beaulieu *et al.*, 2013).

Innerhalb der Unterfamilie der Asteroideae, zu der die Senecioneae gehören, kommt es zu phylogenetischen Konflikten zwischen dem nukleären und plastidären Genomen (z. B. Morgan *et al.*, 2009; Smissen *et al.*, 2011). Innerhalb der Senecioneae wurden diese Konflikte auf Hybridisierung und „*incomplete lineage sorting*“ bezogen (Pelser *et al.*, 2002; Devos *et al.*, 2010; Pelser *et al.*, 2010a; Pelser *et al.*, 2012; Calvo *et al.*, 2013).

Die Tribus Senecioneae besteht aus mehr als 160 Gattungen und über 3000 Arten (Pelser *et al.*, 2007; Nordenstam *et al.*, 2009a) und stellt die größte Tribus innerhalb der Familie dar (Stevens, 2001; Beaulieu *et al.*, 2013; Panero *et al.*, 2014). Der Kenntnisstand über die evolutionäre Verwandtschaft innerhalb der Tribus ist eher gering (Pelser *et al.*, 2007; Nordenstam *et al.*, 2009a) und die Taxonomie bislang nicht eindeutig. Insgesamt gibt es innerhalb der Tribus Senecioneae eine große Variation an sekundären Inhaltsstoffen, wobei Eremophilane und Furanoeremophilane für die Gattungsabgrenzungen innerhalb der Tribus hilfreich sein könnten (Pelser *et al.*, 2005; Nordenstam *et al.*, 2009a).

Schon länger war bekannt, dass *Senecio* in seiner traditionellen Umschreibung nicht monophyletisch ist (z. B. Knox & Palmer, 1995; Pelser *et al.*, 2002; Pelser *et al.*, 2007). *Senecio* ist die größte Gattung in der Tribus und viele Arten der Tribus wurden in der Vergangenheit *Senecio* zugeordnet, oder waren teilweise eigene Gattungen, die später eingegliedert wurden (vgl. Pelser *et al.*, 2007). Dies hängt zum einen mit der hohen Artenzahl in der Tribus zusammen, zum anderen damit, dass morphologische Gruppen nur aufgrund von Merkmalskombinationen eingeteilt werden können, die nicht zwangsläufig in allen Arten der Gruppe vorkommen müssen, und nicht aufgrund einzelner Merkmale (Jeffrey *et al.*, 1977; Jeffrey, 1979). Außerdem stimmen die morphologischen Gruppen häufig nicht mit den karyologischen Gruppen überein (Jeffrey *et al.*, 1977, Jeffrey, 1979, Bremer, 1994; Pelser *et al.*, 2007; Nordenstam *et al.*, 2009a). Die Tribus wurde in der Arbeit von Pelser *et al.* (2007) phylogenetisch untersucht und die Untertriben sowie die Gattung *Senecio* neu umschrieben, da sie keine monophyletischen Linien darstellten. In seiner neuen Umschreibung bildet die Gattung im Kern- und im Chloroplastengenom eine gut unterstützte monophyletische Klade (Pelser *et al.*, 2007). Hierfür müssen viele als *Senecio* beschriebene Arten ausgegliedert werden, dies geschah bisher nur teilweise (z. B. Nordenstam *et al.*, 2009b; Nordenstam & Pelser, 2012). Es wurden allerdings auch schon vor der Arbeit von Pelser *et al.* (2007) viele Arten aus *Senecio* ausgegliedert und bilden heute eigenständige Gattungen, hierzu gehören beispielsweise *Curio* P.V. Heath (Abb. 1c), *Kleinia* Mill. (Abb. 1d) und *Dauresia* B. Nord. & Pelser (Heath, 1997; Nordenstam & Pelser, 2005) aus dem südlichen Afrika, aber z. B. auch *Dendrosenecio* (Hauman ex Hedberg) B. Nord. aus den Hochgebirgen Ostafrikas (Abb. 1e; Nordenstam, 1978).

Damit *Senecio* eine monophyletische Gattung darstellt, müssen andere Arten neu bzw. wieder eingegliedert werden. Zu den einzugliedernden Gattungen gehören *Robinsonia* DC. (Abb. 2f; Pelser *et al.*, 2010b), eine baumähnliche und diözische Gattung, die auf den Juan-Fernández-Inseln endemisch ist, *Aetheolaena* Cass., *Culcitium* Bonpl. (Abb. 2b; Salomón & Freire, 2014) und *Lasiocephalus* Willd. ex Schltdl. (Abb. 2a; Marhold & Sklenář, 2013), die in den Anden vorkommen, sowie die beiden kleinen Gattungen *Hasteola* Raf. (zwei Arten aus Nordamerika; Abb. 2g) und *Iocenes* B. Nord. (monospezifische Gattung aus Patagonien).

Während früher etwa 3000 Arten zu *Senecio* gezählt wurden (Jeffrey *et al.*, 1977; Bremer, 1994), wird heute vermutet, dass 1000 bis 1250 Arten in die Gattung gehören (Pelser *et al.*, 2007; Calvo *et al.*, 2013). Genauere Angaben zur Artenzahl sind nicht möglich, da sich die Gattung in ihrer neuen Umschreibung nicht eindeutig anhand von morphologischen Merkmalen von anderen Gattungen der Tribus unterscheiden lässt, es fehlen Synapomorphien. Die sechs wieder eingegliederten Gattungen weisen teilweise morphologische Merkmale auf, die früher für die Unterscheidung der Gattungen und Untertriben als relevant betrachtet wurden (Pelser *et al.*, 2007). Dies ist auch ein Grund warum manche Wissenschaftler das neue Konzept von *Senecio* nicht anerkennen, einige der eingegliederten Arten sind morphologisch und ökologisch deutlich anders (Dušková *et al.,* 2010; Takayama *et al.,* 2015). Möglicherweise könnten mikromorphologische Merkmale vor allem der Blüte zur Unterscheidung der Gattungen relevant sein (Vincent & Getliffe, 1992; Pelser *et al.,* 2004). Charakteristisch für die Tribus sind die Form und Position der Involukralblätter, die den sogenannten Hüllkelch/das Involukrum an der Infloreszenzbasis bilden. Das Involukrum besteht normalerweise aus einer Reihe gleich großer und gleich geformter Hochblätter, selten sind es mehrere Reihen (Nordenstam *et al.,* 2009a). Die Tribus ist weltweit verbreitet, Zentren der Diversität sind temperate, subtropisch-aride und bergige Regionen (Nordenstam *et al.,* 2009a). Der haploide Chromosomensatz innerhalb der Senecioneae ist häufig x=10 (Pelser *et al.,* 2007; Nordenstam *et al.,* 2009a), jedoch wurden bei viele Arten Abweichungen davon gefunden, auch innerhalb von *Senecio* (Nordenstam, 2007; Nordenstam *et al.,* 2009a).

Die Gattung Senecio *L.*

Der Gattungsname *Senecio* stammt von dem lateinischen Wort „*senex*“ das alter Mann oder Frau bedeutet und eine Anspielung auf die weißen Pappushaare sind, die den weißen Haaren von alten Menschen ähneln sollen (Barkley, 2006). Manche Arten der Gattung sind relativ bekannt, einige aufgrund ihrer Giftigkeit durch Pyrrolizidinalkaloide und den daraus resultierenden wirtschaftlichen Verlusten in der Viehzucht (Rose, 1972; Fu *et al.,* 2004; Stegelmeier, 2011), andere Arten, weil sie invasiv und weit verbreitet sind (z. B. *Senecio madagascariensis* Poir oder *S. inaequidens* DC.; Lafuma *et al.,* 2003; Prentis *et al.,* 2007; Vacchiano *et al.,* 2013).

Laut Pelser *et al.* (2007) bestehen die Köpfchen von *Senecio* entweder nur aus Röhrenblüten oder aus einer Kombination von Röhren- und Zungenblüten. Die Köpfchen bestehen meist aus zwittrigen Einzelblüten, nur die Randblüten sind häufig rein weiblich (z. B. Harvey, 1865; Chater & Walters, 2010). Lediglich die Arten, die auf den Juan-Fernández-Inseln vorkommen, haben diözische Blütenstände (Synonym: *Robinsonia;* Nordenstam *et al.,* 2009a). Häufig sind die Kronblätter gelb, manchmal auch weiß, grün, rosa, purpurn, selten blau (Pelser *et al.,* 2007). Die typische Frucht von *Senecio* sowie den Asteraceae ist die Achäne, die bei *Senecio* gerippt und oft stark behaart ist. Die Früchte haben einen Pappus, dem eine große Bedeutung bei der Ausbreitung durch Wind zugeschrieben wird (Andersen, 1993; Nordenstam *et al.,* 2009a). Die Beblätterung ist meist alternierend (Pelser *et al.,* 2007). Innerhalb der Gattung existieren ein- bis mehrjährige Kräuter, Halbsträucher, Sträucher, Bäume und Lianen (Pelser *et al.,* 2007). Der Typus der Gattung, *Senecio vulgaris* L. (Abb. 3), wie auch Arten aus dem Mittelmeergebiet und den trockenen Regionen des südlichen Afrikas, sind häufig einjährig (Alexander, 1979; Manning

& Goldblatt, 2012; Manning & Bruyns, 2013). *Senecio* ist die einzige Gattung der Tribus, die fast weltweit (außer der Antarktis) verbreitet ist, wobei sie in manchen Regionen nicht einheimisch ist (Westindien; Nordenstam *et al.*, 2009a; Pelser *et al.*, 2007). Der Hauptverbreitungsschwerpunkt von *Senecio* liegt in Südamerika und dem subsaharischen Afrika (Bremer, 1994), allerdings lässt sich eine hohe Artenvielfalt auch in den Winterregengebieten der Erde finden (Nordenstam *et al.*, 2009a). Außerdem ist die Gattung in fast allen Habitaten vertreten, Arten kommen in tropischen wie temperaten Regionen, an der Küste wie auf Bergen und in trockenen wie an feuchten Standorten vor (Nordenstam *et al.*, 2009a). Gründe, die die starke Diversifizierung (ökologisch wie morphologisch) der Gattung erklären könnten, sind bisher unbekannt (Nordenstam *et al.*, 2009a). Pelser *et al.* (2007) konnte zeigen, dass *Senecio* im subsaharischen Afrika entstand und von dort ausgehend die anderen Kontinente mehrmals unabhängig voneinander besiedelt wurden. Datierungen der Gattung schätzen das die Gattung zwischen dem mittleren Miozän und dem Pleistozän entstanden ist (Pelser *et al.*, 2010a; Pelser *et al.*, 2012).

Abbildung 1: Ausgewählte Beispiele von Arten die früher zu *Senecio* gehörten: a) *Delairea odorata* Lem.; b) *Caputia medley-woodii* (Hutch.) B. Nord. & Pelser; c) *Curio roleanus* (H. Jacobsen) P.V. Heath; d) *Kleinia neriifolia* Haw.; e) *Dendrosenecio* cf. *adnivalis* Stapf; f) *Jacobaea vulgaris* Gaertn. Informationen zu den einzelnen Bildern sind im Anhang.

Abbildung 2: Ausgewählte Arten der Gattung *Senecio*: a) *S. superandinus* Cuatrec; b) *S. canescens* (Bonpl.) Cuatrec.; c) *S. mattirolii* Chiov.; d) *S.* cf. *transmarinus* S.Moore; e) *S. masafuerae* (Skottsberg) Pelser; f) *S. elegans* L.; g) *S. suaveolens* (L.) Ell. Informationen zu den einzelnen Bildern sind im Anhang.

Abbildung 3: Der Typus der Gattung - *Senecio vulgaris*. Informationen zur Abbildung sind im Anhang.

Ziele und Methodik der Arbeit

Die Ziele der vorliegenden Arbeit sind die Untersuchung und Beschreibung der Entstehungsgeschichte, Diversifizierung (Kapitel 2 und 3) und Ausbreitung (Kapitel 3 und 4) von *Senecio*. Hierfür wird die Gattung datiert, ihr Ursprungsgebiet näher bestimmt und die Ausbreitung in die Paläarktis und in die Berge Ostafrikas näher untersucht.

Zu diesem Zweck werden Methoden der modernen Pflanzensystematik verwendet. Dazu zählen die Generierung von DNA-Sequenzen mit Hilfe der Sanger-Methode, Rekonstruktionen von Stammbäumen und Merkmalen, sowie biogeographische Untersuchungen. Frühere phylogenetische Untersuchungen der Gattung konzentrierten sich entweder auf Sektionen oder begrenzte Regionen (Comes & Abbott, 2001; Pelser *et al.*, 2002; Calvo *et al.*, 2013). Die tribusweite Phylogenie von Pelser *et al.* (2007), beinhaltet bisher die umfangreichste Stammbaumanalyse der Gattung und umfasste 186 Arten aller Kontinente und vieler beschriebener Sektionen. Dieser Datensatz bildet die Grundlage dieser Studie und wird um weitere Arten erweitert, die zum einen, in den Analysen von Pelser *et al*. (2007) noch nicht eingeschlossen waren, zum anderen um neue, bisher noch nicht untersuchte, subsaharisch afrikanische Arten.

Die Stammbaumrekonstruktionen in der vorliegenden Untersuchung beruhen auf bis zu zwei Markern des Kerngenoms, dem „*internal*“ und „*external transcribed spacer*“ (ITS und ETS) und auf maximal vier Markern des Chloroplastengenoms (*ndh*F Gen, *trn*L Intron und die „*intergenic spacer*“ *trn*L-*trn*F und *ycf*6-*trn*C). Die Verwendung von nukleär ribosomaler DNA ist allerdings nicht unproblematisch, da diese in vielfachen Kopien im Genom vorliegen und es zur Sequenzierung nicht homologer Sequenzen führen kann (vgl. z. B. Álvarez & Wendel, 2003). Jedoch wurden für manche *Senecio*-Arten mehrere Kopien von ITS sequenziert und es konnte gezeigt werden, dass sich die verschiedenen Kopien meistens nicht stark voneinander unterschieden (Pelser *et al.*, 2012). Weitere Arbeiten, die sich mit der Tribus Senecioneae beschäftigten, verwendeten mehr Daten aus dem plastidären Genom (Pelser *et al.*, 2007; Pelser *et al.*, 2010a; Pelser *et al.*, 2012), jedoch zeigen die meisten dieser Sequenzbereiche für *Senecio* keine ausreichende Variation. Daher werden in dieser Arbeit nur die drei Marker verwendet, die davon die höchste Variabilität für *Senecio* aufweisen, sowie ein weiterer Marker (*ycf*6-*trn*C). Dieser wurde in den eben genannten Publikationen nicht verwendet, weist aber relativ viele Sequenzunterschiede für Arten innerhalb der Gattung auf.

Die nachfolgenden drei Kapitel sind der Hauptbestandteil dieser Doktorarbeit. Jedes dieser Kapitel stellt ein eigenständiges Manuskript dar und soll teilweise in einer internationalen

Zeitschrift publiziert werden, weshalb diese in englischer Sprache verfasst wurden. Das **erste Manuskript** (Kapitel 2) beschäftigt sich mit der Diversifizierung sowie der fast weltweiten Ausbreitung von *Senecio*. Hierbei wird eine Phylogenie der Gattung erstellt, die Arten aller Kontinente beinhaltet, diese mit verschiedenen Methoden datiert, Diversifizierungsraten berechnet und eine Rekonstruktion der Habitatpräferenz durchgeführt. Anschließend wird *Senecio* mit anderen großen Gattungen verglichen. Es befasst sich unter anderem mit folgenden Fragestellungen: Stehen der Artenreichtum und die vielfache Ausbreitung auf andere Kontinente von *Senecio* mit ökologischen Eigenschaften in Verbindung? Ist die hohe Artenanzahl von *Senecio* das Ergebnis einer hohen Diversifizierungsrate und gibt es andere Pflanzengattungen die auch jung, artenreich und weit verbreitet sind? Das **zweite Manuskript** (Kapitel 3) konzentriert sich auf die Eingrenzung des Ursprungsgebiets sowie die Besiedelung der Paläarktis durch *Senecio*. Hierfür wird ein Teildatensatz der Phylogenie aus dem ersten Manuskript verwendet und diesem mehr Arten aus dem südlichen Afrika hinzugefügt. Mit Hilfe von verschiedenen Rekonstruktionsmethoden wird die Ausbreitung der Gattung in die Paläarktis untersucht. In diesem Kapitel werden folgende Fragen fokussiert: Sind die beiden paläarktischen Linien, die von Pelser *et al.* (2007) gefunden worden, wirklich unabhängig voneinander entstanden und somit das Ergebnis von zwei Ausbreitungsereignissen? Ist die Besiedelung der Paläarktis das Ergebnis von Fernausbreitung oder wurde die Region durch Migration entlang von Korridoren besiedelt? Die Arten der beiden paläarktischen Kladen weisen unterschiedliche Lebenszyklen auf. Sind dies Anpassungen an unterschiedliche ökologische Bedingungen? Hat sich die annuelle Lebensweise in der Paläarktis neu entwickelt oder war auch schon der nicht paläarktische Vorfahr einjährig? Wann und warum entwickelten sich einjährige und mehrjährige Linien? Das Thema des **dritten Manuskripts** (Kapitel 4) ist die Besiedelung der tropisch afroalpinen Zone der ostafrikanischen Hochgebirge. Die tropisch afroalpine Region stellt ein Inselhabitat dar, weil ähnliche ökologische Bedingungen nur in größerer Distanz zu finden sind. Daher eignet sich diese Region besonders gut für biogeographische Analysen und um den Einfluss von Ausbreitungsereignissen im Vergleich zu Artbildung zu untersuchen. Die tropisch afroalpine Region wurde bisher wenig phylogenetisch untersucht und *Senecio* stellt dort die artenreichste Gattung dar. Für die phylogenetischen Analysen werden vor allem tropisch afroalpine Arten in den Datensatz aufgenommen um die folgende Fragen zu beantworten: Von wo sind die Arten in die tropisch afroalpine Zone eingewandert und waren sie schon vor der Besiedelung an die dort herrschenden ökologischen Bedingungen angepasst? Stellt die Einwanderung ein einmaliges Ereignis mit anschließender Artbildung dar oder wurden die Berge mehrmals unabhängig voneinander besiedelt? Die Ergebnisse werden anschließend mit Ergebnissen von anderen tropisch alpin-ähnlichen Regionen verglichen.

2. Recent cosmopolitan radiation of *Senecio* L. (Asteraceae-Senecioneae)

Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Abtract

Aim Investigations of plant radiations have mainly focused on small species assemblages or more or less restricted areas. Here we investigate the evolutionary history of the nearly cosmopolitan genus *Senecio*, one of the largest genera of angiosperms.

Location Nearly worldwide.

Methods Previously published phylogenies were expanded to represent about 25 % of the genus. One nuclear marker (internal transcribed spacer) as well as three chloroplast markers (*ndh*F, *trn*LF and *trn*C-*ycf*6) were amplified and sequenced. Maximum Parsimony, Maximum Likelihood and Bayesian Inference methods were used to infer the phylogeny, divergence times, biogeographic history and ancestral habitat preference.

Results *Senecio* originated – as previously shown – in sub-Saharan Africa about 10 million years ago (Ma). The crown age of the genus is about 7 Ma with a diversification rate of 0.29-1.48 speciation events Myr^{-1}. In this relatively short time period, all other continents were colonized through long-distance dispersals mainly from Africa. Present seen diversification of clades, which are often restricted to single continents, occurred during the last 5 Myr. Most *Senecio* species as well as the most recent common ancestor prefer either open or disturbed habitats.

Main conclusions Despite its young age and almost cosmopolitan distribution, *Senecio* is one of the most species-rich genera of plants. Accordingly, diversification rates are high compared to the tribe and similar to other recent or continental radiations. The success of *Senecio* is probably related to their preference for open or disturbed habitats, facilitating establishment, in combination with their excellent dispersability. Hence, we postulate that Pliocene climatic changes and mountain uplifting are likely to have contributed to the success of the group, providing ample opportunity to colonize newly opened or disturbed habitats.

Introduction

Species diversification and radiation have intrigued scientists since Darwin studied and described the Galapagos finches (Darwin, 1859). Both terms, diversification and radiation, are often used interchangeably. However, diversification is the process by which the diversity of organisms increases, while radiation is considered to be an increase of diversity of closely related species which share a common ancestor (Abbott *et al.*, 2008). Radiations have often been attributed to ecological factors such as climate, habitat stability and habitat heterogeneity, as well as the ability to adapt, disperse and compete (Ricklefs, 2006; Moore & Donoghue, 2007; Linder, 2008; Rabosky, 2009; Givnish, 2010). Additionally, key innovations, i.e. morphological or ecological traits which promote diversification and therefore lead to radiations, have been credited as drivers of radiations (Böhle *et al.*, 1996; Baldwin & Sanderson, 1998; Hodges, 2000). Radiations can be classified in two categories: adaptive and non-adaptive (Givnish, 1997, 2010), and there is an on-going debate about what exactly constitutes a radiation, and the relevance of species richness, diversification rate, adaptation and colonization of novel habitats have been discussed (Monasterio & Sarmiento, 1991; Givnish, 1997, 2010; Hughes & Eastwood, 2006; Schluter, 2009). In this study, radiation is defined as an increase in diversity within a lineage with respect to species richness, morphology and/or ecology.

Early studies of radiations mainly concentrated on species diversity without considering the time frame of the diversification process (Knox & Palmer, 1995; Böhle *et al.*, 1996). However, time is an important aspect of radiations even though not all angiosperm clades show a positive correlation between age and diversity (Ricklefs & Renner, 1994; Rabosky *et al.*, 2012). Molecular dating methods have enabled researchers to investigate the timing of a radiation as well as differences in diversification rates. Results show that the time span involved in radiations can vary significantly, e.g. *Inga* Mill. with 300 spp. has diversified in the last 10 Million years (Myr; Richardson *et al.*, 2001a), Darwin finches, 15 spp. in 2.3 Myr (Sato *et al.*, 2001) and cichlid fishes, 447-535 spp. in Lake Victoria in 12.4 thousand years (Day *et al.*, 2008). Obviously, the different numbers of species accumulated in different time spans are the result of different diversification rates (Magallón & Sanderson, 2001). For example, Magallón & Castillo (2009) reported that in angiosperms diversification rates ranged from 0.0781 to 0.0909 net speciation events per million years (seMyr^{-1}; speciation events minus extinction events). However, some radiations show much higher rates, e.g. Aizoaceae Martinov: 0.53-11.10 seMyr^{-1} (Klak *et al.*, 2004), *Gaertnera* Lam.: 0.37-0.70 seMyr^{-1} (Malcomber, 2002) and Andean *Lupinus* L. species: 0.72-3.76 seMyr^{-1} (Hughes & Eastwood, 2006; for comparison these rates have here been recalculated using the approach of Magallón & Sanderson [2001] based on crown age estimates and relative extinction rates of 0 and 0.9). Most groups having high diversification rates, such as the examples listed, have diversified in the recent past, where no clear definition of 'recent' radiation exists (Givnish, 2010). This is in accordance with the observation that in general younger radiations have higher net diversification rates than more ancient ones (Linder, 2008). However, this observation is potentially only a methodological artefact. Diversification rates are calculated using present day species numbers and clade ages. Thus, older lineages may be less species-rich today due to extinction in the past, which will lead to lower calculated diversification rates. As extinction rates in general are difficult to estimate (Quental & Marshall, 2010; Rabosky, 2010), extinction as possible cause of low diversification rates can not easily be demonstrated.

Despite different definitions, research on plant radiations has mainly focused on radiations of more or less small species assemblies in more or less restricted areas, such as isolated islands (Baldwin & Sanderson, 1998; Sato *et al.*, 2001; Givnish *et al.*, 2009; Wagstaff & Breitwieser, 2004) or island-like habitats such as lakes or mountains (Knox & Palmer, 1995; Richardson *et al.*, 2001b; Liu *et al.*, 2006; Day *et al.*, 2008). Studies of groups with a non-island-like distribution, often focussed on small species assemblages or on groups, which can only be found on one continent or in one climatic regime, but rarely on groups with a cosmopolitan or nearly cosmopolitan distribution (Hodges, 2000; von Hagen, & Kadereit, 2001; Richardson *et al.*, 2001a; Hughes & Eastwood, 2006; Tank & Olmstead, 2009; Valente *et al.*, 2010; Pirie *et al.*, 2011). A comparison of species-rich angiosperm genera (Tab. 1), where genus rank is taken as a proxy for comparable degrees of morphological similarity, shows that only a few of these large genera have a cosmopolitan distribution. Of those distributed worldwide, most tend to have originated in the early Miocene or earlier, while younger genera are mostly more restricted in their distribution.

This paper focuses on *Senecio* L. (ragworts and groundsels), a genus of nearly cosmopolitan distribution and of young age. Whereas up to 3000 species have been included in *Senecio* in the past (Jeffrey *et al.*, 1977; Bremer, 1994), about 1000 species are accepted in the genus today as the result of a recent molecular phylogenetic analysis of the tribe (Pelser *et al.*, 2007). Nevertheless, *Senecio* still is one of approximately 33 genera of plants that contain more than 700 species and thus belongs to the top 0.0011 % of the most species-rich genera (The Plant List, 2013; Tab. 1). The genus displays wide variation in growth form and ecology and is distributed in all major biomes with centres of diversity in sub-Saharan Africa and South America (Pelser *et al.*, 2007; Nordenstam *et al.*, 2009, Pelser *et al.*, 2010b).

Senecio belongs to the cosmopolitan Asteraceae, which is – with about 24,000 species – the most species-rich angiosperm family (Funk *et al.*, 2009a). Within the family, a number of recent radiations have been investigated, such as the silversword alliance (Heliantheae; Baldwin & Sanderson, 1998), *Dendrosenecio* B. Nord. (Knox & Palmer, 1995), *Brachyglottis* J.R. Forst. & G. Forst. (Wagstaff & Breitwieser, 2004) and the *Ligularia* Duval-*Cremanthodium* Benth.-*Parasenecio* W.W. Sm. & J. Small-complex (Liu *et al.*, 2006), of which the last three belong to the same tribe as *Senecio*, the Senecioneae. Pelser *et al.* (2010a) found a stem age of about 10 Myr for *Senecio* using earlier published secondary fossil calibration points as well as ages of islands to calibrate their phylogeny, and two subclades of *Senecio* were dated to between 4 and 1 Myr using ITS substitution rates (Pelser *et al.*, 2012). This indicates that *Senecio* is likely to be a rather young radiation that accumulated an astonishingly high number of species in combination with a nearly unmatched number of successful colonizations of disjunct areas (Tab. 1, Pelser *et al.*, 2007; Pelser *et al.*, 2010b; Pelser *et al.*, 2012).

Here, we dated the origin of *Senecio* with different dating approaches and calculated the diversification rate of the group using an extended sampling of the genus based on Pelser *et al.* (2007). Additionally we used ancestral area reconstruction in combination with reconstruction of habitat preferences to show that *Senecio* is a young, yet nearly cosmopolitan group that is likely to have diversified due to their ability to colonize open and/or disturbed habitats in a changing world.

Table 1: Angiosperm genera or lineages with more than 700 species based on Frodin (2004), adapted to current generic circumscriptions, and species numbers using recent literature. Distribution data based on Mabberley (2008). Abbreviations: Myr: Million years; N: North, S: South; SE: Southeast, E: East, min.: minimum, esp.: especially.

Genus	**No. species**	**Family**	**Distribution**	**Age [Myr]**	**Reference**
Astragalus L.	3270	Fabaceae	temperate regions of the Northern Hemisphere and S America, E African mountains	s.str.: crown: 9.3-17.7	Wojciechowski, 2005
Bulbophyllum Thouars	2032	Orchidaceae – Epidendroideae, Podochileae	pantropical, centre of diversity: montane forests of Papua New Guinea	crown Epidendroideae: 49	Gustafsson, *et al.,* 2010
Solanum L.	c. 1500-2000	Solanaceae	subcosmopolitan	crown: 17.95	Poczai *et al.,* 2011
Psychotria L.	1951	Rubiaceae	pantropical	stem: 34.9-60.7	Bremer & Eriksson, 2009
Euphorbia L.	1836	Euphorbiaceae	cosmopolitan	stem: 28.99-47.24	Bruyns *et al.,* 2011
Carex L./Cariceae	1795	Cyperaceae	cosmopolitan, centre of diversity in the temperate Northern Hemisphere	stem: 42	Escudero *et al.,* 2012
Begonia L.	1484	Begoniaceae	Pantropical, esp. S America	stem: mid Eocene to early Oligocene	Goodall-Copestake *et al.,* 2009
Dendrobium Sw.	1371	Orchidaceae – Epidendroideae	tropical/warm esp. Asia to Australia	crown Dendrobiinae and Epidendreae: 32	Gustafsson, *et al.,* 2010
Croton L.	1223	Euphorbiaceae	tropical, warm: Australia, Africa, Madagascar	stem: 54.11; crown: 39.29	van Ee *et al.,* 2008
Eugenia L.	1113	Myrtaceae	pantropical	crown Myrteae: min. 37.5	Thornhill *et al.,* 2012
Epidendrum L.	1100	Orchidaceae – Epidendroideae, Laelliinae	neotropical	crown Agrostophyllinae and Epidendreae: 25	Gustafsson, *et al.,* 2010; Gorniak *et al.,* 2010
Piper L.	1055	Piperaceae	tropical	crown: 71.75	Smith *et al.,* 2008
Acacia Mill.	c. 1045 (or 986)	Leguminosae	Australasia	s.str.: crown: 21.0-23.9	Miller *et al.,* 2013
Syzygium P. Browne ex Gaertn.	1041	Myrtaceae	SE Africa to Pacific	Myrtoideae: 77-56	Sytsma *et al.,* 2004
Rhododendron L.	>1000	Ericaceae	Asia, N America, Europe and Australia, highest species diversity in the Himalayas	fossil: seed assigned to the genus: Paleocene (66-56)	Milne, 2004 (citing Zetter & Hesse, 1996)
Senecio L.	c. 1000	Asteraceae	nearly cosmopolitan	stem: ~ 10	Pelser *et al.,* 2010a
Miconia Ruiz & Pav.	1000	Melastomataceae	neotropical	fossil: small heterocolpate pollen from the Plio-Pleistocene	Morley & Dick, 2003 (citing van der Hammen & Gonzaléz Guzman, 1963)
Peperomia Ruiz & Pav.	1000	Piperaceae	tropical warm, esp. America	crown: 57.09	Smith *et al.,* 2008
Vernonia Schreb.	800-1000	Asteraceae	Old World tropical and warm to N America	Veroninae: 14-20	Keeley *et al.,* 2007
Salvia L.	945	Lamiaceae	tropical to temperate	fossils: dated to Lower and Upper Miocene	Emboden, 1964; Müller, 1981
Erica L.	860	Ericaceae	Europe and Africa, highest diversity in the	stem: min. 20	Pers. com. M.D. Pirie; University of Mainz-Germany

Genus	No. species	Family	Distribution	Age [Myr]	Reference
			Greater Cape Floristic Region		
Impatiens L.	850	Balsaminaceae	pantropical and Holarctics	stem: 30.7; crown: 22.5	Janssens *et al.*, 2009
Ficus L.	850	Moraceae	tropical (and warm), esp. Indomalesia to Australia	fossils (achene): early Eocene	Zerega *et al.*, 2005
Phyllanthus L.	833	Phyllanthaceae	tropical warm	fossil: Lower Eocene	Li *et al.*, 2009 (citing Gruas-Cavagnetto & Köhler, 1992)
Allium L.	815	Amaryllidaceae	Eurasia, America, Africa, Sri Lanka and Mexico	crown: 45-50	Gurushidze *et al.*, 2010
Lepanthes Sw.	c. 800	Orchidaceae – Epidendroideae, Pleurothallidinae	neotropical	crown Agrostophyllinae and Epidendreae: 25	Gustafsson, *et al.*, 2010; Gorniak *et al.*, 2010
Anthurium Schott	789	Araceae	neotropical	stem: Paleocene (66-56)	Nauheimer *et al.*, 2012
Indigofera L.	>750	Fabaceae	tropical (and warm)	split between Cape clade from the sister group: 20.91 ± 3.02-26.34 ± 2.02	Galley & Linder, 2006
Eucalyptus L'Hér.	>700	Myrtaceae	Malesia to Australia	crown: min.: 14; fossil pollen: 34	Thornhill *et al.*, 2012
Silene L.	700	Caryophyllaceae	Northern Hemisphere	crown: mean: 12.39	Frajman *et al.*, 2009
Oxalis L.	700	Oxalidaceae	cosmopolitan, esp. S America and Cape	fossils: min: 18	Oberlander, 2009
Crotalaria L.	700	Fabaceae	pantropical; divers in tropical Africa	crown clade of the Crotalarieae is at least 46.3 ± 2.4	Edwards & Hawkins, 2007

Material and Methods

Taxon Sampling, DNA extraction, PCR amplification and sequencing

We sampled 47 previously unsampled *Senecio* species from eastern and southern Africa (Appendix S1.1 in the Supporting Information). In total about 25 % of all *Senecio* species were included in this study using one accession per species except where we have evidence that species are not monophyletic. We extracted total genomic DNA from herbarium material (Appendix S1.1) using DNeasy Plant Kit (Qiagen Inc., Valencia, CA, USA. Qiagen GmbH, Hilden, Germany) according to the manufacturer's MiniProtocol with minor changes. Samples were incubated for 30 min instead of 10 min after adding the lysis buffer and the DNA elution step was done twice using 50 µl respectively and incubated for 20 min. We amplified the nuclear (nr) internal transcribed spacer (ITS) and the chloroplast (cp) *ndh*F gene and *trn*L intron, as well as two cp spacers, *trn*L-*trn*F and *trn*C-*ycf*6. We used standard protocols for amplification, Sanger sequencing and alignments. For most material we were able to amplify the entire ITS region (ITS-1, 5.8S, ITS-2) using external primers 'ITS 18S' (5′-CCT TMT CAT YTA GAG GAA GGA G -3′) and 'ITS 28S' (5′-CCG CTT ATT KAT ATG CTT AAA-3′; Muir & Schlötterer, 1999). For some material ITS-1 and ITS-2 were amplified separately, using primers 'ITS A' (5′-GGA AGG AGA AGT CGT AAC AAG G-3′), 'ITS C' (5′-GCA ATT CAC ACC AAG TAT CGC-3′), 'ITS-B' (5′-CTT TTC CTC CGC TTA TTG ATA TG-3′) and 'ITS-D' (5′-CTC TCG GCA ACG GAT ATC TCG-3′; Blattner, 1999). Amplifications were performed in 20 µl volumes containing 12.86 µl ddH$_2$O, 2 µl buffer, 1 µl 50 mM MgCl$_2$, 0.4 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase (all reaction liquids from NewEngland BioLabs Inc, Ipswich, USA) and 2 µl genomic DNA. Cycling conditions were: 94°C 1 min, 30x (94°C 0.2 min; 52°C 0.3 min; 72°C 1 min), 94°C 0.2 min, 52°C 1.2 min. The *trn*L intron and *trn*L-*trn*F intergenic spacer was amplified together using 'tab C' (5′-CGA AAT CGG TAG ACG CTA CG-3′) and 'tab F' (5′-ATT TGA ACT GGT GAC ACG AG-3′; Taberlet *et al.*, 1991). For some material we were only able to amplify the *trn*L-*trn*F intergenic spacer using 'tab E' (5′-GGT TCA AGT CCC TCT ATC CC-3′; Taberlet *et al.*, 1991) and 'tabF'. Amplifications were performed in 20 µl volumes containing 13.38 µl ddH$_2$O, 2 µl buffer, 0.48 µl 50 mM MgCl$_2$, 0.8µl DMSO, 0.2 µl of 10 mg/ml BSA, 0.8 µl 10 mM dNTP's, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase and 1 µl genomic DNA. Cycling conditions were those described by Shaw *et al.* (2005) for *rpl*16. *Trn*C-*ycf*6 was amplified using '*trn*C(GCA)F' (5′-CCA GTT CRA ATC YGGGTG-3′) and '*ycf*6' (5′-GCC CAA GCR AGA CTT ACT ATA TCC-3′; Shaw *et al.*, 2005). Amplifications were performed in 20 µl volumes containing 12.38 µl ddH$_2$O, 2 µl buffer, 0.48 µl 50mM MgCl$_2$, 0.8 µl DMSO, 0.2 µl of 10 mg/ml BSA, 0.4 µl 10 mM dNTP's, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase and 2 µl genomic DNA. Cycling conditions were those described in Shaw *et al.* (2005) for rpl16. *Ndh*F amplification was carried out as described by Pelser *et al.* (2007). *Ndh*F and *trn*LF showed double bands for some taxa. In those cases, both bands were cut out and purified (Macherey-Nagel; GmbH & Co. KG, Düren, Germany).

PCR products were purified using ExoSAP-IT PCR Clean-Up (Affymetrix, Santa Clara, USA) following the recommended protocol. Cycle sequencing reactions were carried out with BigDye Terminator 3.1 (Applied Biosystems, Foster City, California, U.S.A.) following the recommended protocol with minor modifications (1 µl of BigDye Terminator instead of 2 µl) using the same primers as used for amplification. Purification was done with Sephadex (GE Healthcare, Waukesha, USA) and sequencing of both strands was done on a 'GA3130XL' Genetic Analyser (Applied Biosystems, Carlsbad, USA; Hitachi Ltd., Tokyo, Japan) at Johannes Gutenberg-Universität Mainz (Germany). SEQUENCHER v.4.1.4 (Gene Codes Corporation, Ann Arbor, MI, U.S.A.) was used for file editing. The sequenced regions were checked by eye and adjusted prior to alignment when necessary.

Additionally, cp sequences for the dating analyses of Asteraeae (*ndh*F, *trn*LF and *rbc*L) as well as already available nr and cp sequences of *Senecio* species (ITS, *trn*LF and *ndh*F) were obtained from GenBank (Appendix S1.2).

DNA sequence alignment and phylogenetic reconstruction

Alignments were made with MAFFT v7 (Katoh & Standley, 2013) and adjusted by hand with MACCLADE v. 4.08 (Maddison & Maddison, 2005). Missing data were coded as question marks. Three different datasets were used: 1) an Asteraceae dataset including all described subfamilies and some representatives of the tribe Senecioneae using cp markers (*trn*LF, *ndh*F and *rbc*L; Appendix S1.2); 2) a *Senecio* dataset using the nr ITS region and 3) a *Senecio* dataset of cp markers (*trn*LF, *ndh*F and *trn*C-*ycf*6). More cp markers were available in GenBank, but they do not contribute to the resolution within the genus. Thus, our *Senecio* cp phylogenetic analyses are based on *trn*LF, *ndh*F and *trn*C-*ycf*6 only. Close relatives of *Senecio* according to Pelser *et al.* (2007) were chosen as outgroups: *Crassocephalum crepidioides* (Benth.) S. Moore, *Dendrocacalia crepidifolia* (Nakai) Nakai, *Erechtites valerianifolius* (Link ex Spreng.) DC., *Senecio thapsoides* DC., *Synotis alata* (Wall. ex DC.) C. Jeffrey & Y.L. Chen ex DC., *Sy. cappa* (Buch.Ham. ex D. Don) C. Jeffrey & Y.L. Chen and *Sy. nagensium* (C.B. Clarke) C. Jeffrey &

Y.L. Chen,. Only for *trn*C-*ycf*6 no closely related taxon was available in GenBank. However, as our analyses showed that *S. pergamentaceus* Baker did not fall into the *Senecio* clade, this species was used as outgroup for the *trn*C-*ycf*6 dataset.

Phylogenetic analyses were carried out using Maximum Parsimony (MP) in PAUP* 4.0b10 (Swofford, 2002), Maximum Likelihood (ML) using RAXML v. 8.0.24 (Stamatakis, 2006 run on CIPRES [Miller *et al.*, 2010], using the Blackbox and XSEDE; for differences in the results see text below), and Bayesian Inference (BI) using MRBAYES v 3.2.1. (Ronquist *et al.*, 2012). Substitution models were identified prior to analyses with MODELTEST 3.5 relying on the AIC as criterion (Posada & Crandall, 1998). To code insertions and deletions as binary data (presence/absence), the simple coding method by Simmons & Ochoterena (2000) was used as implemented in SEQSTATE 1.4.1 (Müller, 2005). Gaps were coded in the MP and MRBAYES analyses, and phylogenies with and without gap coding were checked for phylogenetic conflicts (MP: >65 % bootstrap support [BS]; ML: >70 % BS; BI: >0.95 posterior probability [PP]). Settings were as follows: Under MP, 500 replicates with a heuristic search, randomly and stepwise added taxa, tree rearrangement option was tree bisection and reconnection and 500 bootstrap replicates were calculated. Under ML, the ITS and combined cp alignments were partitioned and rate heterogeneity was accounted for where necessary (Appendix S2.1). Under MRBAYES, the ITS and combined cp alignments were partitioned, substitution models were adjusted to the inferred best model, running two independent runs, sampling every 1000th generation; depending on alignment length, number of generations was increased until the TRACER v.1.5 (Rambaut & Drummond, 2007) effective sample size for parameters were >200. After removing a burn-in of 10 %, the two independent runs were combined.

ML calculations using the XSEDE and BlackBox options on CIPRES resulted in different support values for some clades (Fig. 1 & Appendix S2.3). On the one hand, the analysis run using BlackBox (Fig. 1) resulted in a topology similar to that of other analysis methods and yielded support (>75 % BS) for some consanguineus-subclades. On the other hand, XSEDE (Appendix S2.3) placed the species found in the consanguineus-clade in a polytomy basal to other *Senecio* species and revealed support for the New World (NW) 2-clade. As there is no support for the backbone of the phylogeny in any of the analyses, we show the BlackBox results in the main figures as they show greater similarity to the MP and Bayesian analyses.

The *Senecio* cp matrix contains relatively few informative characters (Appendix S2.1). Combining the different cp markers resulted in a decrease of support values of some well-supported clades of the single cp marker phylogenies, even though no supported incongruences had been detected (Appendix S2.4-S2.7). This potentially can be ascribed to the large amount of missing data. Incongruences between individual gene trees were investigated by eye, and we initially combined the nr and cp datasets after removing taxa with incongruent placements supported by significant support. However, this led to the collapse of nodes that were well-supported in the analysis of nr ITS alone. Incongruences between nr and cp gene trees in Senecioneae have been reported previously (Pelser *et al.*, 2007; Pelser *et al.*, 2010a; Pelser *et al.*, 2012; Calvo *et al.*, 2013). The large amount of gene tree conflicts might alternatively be indicative of common hybridisation in *Senecio*, which seems to make an important contribution to speciation in the group (Pelser *et al.*, 2010a; Pelser *et al.*, 2012) and genetic compatibility seems to be generally high (Calvo *et al.*, 2013). Further analyses therefore are based on the ITS dataset only as this region resulted in a much better resolved and supported tree (Fig. 1 & Appendix S2.7).

Molecular clock dating[1]

Ealier dating approaches of *Senecio*/Senecioneae were either based on secondary root calibration and island ages as calibration points (Pelser *et al.*, 2010a) or on ITS substitution rates only (Pelser *et al.*, 2012). We used a recently discovered fossil that suggests that Asteraceae are older than previously thought and that has been placed at the split between Barnadesioideae and the rest of Asteraceae with a minimum age of 47.5 Myr (Barreda *et al.*, 2010). For dating, we first used BEAST v 1.8 (Drummond & Rambaut, 2007; run on CIPRES) on the Asteraceae tree and second RELTIME v. 2.0 beta (Tamura *et al.*, 2012). In an initial analysis, the Asteraceae dataset did not resolve the phylogeny as shown by Funk *et al.* (2009) that was based on much more species and sequence data. We therefore constrained the tree topology accordingly. In BEAST, we chose an exponential distribution as prior for the fossil calibration. The age of the root of the tree was calibrated with a normal distribution of an age between 120 Myr as maximum age (due to many different age estimates of Asteraceae; we used the campanulid age estimated by Bremer [2004]) and the age of the fossil as minimum age. GTR+I+G as substitutions model and an uncorrelated lognormal relaxed clock (ULRC). Additionally, we investigated the effect of using two different tree priors: a Yule and a birth-death process. Two independent runs were conducted and

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[1] Diese Datierungen erfolgten ohne die neue Unterfamilie und ohne das zweite ältere Fossil, da beide zum Zeitpunkt der Datierung noch nicht publiziert waren.

combined using LOGCOMBINER v. 1.7.2 and TREEANNOTATER v. 1.7.2 (Drummond & Rambaut, 2007) when the effective sample size for parameters were >200 as checked with TRACER and after removing a burnin-in of 10 %. RELTIME estimates branch-specific relative rates on the basis of branch length. The input tree was the constraint Asteraceae tree with branch lengths calculated with RAXML (run on CIPRES using XSEDE) and the fossil as calibration point.

The age of *Senecio* as estimated in BEAST from the Asteraceae cp matrix was then used as a secondary calibration point to date the *Senecio* ITS matrix. The mean of the highest posterior density (HPD) values of the stem age of *Senecio* was used as calibration point with a standard deviation of two using a normal distribution. Again, this was done using either a Yule or a birth-death process respectively, and the same priors as above were applied.

Divergence times within *Senecio* were also calculated using minimum and maximum ITS substitution rates reported for Asteraceae (Kay *et al.,* 2006). The analyses were performed in BEAST with an ULRC, the GTR+I+G model and a Yule process as tree prior. Two analyses were carried out, one with the *Senecio* matrix described above and another excluding species with exceptionally long branches (estimated by eye). The excluded species were *S. arnicoides* Hook. & Arn., *S. gregorii* F.Muell., *S. macranthus* A. Rich., *S. neowebsteri* S.F. Blake, S. *pseudoarnica* Less., *S. seminiveus* J. M. Wood & M. S. Evans and *S. trifurcatus* (G.Forst.) Less. The substitution rate was set to uniform with an upper and a lower bound of 0.00783 and 0.00251 substitution site^{-1} Myr^{-1}.

The cp phylogeny of *Senecio* was not dated because an earlier analysis by Pelser *et al*. (2010a) showed that age estimates for the genus obtained from nr and cp phylogenies are similar, and because we did not obtain additional resolution in the cp phylogeny of the genus.

Diversification rates

The diversification rates of *Senecio* were calculated based on different crown age estimates (secondary calibration or substitution rate) obtained with BEAST using the method described in Magallón & Sanderson (2001) implemented in the Geiger package v. 1.99-3.11 (Harmon *et al.,* 2008) in R (R Core Team, 2013) using Rstudio v. 0.97.551 (RStudio, 2013). Shifts in diversification rates within *Senecio* were not calculated as firm knowledge about the exact number of species and clade affiliation of unsampled species is unavailable. In order to be able to compare diversification rates of *Senecio* to the diversification rate of the tribe, we estimated the latter. We used the age estimate of Senecioneae (including HPD) as estimated by us (BEAST estimates) and a conservatively estimated number of 3000 species of Senecioneae according to

Pelser *et al.* (2007). Different relative extinction rates were assumed (ε=0 and ε=0.9) to incorporate the unknown amount of extinction.

Ancestral area reconstruction and character optimisation

Geographical distribution was scored using the species distribution range and not based on the sampling locality, as this is not always known for species downloaded from GenBank. Distribution information is based on Floras, earlier publications and online resources (Harvey, 1865; Tadesse, 2004; Jeffrey & Beentje, 2005; Pelser *et al.*, 2007; African Plant Database, 2012; Calvo *et al.*, 2013; Calflora, 2014; Missouri Botanical Garden, 2014). Areas were coded as North America including Mexico (1), South and Central America (2), Eurasia and North Africa (3), Australasia (including Australia, Malesia, New Zealand and the Pacific; 4) and sub-Saharan Africa (5). Widespread species were coded as multiple states.

We compiled habitat information from Floras, online databases and earlier publications (Appendix S1.3 for information and references). Habitat information was categorized into open/disturbed habitats and non-open/non-disturbed habitats. The open/disturbed category included all species reported to occur in habitats described as open or as experiencing some kind of disturbance, e.g. margins of habitats, rocky grounds, ruderal places or wastelands. The non-open/non-disturbed category included all species reported to grow in stable habitats, e.g. grasslands, forests or shrublands.

Ancestral area and character reconstructions were done using parsimony in MESQUITE 2.75 (Maddison & Maddison, 2011). To integrate phylogenetic uncertainty we used 1951 trees after burn-in of one of the ITS tree files of the MRBAYES analysis without gap coding and mapped the results on the majority rule consensus tree. To account for uncertainty in the habitat reconstruction we ran a parsimony analysis with randomly reshuffled states in Mesquite. Additionally, we coded all unknown habitats as non-open/non-disturbed.

Results

Alignment and Phylogeny

All phylogenetic reconstruction analyses using nr data revealed a monophyletic *Senecio* (Fig. 1 & Appendix S2.2). Within *Senecio*, we were able to identify 13 major clades using nr ITS (Fig. 1). The positions of two species were unresolved and they were not placed in one of the 13 clades (Fig. 1). All but the decurrens-clade are supported with a PP of 0.97 or higher (Fig. 1). Adding indel characters resulted in decreased support for some consanguineus-subclades but increased the support for a clade of sub-Saharan African species, which is nested within the NW 2-clade (Fig. 1). The Aus 2-, NW 1-, NW 2-, doria-, decurrens- and the consanguineus-clades did not receive support using MP or ML-Blackbox (Fig. 1). Only MP with gap coding did not identify the consanguineus-clade, and Aus 1- and the vestitus-clade are nested within the doria-clade in that analysis.

Age estimates and diversification rates

Dating of *Senecio* placed its origin at around 10 Million years ago (Ma; 21.0-4.9; all dating analyses; Tab. 2). ITS rate calibration revealed a crown age of 8.3 Myr (16.0-4.9 [yule process as tree prior]; Tab. 2) and exclusion of species with exceptionally long branches resulted in age differences of about one to 0.1 Myr for most nodes. Age estimates using fossil calibration in BEAST are slightly younger than those using ITS rates with a stem age of 14.6-4.9 Myr and a crown age of 8.5-1.6 Myr (Yule process). Using a birth-death process resulted in similar ages than those under a Yule process. The RELTIME analysis resulted in a stem age estimate of 5.3 Myr which lies within the HPD of the fossil calibration analyses from BEAST. Our analyses showed that *Senecio* colonized other continents from sub-Saharan Africa between 6-3 Ma (Fig. 1), and most clades diversified between 4 and 2 Ma (Tab. 2).

The net diversification rate of tribe Senecioneae ranges from 0.22-0.66 seMyr^{-1} (Tab. 3) and the net diversification rate of *Senecio* is estimated to be 0.88 seMyr^{-1} (using the crown age of the secondary calibration under a Yule process with a relative extinction rate of zero; Tab. 3). However, depending on the method of age estimation and the assumption of the relative extinction rates, the net diversification rate varies from 0.29 to 1.48 seMyr^{-1} (Tab. 3).

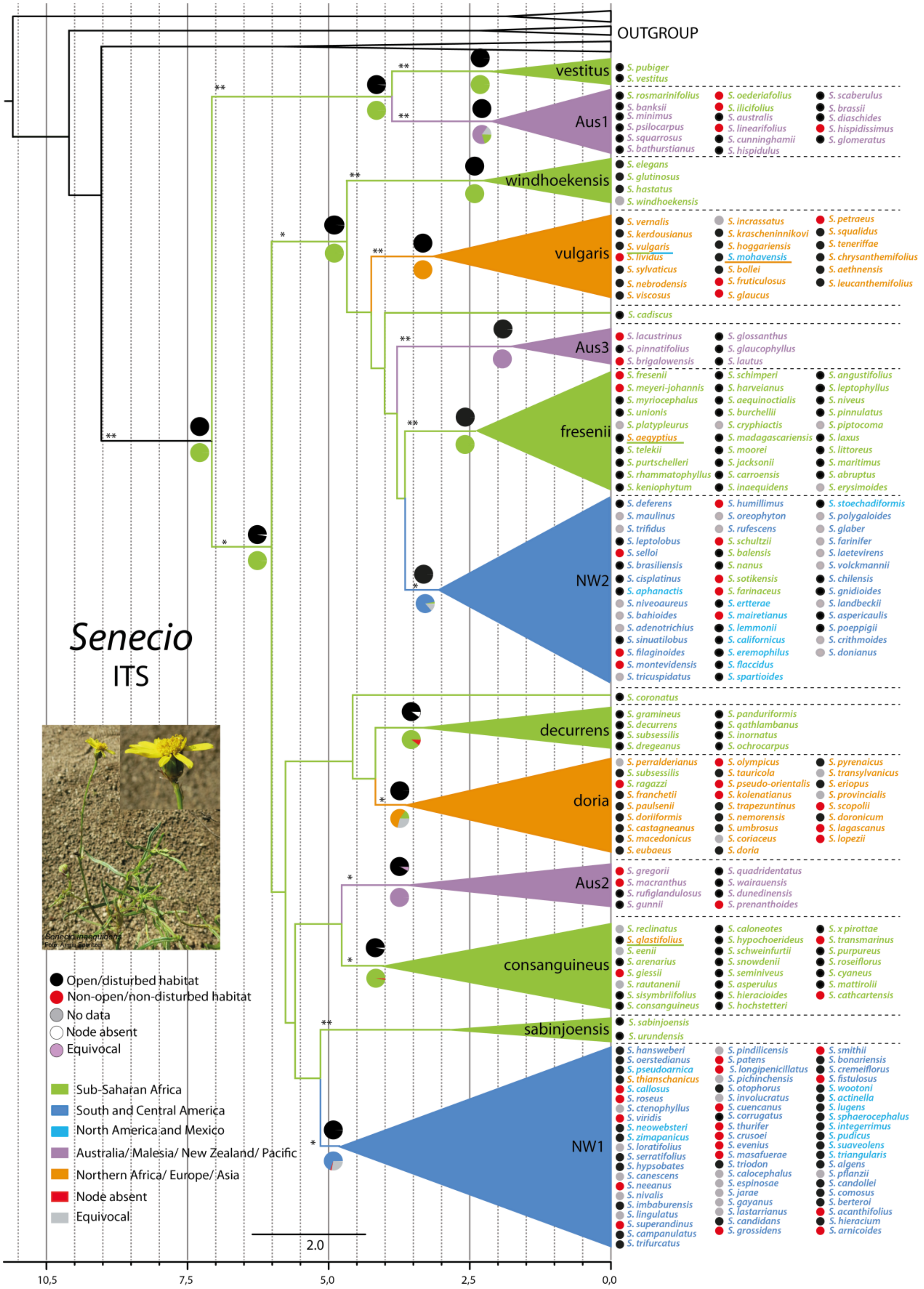

Figure 1: Chronogram of *Senecio* based on nr ITS. Major clades have been collapsed for representation (full phylogenetic reconstructions can be found in Appendix S2). Two stars mark support in Bayesian, Maximum Likelihood and Maximum Parsimony analyses, while one star marks support in Bayesian analysis only. Biogeographic reconstruction is shown along branches, underneath nodes and as colour of species name, and habitat preferences are marked with circles left of species name and are shown above nodes.

Table 2: Results of the molecular dating analyses in Million years ago including the 95% highest posterior density intervals of Senecioneae (excl. *Doronicum*), *Senecio* and clades in *Senecio* (crown ages) using BEAST (under a Yule or a birth-death process) and RelTime. Abbreviations: 2°: secondary calibration; LB: long branch.

Clade	**RelTime fossil calibration**	**BEAST**					
		Fossil calibration		**2° calibration**		**ITS substitution rate**	
		Yule	**Birth-death**	**Yule**	**Birth-death**	**Yule with LB**	**Yule without LB**
Senecioneae stem	19.7	20.9 (28.7 -14.0)	21.4 (28.4-14.3)				
Senecioneae crown	17.8	18.3 (25.7-11.7)	18.7 (25.5-12.1)				
Senecio stem	5.3	9.3 (14.6-4.9)	9.4 (14.5-4.9)	9.0 (12.3-5.7)	9.0 (12.3-5.8)	11 (21.5-6.2)	10.5 (21.0-6.5)
Senecio crown	-	4.5 (8.5-1.6)	4.6 (8.5-1.6)	7.1 (10.0-4.3)	6.8 (9.7-4.2)	8.3 (16.0-4.9)	7.6 (15.1-4.7)
Aus 1-clade				2.1 (3.5-1.0)	2.2 (3.5-1.0)	2.7 (5.4-1.3)	2.5 (5.1-1.3)
Aus 2-clade				3.6 (5.6-1.9)	3.8 (5.7-1.9)	4.4 (8.8-2.3)	3.4 (7.0-1.6)
Aus 3-clade				1.8 (3.1-0.8)	1.7 (3.1-0.7)	2.2 (4.7-0.9)	2.1 (4.3-0.9)
consanguineus-clade				4.0 (6.0-2.2)	4.0 (5.9-2.2)	4.7 (9.2-2.6)	4.1 (8.0-2.3)
decurrens-clade				3.3 (5.2-1.7)	3.4 (5.4-1.7)	4.0 (8.0-1.9)	3.8 (7.6-1.9)
doria-clade				3.6 (5.4-2.1)	3.8 (5.6-2.1)	4.4 (8.4-2.5)	4.1 (8.1-2.5)
fresenii-clade				2.4 (3.7-1.2)	2.4 (3.7-1.3)	2.9 (5.7-1.5)	2.7 (5.3-1.4)
NW 1-clade				4.8 (7.1-2.9)	4.2 (6.2-2.5)	5.8 (11.1-3.6)	5.3 (10.4-3.3)
NW 2-clade				3.0 (4.6-1.7)	3.0 (4.5-1.8)	3.6 (7.0-2. 1)	3.4 (6.7-2.0)
sabinjoensis				2.8 (5.0-1.1)	2.9 (5.2-1.1)	3.6 (7.6-1.1)	3.4 (7.1-1.3)
vestitus-clade				2.1 (4.1-0.7)	2.3 (4.4-0.6)	2.8 (5.4-1.3)	2.8 (6.2-0.8)
vulgaris-clade				3.1 (4.9-1.7)	3.2 (4.8-1.7)	3.8 (7.4-2.0)	3.6 (7.0-2.0)
windhoekensis-clade				2.3 (4.0-0.9)	2.2 (3.8-0.8)	2.7 (8.1-2.2)	2.6 (5.4-1.0)

Table 3: Diversification rates of *Senecio*, calculated following Magallón and Sanderson (2001) and assuming a species richness of 1000 species. Rate calculations were done using different crown age estimates of BEAST including the 95% highest posterior density intervals of the age estimates. Abbreviations: bd – assuming a birth-death process as tree prior; yule - assuming a Yule process as tree prior; Ɛ – relative extinction rate; LB – long branch.

Method of age estimate		diversification rate	
		Ɛ= 0	Ɛ = 0.9
Senecioneae	yule	0.40 (0.28-0.63)	0.31 (0.22-0.48)
	bd	0.39 (0.29-0.60)	0.30 (0.22-0.47)
Senecio (ITS substitution rate)	with LB	0.75 (0.39-1.27)	0.55 (0.29-0.93)
	without LB	0.82 (0.41-1.32)	0.60 (0.30-0.97)
Senecio (secondary calibration)	yule	0.88 (0.62-1.44)	0.64 (0.46-1. 06)
	bd	0.91 (0.64-1.48)	0.67 (0.47-1.08)

Ancestral area reconstruction and character optimisation

Most clades contain species from only one continent (Fig. 1). There are two Eurasian (doria- and vulgaris-clade), two American (NW 1- and NW 2-clade), three Australasian (Aus 1-, Aus 2- and Aus 3-clade) and six sub-Saharan African clades (consanguineus-, decurrens-, fresenii-, sabinjoensis-, vestitus- and windhoekensis-clade). Four of these clades contain species from other continents: Aus 1-, doria- and the NW 2-clade contain sub-Saharan African species, and the NW 1-clade contains an Eurasian species (Fig. 1). Sub-Saharan Africa was reconstructed as the ancestral area of *Senecio* (Fig. 1) with several independent intercontinental colonization events to Eurasia, America and Australasia. South America was reconstructed as the ancestral area of both New World-clades, with at least one dispersal to North America. Open/disturbed and non-open/non-disturbed habitat preferences occur in all clades with a majority of species occurring in open/disturbed habitat. The most recent common ancestor of *Senecio* most likely preferred open/disturbed habitats (Fig. 1 & Appendix S2.9). This pattern does not change when states were randomly reshuffled or when unknown habitat preferences were coded as non-open/non-disturbed habitat (Appendix S2.10 & S2.11).

Discussion

Recent diversification

Irrespective of methods and assumptions, all our dating analyses and ancestral reconstructions indicate that *Senecio* originated most likely during the Mid- to Late-Miocene in sub-Saharan Africa in open or disturbed habitats (Fig. 1 & Tab. 1). The dating results, despite using a newly found fossil which is older than those previously known, are congruent with the dating results by Pelser *et al.* (2010a) and Pelser *et al.* (2012). The genus originated sometime during the Middle Miocene Climate Transition (c.14-8 Ma), when global temperatures continued to decrease after a sharp decline during the Mid-Miocene Crisis (Böhme, 2003). After its origin there seems to have been a time lag until the beginning of the diversification of the group (around 8-7 Ma). Alternatively the time lag could be explained by the fact that we might not have sampled the sister group of *Senecio*, and inclusion of the sister group would push the stem age of the genus towards the crown age. Interestingly, around the same time when *Senecio* started to diversify grasslands expanded, C4-photosynthesis started to become more abundant and humans evolved bipedalism in sub-Saharan Africa (van der Made, 2014). Especially in southern Africa – where *Senecio* is relatively abundant today and which is likely to be the area of origin of the genus – tropical climate and vegetation changed to more seasonal climate and temperate vegetation in the Late-Miocene (Pound *et al.,* 2012).

Around five Ma, i.e. around the start of intercontinental dispersal and onset of diversification of *Senecio*, abrupt cooling affected the southern Ocean when Antarctic Surface water expanded northwards. This resulted in major changes in the biota not only of southern Africa (van Zinderen Bakker & Mercer, 1986), but also on all other continents, which underwent drastic climate changes. At the same time mountain uplifts in South America, Africa and Eurasia took place (Ager, 1975; Haywood *et al.,* 2009; Hoorn *et al.*, 2010) and likely contributed to major changes in climate and vegetation. Thus, the diversification of *Senecio* in southern Africa seems to coincide with a time of major transitions and disturbances in the African landscape, which probably resulted in more open vegetation through aridification (Hoetzel *et al.,* 2013). Furthermore, the climatic changes across the world may have created newly available open and disturbed habitats and empty niches, which provided more opportunity for establishment after dispersal especially for *Senecio* (see below) and would have been starting points for the diversification of the genus in newly colonized areas.

Spatial evolution of Senecio *and open/disturbed habitats*

From sub-Saharan Africa, numerous independent colonization events occurred mainly during the Pliocene (Fig. 1) and resulted in independent radiations in these new areas. At least seven intercontinental long distance-dispersal (LDD) events are evident: two to South America, two to Eurasia and three to Australasia (Fig. 1 & Appendix S2.8; Pelser *et al.*, 2007). At the same time, climatic transitions and disturbances took place in sub-Saharan Africa (Pound *et al.*, 2012).

Additionally to the out-of-Africa intercontinental colonization events, many other dispersal events must have happened to have shaped the current distribution of the group. For example, the colonization of North America reconstructed here to have started from South America or the colonizations of the many islands inhabited by *Senecio* such as Macaronesia or the Juan Fernandez Islands (Coleman *et al.*, 2003; Pelser *et al.*, 2010b). These dispersal events also would have included the dispersal required to explain that *S. massaicus* (Maire) Maire combines genetic material from a Mediterranean and a mainly southern African lineage (Pelser *et al.*, 2012).

Colonizing a new area requires two steps: first dispersal to a new region and then establishment. Asteraceae in general have good dispersability by wind, which is associated with the presence of a hairy (or papery) pappus that is also present in most *Senecio* species. Fruits of *S. vulgaris* L., for example, have been shown to have a low settling velocity, which results in high dispersability (Andersen, 1993). Furthermore, primarily wind-dispersed groups in general may have a higher probability to disperse to new and/or isolated areas compared to non-wind-dispersed groups (Moore & Donoghue, 2007). Especially in the Southern Hemisphere the importance of trans-oceanic long-distance dispersal (LDD) by wind has been reinstated recently (Muñoz *et al.*, 2004; Renner, 2004; Richardson *et al.*, 2004; Sanmartín & Ronquist, 2004; Queiroz, 2005; Pirie *et al.*, 2012). High seed production, similar to good dispersability through the pappus, is common in Asteraceae (Funk *et al.*, 2009) and likely contributes to a high rate of dispersal. *Senecio vulgaris*, for example, can produce more than 12 000 seeds per plant (Lutman *et al.*, 2008). While a pappus and high seed set might seem to suffice for successful colonization of new areas, *Senecio* has a third trait that probably has helped in developing its remarkable species richness and distribution: its habitat preference (Fig. 1). *Senecio* evolved and radiated most likely to a large extent in open and disturbed habitats, which might have facilitated establishment after arrival due to reduced competition (Vilà *et al.*, 2007). This means that the exceptional amount of successful LDD-events in *Senecio* can potentially be related to its ability to be dispersed by wind, its often large number of diaspores and its preference for open and/or distributed habitat(s).

All these properties may have increased colonization success and promoted diversification due to allopatric speciation facilitated by the combined effects of founder events, genetic drift and selection (Yuan *et al.*, 2005; Moore & Donoghue, 2007). Calvo *et al.* (2013), for example, showed for the *Senecio doria*-clade that after colonizing Europe, divergence lead to the evolution of species with almost no overlap in distribution. Thus, despite the good colonization ability of many *Senecio* species, dispersal within clades can be regionally limited, promoting allopatric speciation.

Rapid nearly cosmopolitan radiation

While most radiations previously investigated are either geographically restricted or more or less small in terms of species numbers, our data represent an example of a radiation of a young, species-rich and nearly cosmopolitan genus. The radiation can be considered recent and rapid, especially in the light of the relatively high diversification rate (Tab. 3). The lowest estimated mean diversification rate of the crown clade (0.55 seMyr^{-1}) is in the upper range of the diversification rate of tribe Senecioneae (0.2-0.6 seMyr^{-1}). The overall diversification rate of *Senecio* is comparable to diversification rates documented for other recent radiations (Baldwin & Sanderson, 1998; von Hagen, & Kadereit, 2001; Klak *et al.*, 2004; Valente *et al.*, 2010). However, all these radiations comprise fewer species and/or took place in a limited regional context such as islands or island-like habitats or a single biome (tropical rainforests, winter rainfall area, etc.). The observed phylogenetic conflict between nr and cp sequences of some clades (Appendix S2.2 & S2.7) and the relatively short branches in the tree seem to further support the hypothesis of a rapidly diversifying lineage. Furthermore, the low statistical support inside clades coincides with their low genetic variation and has often been found in recent radiations (Appendix S2.1; Hodges, 2000; Wagstaff & Breitwieser, 2004).

This unique combination of young age (~10 Myr), high species richness (about 1000 spp.) and a nearly cosmopolitan distribution sets the radiation of *Senecio* apart from most other radiations. Many species-rich genera of similar age, such as *Astragalus* L. and *Silene* L., are mostly restricted to the Northern Hemisphere (Mabberley, 2008) or are not monophyletic and thus difficult to compare (*Salvia*: Walker *et al.*, 2004). On the other hand, many cosmopolitan or nearly cosmopolitan and species-rich genera such as *Euphorbia* L., *Carex* L., *Solanum* L. or *Oxalis* L. are clearly older (Tab. 1). There seems to be only one comparably young and widely distributed lineage: the Poa alliance (*Poa* L. and its closest relatives with approximately 775 species). The Poa alliance has a similar age and diversification rate but is more or less restricted to cool or dry environments mostly of the Northern Hemisphere (Hoffmann *et al.*, 2013) whereas *Senecio* is more species rich in the Southern Hemisphere.

The question remains if the high diversification rate found for *Senecio* is exceptional in the context of Senecioneae and Asteraceae. Asteraceae in general are known for their large imbalance of subfamilies in terms of species number (Stevens, 2001). At least two subfamilies are monospecific, and while others are large, these often have much smaller sister-subfamilies (Funk *et al.*, 2009). Senecioneae are believed to be the most species-rich tribe of Asteraceae, with about a third of its species belonging to *Senecio*, the most species-rich genus of the family. The sister clade of *Senecio* is not known, and thus a direct comparison of *Senecio* with closely related lineages is impossible, especially as more and more species originally described as *Senecio* are shown to belong to other lineages in the tribe (Pelser *et al.*, 2007; Pelser *et al.*, 2010a). However, most genera in the Senecioneae are rather species-poor with many monospecific genera (Bremer, 1994), and besides *Senecio* few genera contain more than a moderate number of species and non more than 200 (according to the generic circumscriptions known today). All this shows that the radiation of *Senecio* is remarkable even within Senecioneae and within the whole of Asteraceae. Some authors suggested either morphological or life historical key innovations (Richardson *et al.*, 2001a; Klak *et al.*, 2004; Drummond *et al.*, 2012) and/or adaptation to montane/alpine environments (von Hagen & Kadereit, 2001; Drummond *et al.*, 2012) or to summer draught and seasonality (Valente *et al.*, 2010) to have triggered these radiations. For *Senecio* we postulate that dispersability and the occupation of open and disturbed habitats, facilitating establishment, might have contributed to the wide distribution and strong diversification of the genus in a relatively short time frame.

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Supporting Information

Recent cosmopolitan radiation of *Senecio* L.

Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Appendix S1: Additional information for Material and Methods, including newly added material, GenBank accession numbers and habitat information.

TABLE S1.1: NEWLY SEQUENCED MATERIAL USED IN THIS STUDY[2]. LOWER CASE X INDICATES NEWLY OBTAINED SEQUENCES; MINUS (-) INDICATES THAT NO NEW SEQUENCES WERE OBTAINED. HERBARIUM ABBREVIATIONS: B: BOTANISCHER GARTEN UND BOTANISCHES MUSEUM BERLIN-DAHLEM/GERMANY, BR: BOTANIC GARDEN MEISE/BERLGIUM; C: NATURAL HISTORY MUSEUM OF DENMARK/COPENHAGEN; J: UNIVERSITY OF THE WITWATERSRAND/SOUTH AFRICA, M: BOTANISCHE STAATSSAMMLUNG MÜNCHEN/GERMANY; S: SWEDISH MUSEUM OF NATURAL HISTORY/STOCKHOLM; SIM: STATEN ISLAND INSTITUTE OF ARTS AND SCIENCES/NEW YORK - USA; STA: UNIVERSITY OF ST. ANDREWS/UNITED KINGDOM; UBT: UNIVERSITY OF BAYREUTH/GERMANY; UPS: UNIVERSITY OF UPPSALA/SWEDEN.

Species	**Collector**	**Herb. code**	**ID**	**ITS**	***ndh*F**	***trn*LF**	***trn*C-*ycf*6**
Senecio × pirottae Chiov.	O. Hedberg 726	S	25,1	x	x	x	x
Senecio abruptus Thunb.	J.J. Milton JJM50.1 / ABR3	STA	KAD634	-	-	-	x
Senecio aequinoctialis R.E.Fr.	O. Hedberg 1880	S	5,3	x	x	x	x
Senecio balensis S.Ortiz & Vivero	I. Friis, M.G. Gilbert & K. Vollesen 3424	C	58,1	x	x	x	x
Senecio caloneotes Hilliard	Hilliard & Burtt 16426	S	42,1	x	x	-	x
Senecio cathcartensis O. Hoffm.	Hilliard & Burtt 19079	S	43,1	x	x	x	x
Senecio consanguineus DC.	Dr. R. Seydel 3638	SIM	1026	x	-	x	x
Senecio coronatus (Thunb.) Harv.	Hugo L. 1945 (BR0000013175160)	BR	1002	x	-	x	-
Senecio cryphiactis O.Hoffm.	Giess 10519	M	KAD259	-	-	-	x
Senecio cyaneus O.Hoffm.	P.B. Phillipson 4870	C	17,3	x	-	x	x
Senecio erysimoides DC.	Cron & Goodman 685	J	626	-	-		x
Senecio farinaceus Sch.Bip. ex A.Rich.	Ake Holm 80	S	18,1	x	x	x	x
Senecio fresenii Sch. Bip. ex Oliv. & Hiern	E. Westphal & J.M.C Westphal-Stevels 3139	C	16,4	x	-	x	x
Senecio harveianus MacOwan	Hilliard & Burtt 6939	S	46,1	-	x	x	-

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[2] Da entschieden wurde dieses Manuskript nicht zu veröffentlichen, sind die meisten Sequenzen nochmal als neu sequenziert in den anderen beiden Kapiteln aufgeführt.

Species	**Collector**	**Herb. code**	**ID**	**ITS**	***ndh*F**	***trn*LF**	***trn*C-*ycf*6**
Senecio harveianus MacOwan	James L. Sidey 3247	S	46,2	x	-	-	x
Senecio hieracioides DC.	Hannah I. Stevebs 474/Elemarie van der Watt	SIM	1025	x	-	x	x
Senecio hochstetteri Sch. Bip. ex A. Rich.	P.B. Phillipson 5080	C	19,3	x	x	x	x
Senecio hypochoerideus DC.	Hilliard & Burtt 9613	S	47,1	x	x	x	x
Senecio inornatus DC.	A.J. Salubeni/E.J. Tawakali 3920	C	1009	x	-	x	x
Senecio jacksonii S. Moore	O. Hedberg 1545	S	7,2	x	x	x	x
Senecio keniophytum R. E. Fr.	O. Hedberg 1730	S	4,5	x	x	x	x
Senecio laxus DC.	Cron 669	J	628	-	-	-	x
Senecio mattirolii Chiov.	O. Hedberg 409	S	21,1	x	x	x	x
Senecio meyeri-johannis Engl.	Magnus Fries s.n. (s 12-19541)	S	22,2	x	x	x	x
Senecio moorei R.E.Fr.	M. Thulin & A. Tidigs 167	S	3,5	x	x	x	x
Senecio myriocephalus Sch.Bip. ex A.Rich.	Mesfin Tadesse, C. Puff & O. Ryding 7161	C	23,2	x	-	x	x
Senecio nanus Sch.Bip. ex A.Rich.	R.K. Brummitt 20996	C	59,1	x	x	x	x
Senecio niveus (Thunb.) Willd.	W. Greuter 22177	B	630	-	-	-	x
Senecio ochrocarpus Oliv. & Hiern	Arne Anderberg 1732	S	24,1	x	-	x	x
Senecio oederiafolium DC.	R.D.A. Bayliss BS 6860	SIM	1022	x	-	-	-
Senecio parvifolius DC. syn. of *S. carroensis*	Cron & Goodman 630	J	625	-	-	-	x
Senecio pergamentaceus Baker	H. M. Richards 10563	S	35,1	-	-	-	x
Senecio platypleurus Cufod.	I. Friis, Sally Bidgood, Melaku Wondefrash & Ermias Getachew 10534	C	56,1	x	x	x	x
Senecio purtschelleri Engl.	O. Hedberg 1772	S	2,5	x	x	x	x
Senecio qathlambanus Hilliard	Hilliard & Burtt 15321	S	50,1	x	-	x	x
Senecio ragazzi Chiov.	Hedberg 5665	UPS	62,1	x	-	x	-
Senecio rautanenii S. Moore	Dr. R. Seydel 3525	SIM	1021	x	-	x	x
Senecio reclinatus L.f.	R.D.A. Bayliss BS 4397	SIM	1020	x	-	-	-
Senecio rhammatophyllus Mattf.	O. Hedberg 866	S	27,1	x	-	x	x
Senecio roseiflorus R.E.Fr.	O. Hedberg 1884	S	10,3	x	x	x	x
Senecio rosmarinifolius L.f.	N.S. Pillans 10466	SIM	1030	x	-	-	-

Species	**Collector**	**Herb. code**	**ID**	**ITS**	***ndh*F**	***trn*LF**	***trn*C-*ycf*6**
Senecio sabinjoensis Muschl.	Misimba, Muzinga Matamba 1 (BR0000013175146)	BR	1004	x	-	-	-
Senecio schimperi Sch.Bip. ex A.Rich.	I. Friis, Sally Bidgood, Melaku Wondefrash & Ermias Getachew 10534	C	28,4	x	x	x	x
Senecio schultzii Hochst. ex A. Rich.	Arne Anderberg 1695	S	29,2	x	x	x	x
Senecio schweinfurthii O.Hoffm.	O. Hedberg 1881	S	1,7	x	x	-	x
Senecio seminiveus J. M. Wood & M. S. Evans	Hilliard & Burtt 3776	S	51,1	x	-	-	-
Senecio snowdenii Hutch.	Ake Strid 3579	S	30,1	x	x	x	x
Senecio sotikensis S. Moore	O. Hedberg 871	S	13,2	x	x	x	x
Senecio steudelii Sch.Bip. ex A.Rich.	Ensermu Kelbessa 1447	C	60,1	-	x	x	x
Senecio subsessilis Oliv. & Hiern	K. Schmitt 703	UBT	14,1	x	-	-	-
Senecio subsessilis Oliv. & Hiern	J.A. Mlangwa, P.B Phillipson, H. van Vlaenderen & W. Kindeketa 305	S	14,4	x	x	x	x
Senecio telekii (Schweinf.) O. Hoffm.	O. Hedberg 2290	S	31,2	x	x	x	x
Senecio transmarinus S. Moore	O. Hedberg 682	S	32,4	x	x	x	x
Senecio unionis Sch.Bip. ex A.Rich.	Arne Anderberg 1709	S	33,1	x	x	x	x
Senecio urundensis S. Moore	S.Lisowski 93978 (BR0000013175139)	BR	1005	x	-	-	-

Table S1.2: Sequences obtained from Genbank. Marker indicated at the beginning of the column followed by species name, Author and GenBank accession numbers.

ITS: *Crassocephalum crepidioides* (Benth.) S. Moore: EF538173; *Dendrocacalia crepidifolia* (Nakai) Nakai: GU818543; *Erechtites valerianifolius* (Link ex Spreng.) DC.: EF538199; *S. abruptus* Thunb.: JN789733; *S. acanthifolius* Hombr. & Jacq., ex Decne.: EF538238; *S. actinella* Greene: L33213, L33183; *S. adenotrichius* DC.: EF538295; *S. aegyptius* L.: AJ400777; *S. aethnensis* Jan ex DC.: AJ400779; *S. algens* Wedd.: EF538296; *S. angustifolius* (Thunb.) Willd.: JN789735; *S. aphanactis* Greene: AF457430; *S. arenarius* M. Bieb.: AF457421; *S. arnicoides* Wall.: EF538298; *S. aspericaulis* J. Rémy: EF538299; *S. asperulus* DC.: EF538300; *S. australis* Willd.: EF538302; *S. bahioides* Hook. & Arn.: EF538304; *S. banksii* Hook.f.: EF538305; *S. bathurstianus* (DC.) Sch.Bip.: KC696056; *S. berteroi* (De Candolle) Pelser: AF459957; *S. bollei* Sunding & G.Kunkel: JN789736; *S. bonariensis* Hook. & Arn: EF538306; *S. brasiliensis* (Spreng.) Less.: GU818641; *S. brassii* Belcher: EF538307; *S. brigalowensis* I. Thomps.: KC696059; *S. burchellii* DC.: EF538309; *S. cadiscus* B.Nord. & Pelser: GU818506; *S. californicus* DC.: AF097536; *S. callosus* Sch.Bip. ex Klatt: EF538310; *S. calocephalus* Poepp. & Endl.: HM050325; *S. campanulatus* Sch.Bip. ex Klatt: EF538149; *S. candidans* DC.: HM050326; *S. candollei* Wedd.: EF538311; *S. canescens* (Bonpl.) Cuatrec.: EF538176; *S. carroensis* DC.: JN789741; *S. castagneanus* DC.: JX895508; *S. chilensis* Less.: EF538313; *S. chrysanthemifolius* Poir.: AJ400780; *S. cisplatinus* Cabr.: EF538314; *S. comosus* Sch.Bip. ex Wedd.: EF538316; *S. consanguineus* DC.: AF457420; *S. coriaceus* Aiton: EF538317; *S. corrugatus* (Philippi) Pelser: EF028715, EF028708; *S. cremeiflorus* Mattf.: EF538320; *S. crithmoides* Hook. & Arn.: EF538321; *S. crusoei* Pelser: EF538290; *S. cryphiactis* O. Hoffm.: JN789742; *S. ctenophyllus* Phil.: EF538322; *S. cuencanus* Hieron.: GU289943; *S. cunninghamii* DC.: EF538323; *S. decurrens* DC.: EF538324; *S. deferens* Griseb.: EF538325; *S. diaschides* D.G. Drury: EF538328; *S. donianus* Hook. & Arn: EF538329; *S. doria* L.: AF459946; *S. doriiformis* DC.: JX895507; *S. doronicum* (L.) L.: EF538330; *S. dregeanus* DC.: EF538331; *S. dunedinensis* Belcher: AY554109; *S. eenii* (S. Moore) Merxm.: AF457425; *S. elegans* L.: GU818642; *S. eremophilus* Richardson: AF459945; *S. eriopus* Willk.: JX895291; *S. ertterae* T.M. Barkley: AF457433; *S. erysimoides* DC.: JN789743; *S. espinosae* Cabr.: EF538332; *S. eubaeus* Boiss. & Heldr.: JX895245; *S. evenius* (Philippi) Pelser: EF028714, EF028707; *S. farinifer* Hook. & Arn: EF538333; *S. filaginoides* DC.: EF538334; *S. fistulosus* Poepp. ex DC.: EF538335; *S. flaccidus* Less.: EF538336; *S. franchetii* C. Winkl.: EF538337; *S. fruticulosus* Sibth. & Sm.: JN789744; *S. gayanus* DC.: GU818649; *S. giessii* Merxm.: AF457418; *S. glaber* Less.: EF543651, EF543649; *S. glastifolius* L. f.: EF538340; *S. glaucophyllus* Cheesem.: EU812813; *S. glaucus* L.: JN789745; *S. glomeratus* Desf. ex Poir.: EU331117; *S. glossanthus* (Sond.) Belcher: KC696060; *S. glutinosus* Thunb.: AF457427; *S. gnidioides* Phil.: EF538341; *S. gramineus* Harv.: GU818650; *S. gregorii* F.Muell.: GU818651; *S. grossidens* Dusén ex Malme: EF538342; *S. gunnii* (Hook. f.) Belcher: EF538343; *S. hansweberi* Cuatrec.: EF538344; *S. hastatus* L.: EF538345; *S. hieracium* J.Rémy: GU818652; *S. hispidissimus* I. Thomps.: GU818657; *S. hispidulus* A. Rich.: JX895506; *S. hoggariensis* Batt. & Trab.: DQ208190; *S. humillimus* Sch. Bip.: EF538347; *S. hypsobates* Wedd.: EF538348; *S. ilicifolius* L.: GU818662; *S. imbaburensis* Sklenář & Marhold: GU290009; *S. inaequidens* DC.: AF459943; *S. incrassatus* Lowe: JN789807; *S. integerrimus* Nutt.: EF538349; *S. involucratus* (Kunth) DC.: EF538150; *S. jarae* Phil.: EF538350; *S. kerdousianus* Gómiz & Llamas: JN789808; *S. kolenatianus* C.A. Mey.: JX895252; *S. krascheninnikovii* Schischk.: AF457437; *S. lacustrinus* I. Thomps.: KC696061; *S. laetevirens* Phil.: EF538352; *S. lagascanus* DC.: JX895354; *S. landbeckii* Phil.: EF538353; *S. lastarrianus* J.Rémy in Gay: GU818663; *S. lautus* (Willd.) G. Forst. ex Willd.: EU812814; *S. laxus* DC.: JN789809; *S. lemmonii* A. Gray: AF457432; *S. leptolobus* DC.: EF538355; *S. leptophyllus* DC.: JN789810; *S. leucanthemifolius* Poir.: JN789811; *S. linearifolius* A. Rich.: KC696064; *S. lingulatus* (Schltdl.) Cuatrec.: GU290004; *S. littoreus* Thunb.: JN789812; *S. lividus* L.: AJ400795; *S. longipenicillatus* Schultz-Bip. ex Sandw.: GU290029; *S. lopezii* Boiss.: JX895264; *S. loratifolius* Greenm.: AF161643, AF161693; *S. lugens* Richardson: L33196, L33226; *S. macedonicus* Griseb.: JX895510; *S. macranthus* A. Rich.: EF538358; *S. madagascariensis* Poir.: GQ478106; *S. mairetianus* DC.: EF538359; *S. maritimus* L. f.: JN789816; *S. masafuerae* (Skottsberg) Pelser: EF028717, EF028710; *S. maulinus* Reiche: JN789901; *S. minimus* Poir.: EU331119; *S. mohavensis* A. Gray: AF457435; *S. montevidensis* (Spreng.) Baker: EF538361; *S. nebrodensis* L.: JN789902; *S. neeanus* Cuatrec.: EF538177; *S. nemorensis* L.: AF459937; *S. neowebsteri* S.F. Blake: AF161694, AF161644; *S. nivalis* (Kunth) Cuatrec.: GU289960; *S. niveoaureus* Cuatrec.: EF538178; *S. niveus* (Thunb.) Willd.: JN789903; *S. oerstedianus* Benth.: EF538362; *S. olympicus* Boiss.: JX895511; *S. oreophyton* J.Rémy: EF538393; *S. otophorus* Wedd.: GU289949; *S. oxyriifolius* DC.: AF459936; *S. panduriformis* Hilliard: EF538364; *S. patens* (Kunth) DC.: EF538151; *S. paulsenii* O. Hoffm. ex Pauls.: JX895235; *S. perralderianus* Coss.: EF538365; *S. petraeus* Boiss. & Reut.: JN789906; *S. pflanzii* (Perkins) Cuatrec.: EF538179; *S. pichinchensis* (Cuatrec.) Cuatrec.: GU290022; *S. pindilicensis* Hieron.: GU290014; *S. pinnatifolius* A. Rich: GU81867; *S. pinnulatus* Thunb.: JN789907; *S. piptocoma* O. Hoffm. ex Schinz: JN789908; *S. poeppigii* Cuatrec.: EF543650, EF543652; *S. polygaloides* Phil.: EF538367; *S. prenanthoides* A. Rich.: GU818681; *S. provincialis* (L.) Druce: JX895383; *S. pseudoorientalis* Schischk.: JX895512.; *S. pseudoarnica* Less.: AF161695, AF161645; *S. psilocarpus*

Belcher & Albr.: GU818692; *S. pubiger* L.: EF538368; *S. pudicus* Greene: EF538369; *S. purpureus* L.: EF538370; *S. pyrenaicus* L.: EF538371; *S. quadridentatus* Labill.: AF422134; *S. roseus* Sch. Bip.: EF538373; *S. rufescens* DC.: EF538374; *S. rufiglandulosus* Colenso.: AF422135; *S. scaberulus* Hook. f.: EF538378; *S. scopolii* Hoppe & Hornsch. ex Bluff & Fingerh.: JX895513; *S. selloi* (Spreng.) DC.: EF538379; *S. serratifolius* (Meyen & Walp.) Cuatrec.: EF538180; *S. sinuatilobus* DC.: EF538380; *S. sisymbriifolius* DC.: EF538381; *S. smithii* DC.: EF538382; *S. spartioides* Torr. & A. Gray: EF538383; *S. sphaerocephalus* Greene: AF161646; *S. squalidus* L.: JN789909; *S. squarrosus* A. Rich.: GU818703; *S. stoechadiformis* DC.: EF538385; *S. suaveolens* (L.) Ell.: EF538222; *S. superandinus* Cuatrec: EF538248; *S. sylvaticus* L.: AF459928; *S. tauricolus* V. A. Matthews: GU817570.; *S. teneriffae* Sch. Bip.: JN789910; *S. thapsoides* DC.: EF538388; *S. thianschanicus* Regel & Schmalh.: AY176156; *S. thurifer* (Decaisne) Pelser: EF028718; *S. transsylvanicus* Boiss.: JX895306; *S. trapezuntinus* Boiss.: JX895514; *S. triangularis* Hook.: EF538389.; *S. tricuspidatus* Hook. & Arn.: EF538390; *S. trifidus* Hook. & Arn: EF538391; *S. trifurcatus* (G.Forst.) Less.: HM050327; *S. triodon* Phil.: GU818707; *S. umbrosus* Waldst. & Kit.: JX895447; *S. vernalis* Waldst. & Kit.: AJ400806; *S. vestitus* P.J. Bergius: GU818708; *S. viridis* Phil.: EF538394; *S. viscosus* L.: AF459925; *S. volckmannii* Phil.: EF538395; *S. vulgaris* L.: AJ400811; *S. wairauensis* Belcher: EF538397; *S. windhoekensis* Merxm.: AF457426; *S. wootonii* Greene: EF538398; *S. zimapanicus* Hemsl.: AF161686, AF161636; *Synotis cappa* (Buch.Ham. ex D. Don) C. Jeffrey & Y.L. Chen: EF538402; *Synotis nagensium* (C.B. Clarke) C. Jeffrey & Y.L. Chen: AF459922

***trn*LF**: *Abrotanella emarginata* (Gaudich.) Cass.: EF538089; *Acicarpha spathulata* R. Br.: EU385031; *Boopis anthemoides* Juss.: EU547627; *Carduoideae sp* Cass. ex Sweet: JQ303111; *Carthamus oxyacanthus* M. Bieb.: HM002884; *Cnicothamnus lorentzii* Griseb.: EU385054; *Corymbium glabrum* L.: EU385055; *Crassocephalum crepidioides* (Benth.) S. Moore: EF028722; *Dasyphyllum* Kunth: EU841077; *Doronicum pardalianches* L.: EF538098; *Erechtites valerianifolius* (Link ex Spreng.) DC.: EF538100; *Gymnarrhena micrantha* Desf.: EU385076; *Hecastocleis shockleyi* A. Gray: EU385077; *Helianthus tuberosus* L.: GU818008; *Hirpicium gazanioides (Harv.)* Roessler: AY504808; *Jacobaea vulgaris* Gaertn.: EF028725; *Linzia* Sch. Bip. ex Walp.: EF155880; *Packera eurycephala* (Torr. & A. Gray) W.A. Weber & Á. Löve: EF538113; *Pertya scandens* (Thunb. ex Murray) Sch. Bip.: EU385101; *S. abruptus* Thunb.: JN789959; *S. acanthifolius* Hombr. & Jacq., ex Decne.: EF538104; *S. aegyptius* L.: JN789960; *S. aethnensis* Jan ex DC.: EU195499; *S. algens* Wedd.: GU818058; *S. angustifolius* (Thunb.) Willd.: JN789961; *S. arnicoides* Wall.: GU818059; *S. berteroi* (De Candolle) Pelser: EF538142; *S. bollei* Sunding & G.Kunkel: JN789962; *S. brasiliensis* (Spreng.) Less.: GU818061; *S. burchellii* DC.: JN789963; *S. cadiscus* B.Nord. & Pelser: GU817980; *S. campanulatus* Sch.Bip. ex Klatt: HM050374; *S. carroensis* DC.: JN790001; *S. chilensis* Less.: EF538122; *S. comosus* Sch.Bip. ex Wedd.: GU818062; *S. corrugatus* (Philippi) Pelser: HM050371; *S. cremeiflorus* Mattf.: HM050375; *S. crusoei* Pelser: EF538118; *S. cryphiactis* O. Hoffm.: JN789969; *S. ctenophyllus* Phil.: GU818063; *S. elegans* L.: GU818064; *S. erysimoides* DC.: JN789970; *S. evenius* (Philippi) Pelser: GU818055; *S. fistulosus* Poepp. ex DC.: GU818065; *S. flaccidus* Less.: GU818066; *S. fruticulosus* Sibth. & Sm.: JN789971; *S. gayanus* DC.: GU818067; *S. glastifolius* L. f.: JN789972; *S. gramineus* Harv.: GU818068; *S. gregorii* F.Muell.: GU818069; *S. grossidens* Dusén ex Malme: HM050376; *S. hieracium* J.Rémy: GU817913; *S. hispidissimus* I. Thomps.: GU818071; *S. hypsobates* Wedd.: GU818073; *S. ilicifolius* L.: GU818074; *S. inaequidens* DC.: JN789979; *S. incrassatus* Lowe: JN789983; *S. integerrimus* Nutt.: GU818075; *S. involucratus* (Kunth) DC.: EF538090; *S. jarae* Phil.: EF538125; *S. lastarrianus* J.Rémy in Gay: GU818076; *S. laxus* DC.: JN789985; *S. leucanthemifolius* Poir.: JN789988; *S. littoreus* Thunb.: JN789989; *S. lividus* L.: JN789990; *S. madagascariensis* Poir.: JN789991; *S. mairetianus* DC.: EF538128; *S. maritimus* L. f.: JN789992; *S. masafuerae* (Skottsberg) Pelser: GU817945; *S. maulinus* Reiche: JN789997; *S. minimus* Poir.: JN789998; *S. nebrodensis* L.: JN789999; *S. nemorensis* L.: EF028730; *S. niveoaureus* Cuatrec.: GU818078; *S. niveus* (Thunb.) Willd.: JN790000; *S. oerstedianus* Benth.: GU817950; *S. oreophyton* J.Rémy: GU818079; *S. patens* (Kunth) DC.: GU818080; *S. petraeus* Boiss. & Reut.: JN790003; *S. pflanzii* (Perkins) Cuatrec.: EF538096; *S. pinnatifolius* A. Rich: GU818081; *S. pinnulatus* Thunb.: JN790004; *S. piptocoma* O. Hoffm. ex Schinz: JN790005; *S. polygaloides* Phil.: GU818082; *S. prenanthoides* A. Rich.: GU818083; *S. psilocarpus* Belcher & Albr.: GU818084; *S. roseus* Sch. Bip.: GU818085; *S. squarrosus* A. Rich.: GU817964; *S. suaveolens* (L.) Ell.: EF538102; *S. tauricolus* V. A. Matthews: GU818087; *S. teneriffae* Sch. Bip.: JN790010; *S. thapsoides* DC.: EF538137; *S. thianschanicus* Regel & Schmalh.: AF468168; *S. thurifer* (Decaisne) Pelser: HM050372; *S. trifurcatus* (G.Forst.) Less.: HM050373; *S. triodon* Phil.: GU818088; *S. vernalis* Waldst. & Kit.: JN789987; *S. vestitus* P.J. Bergius: GU818089; *S. viscosus* L.: EF028734; *S. vulgaris* L.: EF538139, JQ041866; *Schlechtendalia luzulaefolia* Less.: EU841085; *Stifftia* J.C. Mikan: JF920298; *Synotis nagensium* (C.B. Clarke) C. Jeffrey & Y.L. Chen: EF028735; *Trixis* P. Browne: EU385120

***ndh*F:** *Abrotanella emarginata* (Gaudich.) Cass.: AJ012679; *Acicarpha spathulata* R. Br.: EU385125; *Boopis anthemoides* Juss.: L39384; *Carduoideae sp* Cass. ex Sweet: JQ303120; *Carthamus oxyacanthus* M. Bieb.:

KC589940; *Cnicothamnus lorentzii* Griseb.: AF233823; *Corymbium glabrum* L.: EU385148; *Crassocephalum crepidioides* (Benth.) S. Moore: EF53795; *Dasyphyllum* Kunth: L39392; *Doronicum pardalianches* L.: AY723254; *Erechtites valerianifolius* (Link ex Spreng.) DC.: EF537965; *Gymnarrhena micrantha* Desf.: EU385170; *Hecastocleis shockleyi* A. Gray: EU385171; *Helianthus tuberosus* L.: GU817867; *Jacobaea vulgaris* Gaertn.: AB530940; *Packera eurycephala* (Torr. & A. Gray) W.A. Weber & Á. Löve: EF537982; *Pertya scandens* (Thunb. ex Murray) Sch. Bip.: EU385195; *S. abruptus* Thunb.: JN790011; *S. acanthifolius* Hombr. & Jacq., ex Decne.: EF537970; *S. aegyptius* L.: JN790012; *S. aethnensis* Jan ex DC.: JN790050; *S. algens* Wedd.: GU817905; *S. angustifolius* (Thunb.) Willd.: JN790013; *S. arnicoides* Wall.: GU817801; *S. berteroi* (De Candolle) Pelser: EF537987; *S. bollei* Sunding & G.Kunkel: JN790014; *S. brasiliensis* (Spreng.) Less.: GU817820.; *S. burchellii* DC.: JN790015; *S. cadiscus* B.Nord. & Pelser: GU817794; *S. calocephalus* Poepp. & Endl.: HM050331; *S. campanulatus* Sch.Bip. ex Klatt: HM050328; *S. candidans* DC.*:* HM050333; *S. carroensis* DC.: JN790045; *S. chilensis* Less.: EF537992; *S. comosus* Sch.Bip. ex Wedd.: GU817907; *S. corrugatus* (Philippi) Pelser: HM050329; *S. crusoei* Pelser: GU817903; *S. cryphiactis* O. Hoffm.: JN790017; *S. ctenophyllus* Phil.: GU817804; *S. elegans* L.: GU817908; *S. erysimoides* DC.: JN790018; *S. evenius* (Philippi) Pelser: GU817902; *S. fistulosus* Poepp. ex DC.: GU817909; *S. flaccidus* Less.: GU817910; *S. fruticulosus* Sibth. & Sm.: JN790019; *S. gayanus* DC.: GU817911; *S. glastifolius* L. f.: JN790020; *S. gramineus* Harv.: GU817802; *S. gregorii* F.Muell.: GU817912; *S. hieracium* J.Rémy: GU817913; *S. hispidissimus* I. Thomps.: GU817914; *S. hoggariensis* Batt. & Trab.: JN789978; *S. hypsobates* Wedd.: GU817822; *S. ilicifolius* L.: GU817915; *S. inaequidens* DC.: JN790027; *S. incrassatus* Lowe: JN790029; *S. integerrimus* Nutt.: GU817916; *S. involucratus* (Kunth) DC.: EF537952; *S. jarae* Phil.: EF537997; *S. kerdousianus* Gómiz & Llamas: JN789984; *S. lastarrianus* J.Rémy in Gay: GU817823; *S. lautus* (Willd.) G. Forst. ex Willd.: KC695942; *S. laxus* DC.: JN790030; *S. leptophyllus* DC.: JN790031; *S. leucanthemifolius* Poir.: JN790033; *S. littoreus* Thunb.: JN790034; *S. lividus* L.: JN790035; *S. madagascariensis* Poir.: JN790036; *S. mairetianus* DC.: EF538001; *S. maritimus* L. f.: JN790037; *S. masafuerae* (Skottsberg) Pelser: GU817818; *S. maulinus* Reiche: JN790042; *S. nebrodensis* L.: JN790043; *S. nemorensis* L.: AY723209; *S. niveoaureus* Cuatrec.: GU817918; *S. niveus* (Thunb.) Willd.: JN790044; *S. oerstedianus* Benth.: GU817919; *S. oreophyton* J.Rémy: GU817920; *S. patens* (Kunth) DC.: GU817795; *S. petraeus* Boiss. & Reut.: JN790047; *S. pflanzii* (Perkins) Cuatrec.: EF537960; *S. pinnatifolius* A. Rich: GU817922; *S. piptocoma* O. Hoffm. ex Schinz: JN790049; *S. polygaloides* Phil.: GU817923; *S. prenanthoides* A. Rich.: GU817924; *S. psilocarpus* Belcher & Albr.: GU817925; *S. roseus* Sch. Bip.: GU817926; *S. squalidus* L.: JN790007; *S. squarrosus* A. Rich.: GU817927; *S. suaveolens* (L.) Ell.: EF537968; *S. tauricolus* V. A. Matthews: GU817929; *S. thapsoides* DC.: EF538014; *S. thianschanicus* Regel & Schmalh.: AY723207; *S. thurifer* (Decaisne) Pelser: HM050330; *S. trifurcatus* (G.Forst.) Less.: HM050334; *S. triodon* Phil.: GU817930; *S. vernalis* Waldst. & Kit.: JN790032; *S. vestitus* P.J. Bergius: GU817824; *S. viscosus* L.: EF538016; *S. vulgaris* L.: EF538017; *Schlechtendalia luzulaefolia* Less.: L39395; *Stifftia* J.C. Mikan: L39399; *Synotis alata* (Wall. ex DC.) C. Jeffrey & Y.L. Chen ex DC.: AY723217; *Synotis nagensium* (C.B. Clarke) C. Jeffrey & Y.L. Chen: EF538018; *Trixis* P. Browne: L39406; *Wunderlichia mirabilis* Riedel ex Baker: EU385122

***rbc*L**: *Acicarpha spathulata* R. Br.: EU384939; *Boopis anthemoides* Juss.: L13860; *Carduoideae sp* Cass. ex Sweet: JQ303118; *Carthamus oxyacanthus* M. Bieb.: KC589814; *Cnicothamnus lorentzii* Griseb.: EU384961; *Corymbium glabrum* L.: EU384962; *Crassocephalum crepidioides* (Benth.) S. Moore: GU817753; *Dasyphyllum* Kunth: L13863; *Erechtites valerianifolius* (Link ex Spreng.) DC.: EF537965; *Gymnarrhena micrantha* Desf.: EU384983; *Hecastocleis shockleyi* A. Gray: EU384984; *Helianthus tuberosus* L.: GU817765; *Jacobaea vulgaris* Gaertn.: GU817769; *Packera eurycephala* (Torr. & A. Gray) W.A. Weber & Á. Löve: GU817778; *Pertya scandens* (Thunb. ex Murray) Sch. Bip.: EU385008; *S. burchellii* DC.: AM234911; *S. vulgaris* L.: HM850347; *Schlechtendalia luzulaefolia* Less.: AY874431; *Stifftia* J.C. Mikan: EU385020; *Trixis* P. Browne: EU385025; *Wunderlichia mirabilis* Riedel ex Baker: EU385217

TABLE S1.3: HABITAT INFORMATION FOR THE DIFFERENT SPECIES AND THEIR ASSIGNMENT INTO CATEGORIES. CATEGORY 1: OPEN/DISTURBED; CATEGORY 2: NON-OPEN/NON-DISTURBED. MINUS (-) INDICATES THAT THERE WAS NO DATA OR ASSIGMENT TO A CATEGORY.

Species	Habitat description	Habitat category	Resource
S. abruptus	Sandy moist ground, stony slopes	1	Harvey, 1865; Manning & Goldblatt, 2012
S. acanthifolius	Frequent in the very wet forests of the southern Andes	2	Cabrera, 1949
S. actinella	In duff, rocky woodlands, especially in pine-dominated areas	1	Barkley, 2006
S. adenotrichius	Endemic species of the low mountains of central Chile	-	Cabrera, 1949
S. aegyptius	Banks of the Nil, oasis, river bed, roadside ditches, margins	1	Alexander, 1979; Tadesse, 2004
S. aequinoctalis	Moist sites in afro-alpine grasslands, shallow soil over rocks	1	Jeffrey & Beentje, 2005
S. aethnensis	Lava slopes	1	Chater & Walters, 2010
S. algens	Between rocks	1	Cabrera, 1999
S. angustifolius	Stony flats and slopes	1	Manning & Goldblatt, 2012
S. aphanactis	Dry, open ground, especially alkaline flats	1	Barkley, 2006
S. arenarius	Sandy ground, sandy and gravelly flats and washes	1	Harvey, 1865; Manning & Goldblatt, 2012
S. arnicoides	Common grass in the lowlands of central Chile	2	Cabrera, 1949
S. aspericaulis	Damp places	1	Cabrera, 1999
S. asperulus	Grows socially in poor stony soil, weed along roadside	1	Hilliard, 1977
S. australis	Offshore islands on rock ledges, in short grasses and coastal herbs growing amongst petrel and diving petrel burrows	1	New Zealand Plant Conservation Network, 2014
S. bahioides	Endemic species of the low mountains of Pacific coast	-	Cabrera, 1949
S. balensis	Grasslands on shallow and seasonally waterlogged soils	1	Ortiz & Vivero, 2005
S. banksii	Usually on coastal cliffs, often limestone	1	Webb *et al.*, 1988
S. bathurstianus	mainly in disturbed sites, often in poorer soils and often associated with rocky outcrops, e.g. sandstone or granite, in drier forest and woodland	1	Thompson, 2004a; The Plant Information Network System, 2014
S. berteroi	Inhabiting the scrub located in the high mountains and forests in the humid gorge, high parts of the central section, generally in low open forest	1	Skottsberg, 1921
S. bollei	Maritime zone	1	Pitart & Proust, 1909
S. bonariensis	edge of the permanent bodies of water, aquatic plant	1	Departamento de Biologia, Bioquimica y Farmacia, Universidad Nacional del Sur, 2006
S. brasiliensis	In wet fields, vegetation in low fields, swamps and moist soils, forests, disturbed ground, roadsides, damp grassland, river banks, lake margins	1	Cabrera, 1999; Cabrera *et al.*, 2009; Hind, 2011
S. brassii	Alpine grassland, often boggy or peaty, on piles of rock debris, along roadsides, in tree-fern savanna and fire-induced meadows	1	Belcher, 1982
S. brigalowensis	Grass plains	2	The Plant Information Network System, 2014

Species	**Habitat description**	**Habitat category**	**Resource**
S. burchellii	Sandy and stony slopes	1	Manning & Goldblatt, 2012
S. cadiscus	Vernal pools on shale	1	Nordenstam *et al.*, 2009
S. californicus	Sandy, dry or drying sites, especially near coast	1	Barkley, 2006
S. callosus	Most often found in coniferous or coniferous-oak forests	2	Williams, 1976
S. calocephalus	Endemic species of southern Chile, which grows in the high mountains	-	Cabrera, 1949
S. caloneotes	Wet rocky places	1	Hilliard, 1977
S. campanulatus	Disturbed cloud forest margins, roadsides, secondary scrub	1	Hind, 2011
S. candidans	Coast	1	Cabrera, 1999
S. candollei	Frequent on the banks of streams	1	Cabrera, 1999
S. canescens	Very humid páramo	-	Ramsay, 2001
S. carroensis	Stony, rocky places	1	Harvey, 1865
S. castagneanus	Rocky slopes, forest clearings	1	Matthews, 1975
S. cathcartensis	Grassland, damp or even wet places	2	Hilliard, 1977
S. chilensis	In the district of deciduous forest, common in sandy soils or volcanic	1	Cabrera, 1999
S. chrysanthemifolius	Occurs on volcano	1	Brennan *et al.*, 2009
S. cisplatinus	Present in the grassland, frequently occurs in edges and cores of sandy patches	1	de Freitas *et al.*, 2010
S. comosus	Amongst rocks, in derelict mining areas	1	Hind, 2011
S. consanguineus	Favours river banks	1	Hilliard, 1977
S. coriaceus	-	-	-
S. coronatus	Grows in grassland usually in large colonies, on rocky soils	1	Hilliard, 1977; Pooley, 2003
S. corrugatus	Common on ridges, abundant in the higher parts, where it forms a conspicuous feature in the vegetation of the rocky crest	2	Skottsberg, 1921
S. cremeiflorus	wet environments, ditches, streams and lakes	1	Sánchez & Lupo, 2009
S. crithmoides	Endemic species from the high mountains	-	Cabrera, 1949
S. crusoei	In the shrubberies of the ridges	2	Skottsberg, 1921
S. cryphiactis	-	-	-
S. ctenophyllus	Endemic species from the mountains	-	Cabrera, 1949
S. cuencanus	Within high Andean cloud forests and shrublands paramos	2	Silva-Moure *et al.*, 2014
S. cunninghamii	Most frequent near areas of temporary impeded drainage on sand or clay, and less frequent on hillsides or open stony plains; various soils, commonly associated with watercourses or in drains or depressions in shrubland, woodland and forest	1	Lawrence, 1985; Thompson, 2004b
S. cyaneus	Upland grassland and heath zone, less often in forest margin	1	Jeffrey & Beentje, 2005
S. decurrens	Open grassland	1	Hilliard, 1977
S. deferens	Vegetation in forest and open fields	1	Cabrera *et al.*, 2009
S. diaschides	Alluvial soils adjacent to swamps and rivers, in forest and woodland	1	Thompson, 2004a
S. donianus	Endemic species from the high mountains of Coquimbo	-	Cabrera, 1949

Species	**Habitat description**	**Habitat category**	**Resource**
S. doria	Damp meadows and woods, open woodland and scrubs, saline steppes, meadows and marshes	1	Chater & Walters, 2010
S. doriiformis	Rocky places, streamsides	1	Matthews, 1975
S. doronicum	Grassy and rocky places	1	Chater & Walters, 2010
S. dregeanus	Open grassland	1	Hilliard, 1977
S. dunedinensis	Scrubland, grassland and rocky places	1	Webb *et al.*, 1988
S. eenii	-	-	-
S. elegans	Sandy ground, near the sea shore	1	Harvey, 1865
S. eremophilus	Grassy or open, rocky sites, damp and drying habitats in conifer dominated areas, especially road cuts and other disturbed sites	1	Barkley, 2006
S. eriopus	Rocky places	1	Chater & Walters, 2010
S. ertterae	Talus slopes of greenish yellow ash tuff	1	Barkley, 2006
S. erysimoides	-	-	-
S. espinosae	Has only been found in the province of Talea	-	Cabrera, 1949
S. eubaeus	Rocky places	1	Chater & Walters, 2010
S. evenius	Along the higher ridges, at the limit of the forest among brushwood or in the humid *Dicksonia*-rich woods	2	Skottsberg, 1921
S. farinaceus	*Erica arborea* scrub, afroalpine grassland	2	Tadesse, 2004
S. farinifer	Endemic species of the low mountains of central Chile	-	Cabrera, 1949
S. filaginoides	Highly polymorphic, frequent in dry, sandy places of the Andes	2	Cabrera, 1999
S. fistulosus	Common in very wet meadows on both sides of the Andes Mountains	2	Cabrera, 1999
S. flaccidus	Dry, open sandy or rocky plains, streambeds and canyons, rocky sites, usually areas with continual mild disturbance, especially desert basins and washes	1	Barkley, 2006
S. franchetii	Forests and stony slopes	1	Shishkin, 1995
S. fresenii	*Juniperus* forest at high altitudes, *Erica arborea* bushland, well drained grassy slopes in afroalpine meadow	2	Tadesse, 2004
S. fruticulosus	Grows in phrygana and damp places	2	Jahn & Schönfelder, 1995
S. gayanus	Endemic species from the high mountains of central Chile	-	Cabrera, 1949
S. giessii	Sandy and gravelly flats	2	Manning & Bruyns, 2013
S. glaber	Endemic species of not very high mountains of central Chile	-	Cabrera, 1949
S. glastifolius	Forest margins	1	Goldblatt. 2000
S. glaucophyllus	Mostly limestone, mainly in stony ground, coast	1	Webb *et al.*, 1988
S. glaucus	Shrub-steppes, desert, river banks	2	Alexander, 1979
S. glomeratus	Common in waste places, especially roadsides and stony sites, forest margins and clearings, coastal sands and cliffs, also in shrubland, grasslands and swamps	1	Webb *et al.*, 1988; Thompson, 2004a
S. glossanthus	Grows in seasonally wet areas, on gilgai plains and clay pans, on clay, clayey sand, or sand over granite, laterite or limestone, in shrubland and low woodland	1	Thompson, 2005a
S. glutinosus	rRocky, mostly sandstone slopes	1	Manning & Goldblatt, 2012

Species	Habitat description	Habitat category	Resource
S. gnidioides	Vegetation on rocky soils	1	Cabrera, 1999
S. gramineus	Grows in short turf and in crevices of rock sheets, grassland, mainly on the summit, around margins of rock sheets and stony ridges	1	Hilliard, 1977; Pooley, 2003; Manning & Goldblatt, 2012
S. gregorii	Arid and semi-arid regions, mainly in far-western plains	2	The Plant Information Network System, 2014
S. grossidens	Vegetation in wetland soils	2	Lawrence, 1985; Cabrera *et al.*, 2009
S. gunnii	Disturbed sites, woodlands, grasslands, herb fields and open shrubland	1	Thompson, 2004a; The Plant Information Network System, 2014
S. hansweberi	Rocky, gravel beds	1	Cuatrecasas, 1982
S. harveianus	Rocky outcrops, bare places on mountains	1	Pooley, 2003
S. hastatus	Rocky slopes	1	Manning & Goldblatt, 2012
S. hieracioides	Socially in poor grasslands, and among rocks often becoming a weed along roadsides	1	Hilliard, 1977
S. hieracium	Open forests of *Nothofagus*, in meadows and wet places	1	Cabrera *et al.*, 1999
S. hispidissimus	Sandy soils in heathlands, woodlands and shrublands	2	Thompson, 2004a
S. hispidulus	Waste places, forest margins and clearings, coastal sites, riverbeds and damp areas; forest and woodlands	1	Webb *et al.*, 1988; Thompson, 2004a
S. hochstetteri	Grassland, occasionally in forest margins or wooded grassland, open bushland	1	Tadesse, 2004; Jeffrey & Beentje, 2005
S. hoggariensis	Montane sandy river beds and fallow fields	1	Alexander, 1979
S. humillimus	Meadows on moist soils	2	Cabrera, 1999
S. hypochoerideus	Grows socially on rocky, grassy mountain slopes	1	Hilliard, 1977
S. hypsobates	Boggy depression and stream sides in *Espeletia* páramo	1	Ramsay, 2001
S. ilicifolius	Clay flats and slopes	2	Manning & Goldblatt, 2012
S. imbaburensis	Rocky habitats in the (super)paramo belt, but there is a remarkable record from lower altitudes of the Andean montane forest	1	Sklenář, 2001
S. inaequidens	Among rock outcrops on steep, moist, grassy mountain slopes and along rocky watercourses, weed along roadside, disturbed areas	1	Hilliard, 1977
S. incrassatus	-	-	-
S. inornatus	Upland grassland, forest margins, may be abundant near streams, moist grass slopes, streambanks	1	Pooley, 2003; Jeffrey & Beentje, 2005
S. integerrimus	Moist openings in coniferous woodlands, open prairies and plains, meadow grasslands from foothills to above timberline	1	Barkley, 2006
S. involucratus	-	-	-
S. jacksonii	On thin soil over rocks and rocky ground, swampy grassland	1	Jeffrey & Beentje, 2005
S. jarae	High mountains of northern Chile and north-western Argentina	-	Cabrera, 1949

Species	Habitat description	Habitat category	Resource
S. keniophytum	Boggy ground near streams or lakes, may grow close to snow line or glacier lakes in shelter of rocks, disturbed soils beside glaciers and streams	1	Agnew & Agnew, 1994; Jeffrey & Beentje, 2005
S. kerdousianus	Grows in the shadiest and wettest parts of a road-side ditch, and on terraces above the road, below fallen rocks and at the base of vertical rocks	1	Gómiz & Llamas, 2005
S. kolenatianus	Subalpine and alpine damp meadows	2	Shishkin, 1995
S. krascheninnikovii	Mountain spruce forests, gravel beds of mountain streams, near rocks, stony sloped, gravely slopes and sandy places	1	Jeffrey & Chen Yi-Ling, 1984; Shishkin, 1995
S. lacustrinus	Sandy or loamy soils, usually associated with ephemeral lakes and other water sources	2	Thompson, 2005b
S. laetevirens	Endemic species of the Cordillera de Santiago in Chile	-	Cabrera, 1949
S. lagascanus	Dry places	2	Chater & Walters, 2010
S. landbeckii	Endemic to the mountains	-	Cabrera, 1949
S. lastarrianus	Endemic species from the high mountains of central Chile	-	Cabrera, 1949
S. lautus	Coastal cliffs, turf, sand and rocks	1	Webb *et al.*, 1988
S. laxus	Waste ground, sandy slopes	1	Harvey, 1865; Goldblatt & Manning, 2000
S. lemmonii	Rocky sites in deserts	1	Barkley, 2006
S. leptolobus	At the coast	1	Giehl, 2012
S. leptophyllus	Dry stony karroid slopes	1	POSA Flora (2007)
S. leucanthemifolius	Maritime sands and rocks, agrestal and ruderal forest clearings, roadsides, hillsides	1	Chater & Walters, 2010
S. linearifolius	Woodlands and forest	2	Thompson, 2004a
S. lingulatus	-	-	
S. littoreus	Sandy ground and near cultivations, mainly coastal sands	1	Harvey, 1865; Manning & Goldblatt, 2012
S. lividus	Under cover of pine trees, cork oaks and thickets, in acid soils, sometimes humid	2	Sociedade Portuguesa de Botânica, 2014
S. longipenicillatus	Moorland, populations have a greater development in the galleries formed by rocks, shrubs, where moisture collects on the ground and moss growth is favoured (*Espeletia* spp.)	2	Silva-Moure *et al.*, 2014
S. lopezii	Woods, shady places	2	Chater & Walters, 2010
S. loratifolius	-	-	
S. lugens	Moist meadows, gravelly streambeds, open woods in alpine or boreal sites	1	Barkley, 2006
S. macedonicus	Mountains and rocky slopes	1	Chater & Walters, 2010
S. macranthus	Moist gullies in sclerophyll forest	2	The Plant Information Network System, 2014
S. madagascariensis	Dunes and strand, forest, thicket	1	Madagascar Catalogue, 2014
S. mairetianus	Alpine meadows and pine forest	2	García-Pérez, 1985
S. maritimus	Sea shores, coastal dunes and slopes	1	Harvey, 1865; Manning & Goldblatt, 2012
S. masafuerae	High ridges, generally growing in fernbeds	2	Skottsberg, 1921
S. mattirolii	Open stony and grassy areas, often near stream sides or glaciers	1	Jeffrey & Beentje, 2005
S. maulinus	Endemic species of the Cordillera of Talca	-	Cabrera, 1949

Species	Habitat description	Habitat category	Resource
S. meyeri-johannis	Moist peaty soil in upper moorlands, afro-alpine grasslands, seepage areas	2	Jeffrey & Beentje, 2005
S. minimus	Waste places, open forest, forest margin and clearings, occasionally in shrubland, swamps and coastal habitats, rich soils in moister sites such as beside swamps and streams, in forest and woodland	1	Webb *et al.*, 1988; Thompson, 2004a
S. mohavensis	Sandy or rocky washes, desert flats,	1	Barkley, 2006
S. montevidensis	Frequent in the dunes and sandy soils, lives on rocky ground	1	Baker, 1884; Cabrera, 1999
S. moorei	Open spaces in upland forest, glades in bamboo, heath zone, near swamps or moist sites, montane grassland	1	Jeffrey & Beentje, 2005
S. myriocephalus	Margins of *Hagenia-Schefflera* forest, *Podocarpus* forest, usually in forest clearings	1	Tadesse, 2004
S. nanus	*Erica arborea* bushland, moist high altitude grassland, especially in depression on flat, rocky places	1	Tadesse, 2004
S. nebrodensis	Rocky places	1	Chater & Walters, 2010
S. neeanus	Sajama high-Andean bunch-grassland	2	Hind, 2011
S. nemorensis	Coniferous and birch aspen forests, their edges, in pine woodlands, scrubs, meadows along edges of marshes, river banks, mountains ascending almost to the upper treeline, open places in forests	1	Shishkin, 1995; Chen *et al.*, 2011
S. neowebsteri	High talus slopes	1	Barkley, 2006
S. nivalis	-	-	-
S. niveoaureus	-	-	-
S. niveus	Stony slopes, dry river banks	1	Manning & Bruyns, 2013
S. ochrocarpus	*Juniperus* forest in moist or shaded situations, *Erica arborea* bushland below afroalpine meadows, sometimes along river banks and in open grassland on mountains	1	Tadesse, 2004
S. oederiafolius	Damp grassland	2	Goldblatt & Manning, 2000
S. oerstedianus	Open and forest slopes of the western volcanoes	1	Williams, 1976
S. olympicus	Sloping meadows	2	Matthews, 1975
S. oreophyton	Species from the high mountains of Atacama and Coquimbo and neighbouring regions	-	Cabrera, 1949
S. otophorus	In the transition from high Andean forest and wilderness	1	Silva-Moure *et al.*, 2014
S. panduriformis	Grows in scrubs on forest margins	1	Hilliard, 1977
S. patens	Wet, within the cloud forest and high Andean forest top	2	Silva-Moure *et al.*, 2014
S. paulsenii	Stony and rubbly slopes, on talus and rocks	1	Shishkin, 1995
S. perralderianus	-	-	
S. petraeus	Limestone rocks	2	Chater & Walters, 2010
S. pflanzii	-	-	-
S. pichinchensis	-	-	-
S. pindilicensis	-	-	-
S. pinnatifolius	Dry hills, coastal dunes, forest, woodland and scrubland, often at margins of rainforests, sometimes in cleared areas; rocky environments	1	The Plant Information Network System, 2014

Species	**Habitat description**	**Habitat category**	**Resource**
S. pinnulatus	Casual in fields and waste places, moist sandy slopes	1	Manning & Goldblatt, 2012
S. piptocoma	-	-	-
S. platypleurus	-	-	-
S. poeppigii	Sandy or rocky soils	1	Cabrera, 1999
S. polygaloides	Endemic species from the high mountains of central Chile and neighboring regions of Argentina	-	Cabrera, 1949
S. prenanthoides	sandy soils, scrub, woodland and forests	2	Thompson, 2004a
S. provincialis	-	-	
S. pseudoarnica	Sandy-gravelly ocean shores and upper beaches	1	Barkley, 2006; Chen *et al.*, 2011
S. pseudoorientalis	Grassy slopes, damp places, steppe, subalpine and alpine meadows,	2	Matthews, 1975, Shishkin, 1995
S. psilocarpus	Volcanic clays or peaty soils; herb-rich winter-wet swamps	1	Thompson, 2004a; Royal Botanic Gardens Melbourne, 2012
S. pubiger	Dry stony clay, often disturbed sites	1	Manning & Goldblatt, 2012
S. pudicus	Rocky, damp or drying hillsides, often coniferous and aspen woodland	1	Barkley, 2006
S. purpureus	Marshy ground by streams or in swamp edges, in ruderal sites such as road-sides and cultivation, moist slopes, esp. after fire	1	Jeffrey & Beentje, 2005; Manning & Goldblatt, 2012
S. purtschelleri	Damp sites in afro-alpine zone, usually in rock crevices or in shelter of rock, may be only flowering plant on rock screes, also in upper giant heath belt, marshy streamsides in afroalpine	1	Agnew & Agnew, 1994; Jeffrey & Beentje, 2005
S. pyrenaicus	Grassy and rocky places	1	Chater & Walters, 2010
S. qathlambanus	Damp subalpine and alpine grassland, on steep slopes and along watercourses	1	Carbutt & Edwards, 2006
S. quadridentatus	Waste places, riverbeds and other stony places, cliffs and rock outcrops, also occasional in shrubland and grassland, cleared land	1	Webb *et al.*, 1988; Thompson, 2004a
S. ragazzi	Montane grassland on sloping ground, *Erica arborea-Hagenia abyssinica* forest, bamboo thicket	2	Tadesse, 2004
S. rautanenii	-	-	-
S. reclinatus	-	-	-
S. rhammatophyllus	Moorlands with grasses and giant heath, highland forest edges and tree lines	1	Agnew & Agnew, 1994; Jeffrey & Beentje, 2005
S. roseiflorus	Giant heath and *Stoebe-Protea* zone, rocky moorland, streamsides, dried alpine zones	1	Agnew & Agnew, 1994; Jeffrey & Beentje, 2005
S. roseus	*Pinus* forest with grassland and alpine meadows and subalpine	2	García-Pérez, 1985
S. rosmarinifolius	sandy and stony slopes	1	Manning & Goldblatt, 2012
S. rufescens	-	-	-
S. rufiglandulosus	Stream sides, forest margins, shrubland, banks, cliffs and roadsides	1	Webb *et al.*, 1988
S. sabinjoensis	Heath zone, mossy crevice on bare lava slope	1	Jeffrey & Beentje, 2005
S. scaberulus	Coastal habitats, scrubland, forest margins and clearings	1	Webb *et al.*, 1988

Species	**Habitat description**	**Habitat category**	**Resource**
S. schimperi	Riverine forest, *Juniperus-Olea* forest, *Juniperus-Podocarpus* forest, low open scrub, grassland, roadside ditches, arable land, waste or fallow fields	1	Tadesse, 2004
S. schultzii	Afroalpine meadows	2	Tadesse, 2004
S. schweinfurtii	Common in disturbed places in montane and alpine grassland	1	Agnew & Agnew, 1994
S. scopolii	Dry places	2	Chater & Walters, 2010
S. selloi	Sandy or dry soils	2	Cabrera, 1999
S. seminiveus	Rounded clumbs on cliff faces or sprawled over rock sheets or in the crevices of rock sheets	1	Hilliard, 1977
S. serratifolius	in streams, amongst rock outcrops, stream margins and boggy areas	1	Cabrera, 1999
S. sinuatilobus	on the coast	1	Cabrera, 1949
S. sisymbriifolius	Shaded places among rocks	1	Manning & Bruyns, 2013
S. smithii	Moist thickets	2	Reiche, 1905
S. snowdenii	From clearings in the bamboo zone almost to the summit, in grassland or afro-alpine bushlands, moorland	1	Agnew & Agnew, 1994; Jeffrey & Beentje, 2005
S. sotikensis	Marshy ground, grassland	2	Jeffrey & Beentje, 2005
S. spartioides	Open, dry, disturbed sites, especially stream banks and hillsides	1	Barkley, 2006
S. sphaerocephalus	Open meadows, especially in coniferous associations	1	Barkley, 2006
S. squalidus	Roadsides, walls, wasteland, woodland and scrub, also on disturbed rocky ground	1	Chater & Walters, 2010
S. squarrosus	Sandy or clay soils, open forest and woodlands	1	Thompson, 2004a
S. stoechadiformis	*Abies religiosa* forest with patches of *Juniperus* scrub, Tufa hillside vegetation of open oak, in *Quercus* scrub, xeric with *Verbesina* and *Eupatorium*, preferably in areas affected by disturbance	1	García-Pérez, 1985
S. suaveolens	Rich woods, shaded, wet areas bordering streams	1	Barkley, 2006
S. subsessilis	Montane bushland, giant heath, *Hagenia* woodland/forests, bamboo, often in clearings and possibly a pioneer there, at edges of montane rain forest, remnant forests or woodland on mountain slopes, occasionally along river or stream banks, bamboo forest	1	Agnew & Agnew, 1994; Tadesse, 2004; Jeffrey & Beentje, 2005
S. superandinus	Grass páramo with *Espeletia* and some rocks	2	Ramsay, 2001
S. sylvaticus	Wood margins, disturbed ground, sandy soils; forest edges, pine woods, edges of marshes, sandbars, cut-over areas, and burned clearings in forests	1	Shishkin, 1995; Chater & Walters, 2010
S. tauricolus	Steppe, rocky slopes, scrub	1	Matthews, 1975
S. telekii	Dry stony slopes, scree, stony gravel, in rock crevices, in the lower part of its range in open giant heath, in the upper part of its range in the shelter of rocks, or even next to glacier	1	Jeffrey & Beentje, 2005
S. teneriffae	Roadsides, forest clearings	1	Gilmer & Kadereit, 1989
S. thianschanicus	Old moraines, gravel beds, scrubs, forest edges at treeline, on stony slopes, grassy slopes, open wet places, streamsides	1	Shishkin, 1995; Chen *et al.*, 2011

Species	**Habitat description**	**Habitat category**	**Resource**
S. thurifer	On the ridges, among shrubs and small trees	2	Skottsberg, 1921
S. transmarinus	Forest, moorland, *Dendrosenecio* forest, bamboo zone, floating swamp	2	Jeffrey & Beentje, 2005
S. transylvanicus	-	-	
S. trapezuntinus	Stony ground	1	Matthews, 1975
S. triangularis	Damp places, open woodlands, especially rocky stream banks in coniferous forests	1	Barkley, 2006
S. tricuspidatus	Endemic species of southern Patagonia and Tierra del Fuego	-	Cabrera, 1949
S. trifidus	SIn the high mountains of Rioja	-	Cabrera, 1949
S. trifurcatus	Moist places in the southern mountain ranges, it has been found around the meadows and along streams	1	Cabrera, 1999
S. triodon	Vegetation on rocks in forest	1	Cabrera, 1999
S. umbrosus	Forest edges in river valleys	1	Shishkin, 1995
S. unionis	Open slopes in *Erica arborea* scrubland, rocky places in afroalpine vegetation	1	Tadesse, 2004
S. urundensis	Grassland and sparsely wooded grassland, esp. where burned	1	Jeffrey & Beentje, 2005
S. vernalis	Sandy meadows, stony slopes, logged areas, scrubs, railroad embankments, field borders, waste places, fields, open habitats	1	Matthews, 1975; Shishkin, 1995; Chater & Walters, 2010
S. vestitus	Rocky sandstone slopes	1	Manning & Goldblatt, 2012
S. viridis	arid soils	2	Cabrera, 1999
S. viscosus	Coastal and river sands, railroad embankments, near dwellings, waste grounds, open sandy or gravelly habitats, rocky slopes, woodland	1	Matthews, 1975; Shishkin, 1995; Chater & Walters, 2010
S. volckmannii	Endemic species of the Cordillera of Coquimbo	-	Cabrera, 1949
S. vulgaris	Dwellings, kitchen gardens, crops, parks, railroad embankments, sandy banks of rivers and lakes, forest edges, cultivated land, wasteland, maritime sands	1	Shishkin, 1995; Chater & Walters, 2010
S. wairauensis	Stony or wet sides in open forests, forest margins and clearings, shrubland, grassland or disturbed areas	1	Webb *et al.*, 1988
S. windhoekensis	-	-	-
S. wootonii	Damp or drying sites, often in rocky, moderately disturbed sites	1	Barkley, 2006
S. x pirottae	Open stony area	1	Jeffrey & Beentje, 2005
S. zimapanicus	Gravelly soils and stream banks in pine woodlands	1	Freeman & Barkley, 1995

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Thompson, I.R. (2004b) Taxonomic studies of Australian *Senecio* (Asteraceae): 2. The shrubby, discoid species and the allied radiate species *Senecio linearifolius*. *Muelleria*, **20**, 67–110.

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Appendix S2: Additional results regarding phylogenetic reconstructions, ancestral area and habitat preference reconstructions.

TABLE S2.1: ALIGNMENT LENGTH, SUBSTITUTION MODELS AND INFORMATIVE CHARACTERS OF DNA REGIONS.

Dataset	Marker	Substitution model	# of sequenced species	Alignment length in bp (without gaps)	Excl. bases	# of variable positions/ informative characters	# of gaps/ informative gaps
Senecio (including outgroup)	ITS	GTR+G+I	258	694	0	420/303	94/34
	*trn*LF	GTR+I	125	849	0	75/39	38/14
	*ndh*F	TVM+G	111	386	0	36/11	2/1
	*trn*C-*ycf*6	F81+I+G	45	804	28	81/32	32/13
Asteraceae	*ndh*F	TVM+I+G	26	1720	0	246/90	-
	*trn*LF		28	823	0	190/70	-
	*rbc*L		21	1432	0	192/74	-

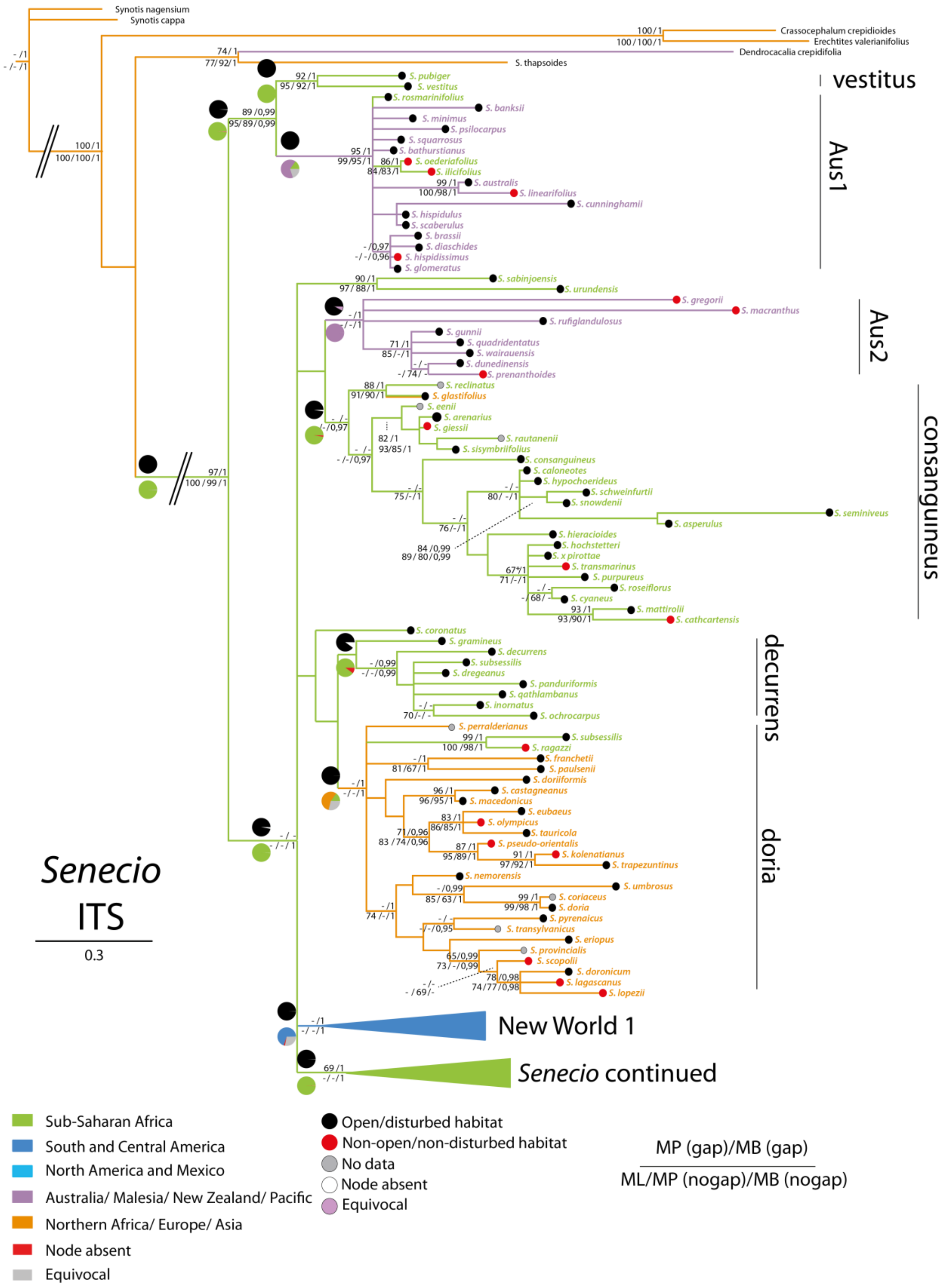
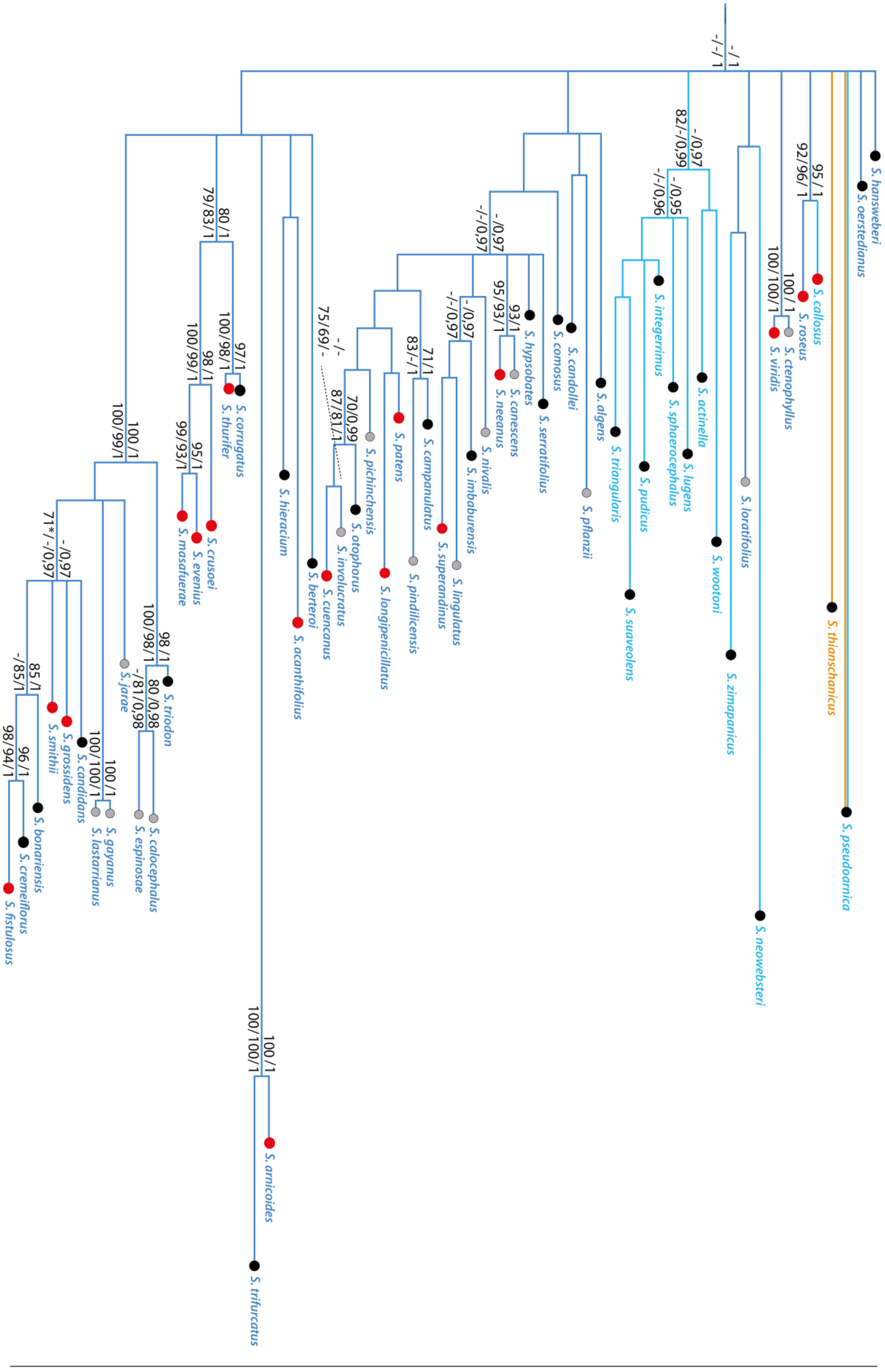
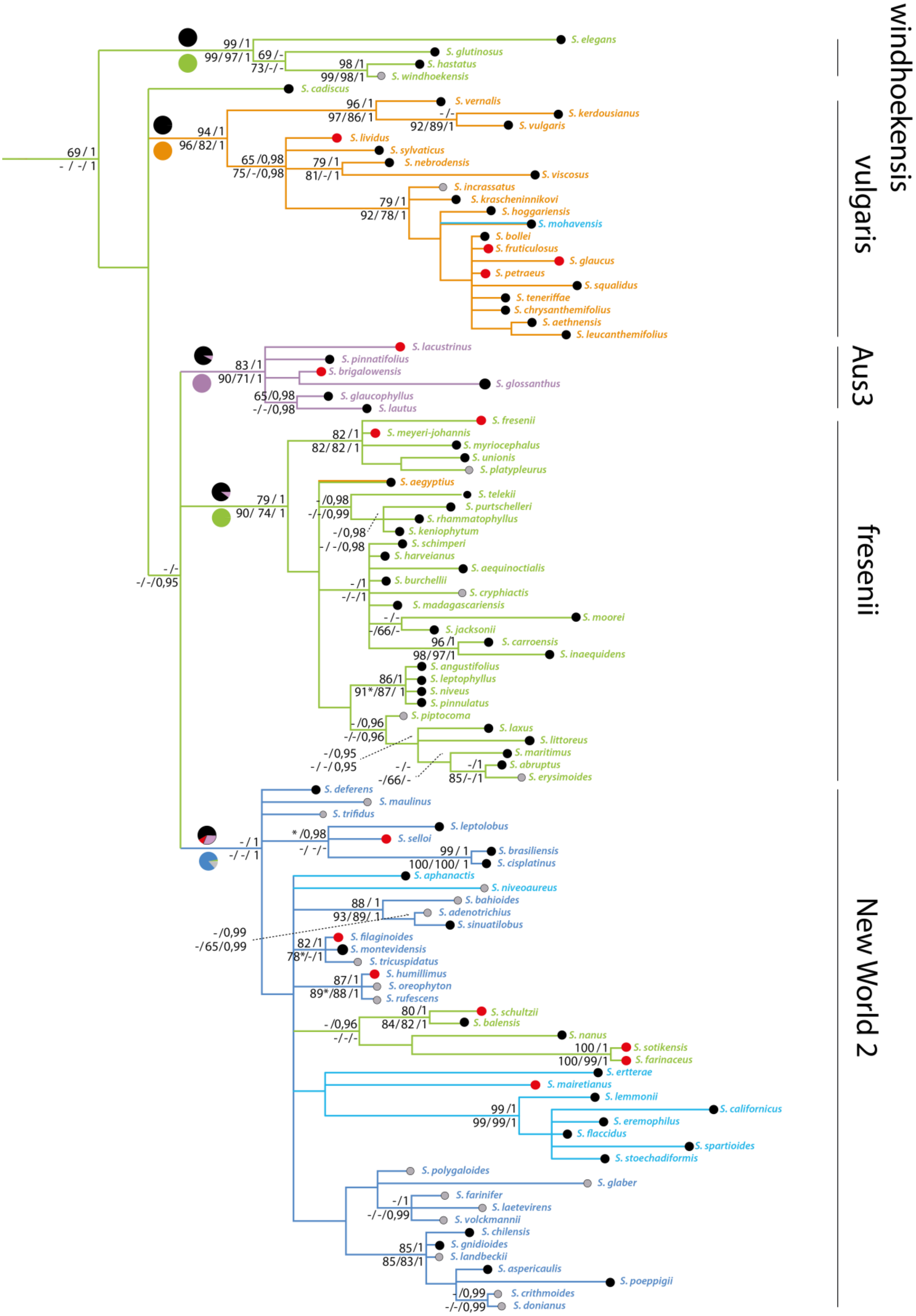


Figure S2.2: Phylogenetic reconstruction of *Senecio* based on nr ITS majority rule consensus tree, calculated with MrBayes. Support values for Maximum Parsimony (MP; >65) and Bayesian statistics using MrBayes (MB; >0.95) with gap coding are shown above and values for Maximum Likelihood (ML; >70), MP and MB without gap coding below branches. Asterisk mark minor differences between support values inside clades resulting from different analyses. Biogeographic reconstruction is shown along branches and underneath nodes and habitat preferences are marked with circles at tips and are shown above nodes. Figure continued on next two pages.


-/-/1
- /1
S. hansweberi
S. oerstedianus
S. pseudoarnica
S. thianschanicus
95/1
92/96/1
S. callosus
S. roseus
100/1
100/100/1
S. ctenophyllus
S. viridis
S. loratifolius
S. zimapanicus
S. neowebsteri
-/0,97
82/-/0,99
S. actinella
S. wootoni
-/0,95
-/-/0,96
S. lugens
S. sphaerocephalus
S. integerrimus
S. pudicus
S. suaveolens
S. triangularis
S. algens
S. candollei
S. pflanzii
S. comosus
-/0,97
-/-/0,97
S. serratifolius
S. hypsobates
93/1
95/93/1
S. canescens
S. neeanus
S. nivalis
-/0,97
-/-/0,97
S. imbaburensis
S. lingulatus
S. superandinus
71/1
83/-/1
S. campanulatus
S. pindilicensis
S. patens
S. longipenicillatus
S. pichinchensis
70/0,99
87/81/1
-/-
75/69/-
S. otophorus
S. involucratus
S. cuencanus
S. hieracium
S. berteroi
S. acanthifolius
80/1
79/83/1
97/1
100/98/1
S. corrugatus
S. thurifer
98/1
100/99/1
S. crusoei
95/1
99/93/1
S. evenius
S. masafuerae
100/1
100/99/1
98/1
100/98/1
S. triodon
80/0,98
-/81/0,98
S. calocephalus
S. espinosae
S. jarae
100/1
100/100/1
S. gayanus
S. lastarrianus
S. candidans
-/0,97
71*/-/0,97
S. grossidens
S. smithii
85/1
-/85/1
S. bonariensis
96/1
98/94/1
S. cremeiflorus
S. fistulosus
100/1
100/100/1
S. arnicoides
S. trifurcatus

New World 1


windhoekensis
vulgaris
Aus3
fresenii
New World 2
69 / 1
- / -/ 1
99 / 1
99/ 97/ 1
S. elegans
69 /-
73/-/ -
S. glutinosus
98 /1
99/ 98/1
S. hastatus
S. windhoekensis
S. cadiscus
94 / 1
96/ 82/ 1
96 / 1
97/ 86/ 1
S. vernalis
- /-
92/ 89/1
S. kerdousianus
S. vulgaris
65 /0,98
75/-/0,98
S. lividus
S. sylvaticus
79 / 1
81/-/ 1
S. nebrodensis
S. viscosus
79 / 1
92/ 78/ 1
S. incrassatus
S. krascheninnikovi
S. hoggariensis
S. mohavensis
S. bollei
S. fruticulosus
S. glaucus
S. petraeus
S. squalidus
S. teneriffae
S. chrysanthemifolius
S. aethnensis
S. leucanthemifolius
83 / 1
90/71/ 1
S. lacustrinus
S. pinnatifolius
S. brigalowensis
S. glossanthus
65/0,98
-/-/0,98
S. glaucophyllus
S. lautus
- /-
-/-/0,95
79 / 1
90/ 74/ 1
82 / 1
82/ 82 / 1
S. fresenii
S. meyeri-johannis
S. myriocephalus
S. unionis
S. platypleurus
S. aegyptius
- /0,98
-/-/0,99
S. telekii
S. purtschelleri
S. rhammatophyllus
-/0,98
S. keniophytum
- / -/0,98
S. schimperi
S. harveianus
S. aequinoctialis
- /1
-/-/1
S. burchellii
S. cryphiactis
S. madagascariensis
- /-
-/66/-
S. moorei
S. jacksonii
96 /1
98/ 97/1
S. carroensis
S. inaequidens
86/1
91*/87/ 1
S. angustifolius
S. leptophyllus
S. niveus
S. pinnulatus
- /0,96
-/-/0,96
S. piptocoma
S. laxus
S. littoreus
-/0,95
-/ -/ 0,95
S. maritimus
- /-
-/66/ -
-/1
85/-/1
S. abruptus
S. erysimoides
- / 1
-/ -/ 1
S. deferens
S. maulinus
S. trifidus
* /0,98
-/ -/-
S. leptolobus
S. selloi
99 / 1
100/ 100/ 1
S. brasiliensis
S. cisplatinus
S. aphanactis
S. niveoaureus
88 / 1
93/ 89/ 1
S. bahioides
S. adenotrichius
S. sinuatilobus
- /0,99
-/65/0,99
82 /1
78*/-/1
S. filaginoides
S. montevidensis
S. tricuspidatus
87/1
89*/88 /1
S. humillimus
S. oreophyton
S. rufescens
- /0,96
-/-/-
80 /1
84/ 82 /1
S. schultzii
S. balensis
S. nanus
100 / 1
100/ 99/1
S. sotikensis
S. farinaceus
S. ertterae
S. mairetianus
99 /1
99/ 99/1
S. lemmonii
S. californicus
S. eremophilus
S. flaccidus
S. spartioides
S. stoechadiformis
S. polygaloides
S. glaber
-/1
-/-/0,99
S. farinifer
S. laetevirens
S. volckmannii
S. chilensis
85/1
85/83/1
S. gnidioides
S. landbeckii
S. aspericaulis
S. poeppigii
- /0,99
-/-/0,99
S. crithmoides
S. donianus

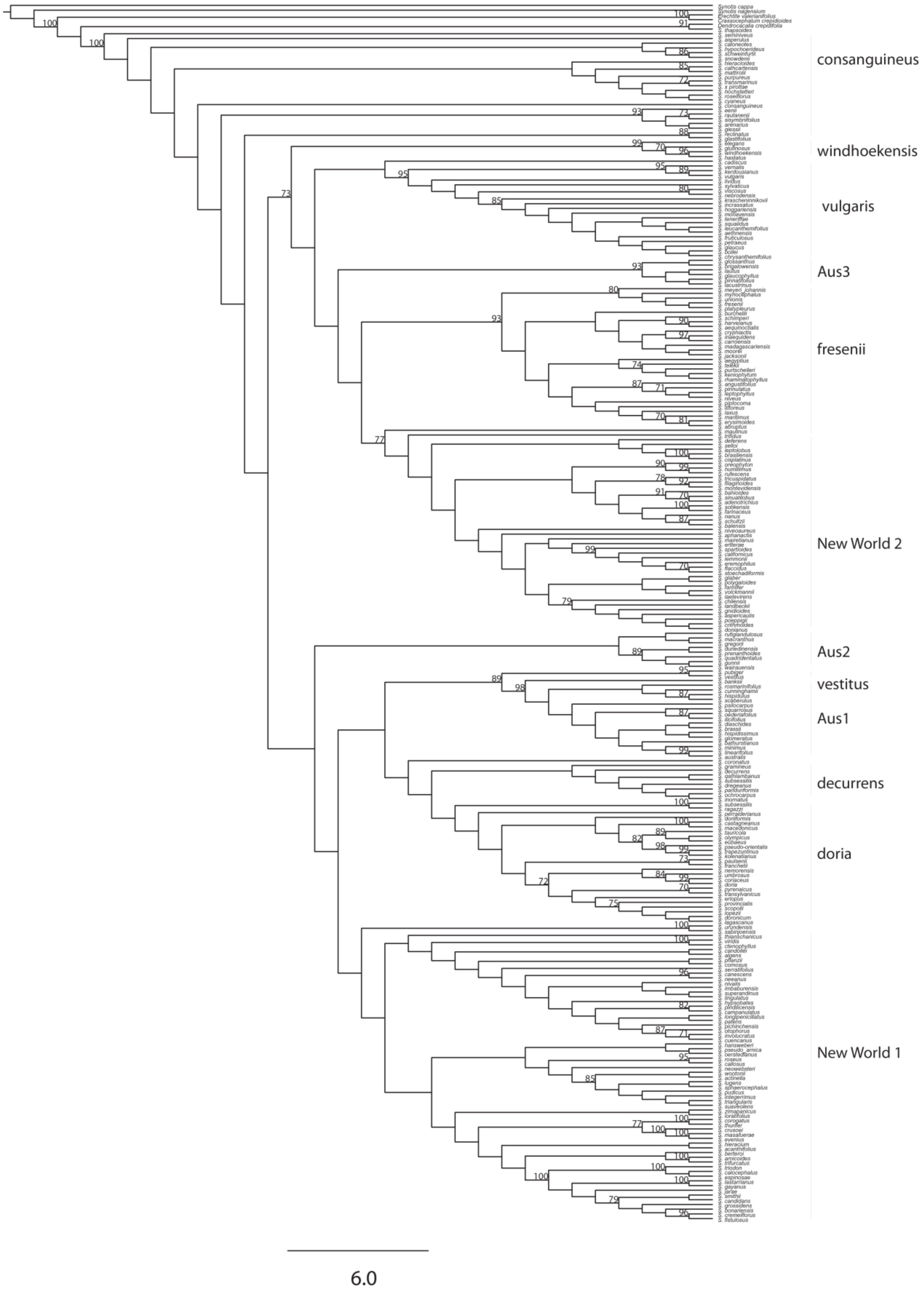


FIGURE S2.3: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON THE ITS MAJORITY RULE CONSENSUS TREE. RUN ON CIPRES USING RAxML XSEDE. SUPPORT VALUES OF MAXIMUM LIKELIHOOD BOOTSTRAP VALUES >70 ARE SHOWN.

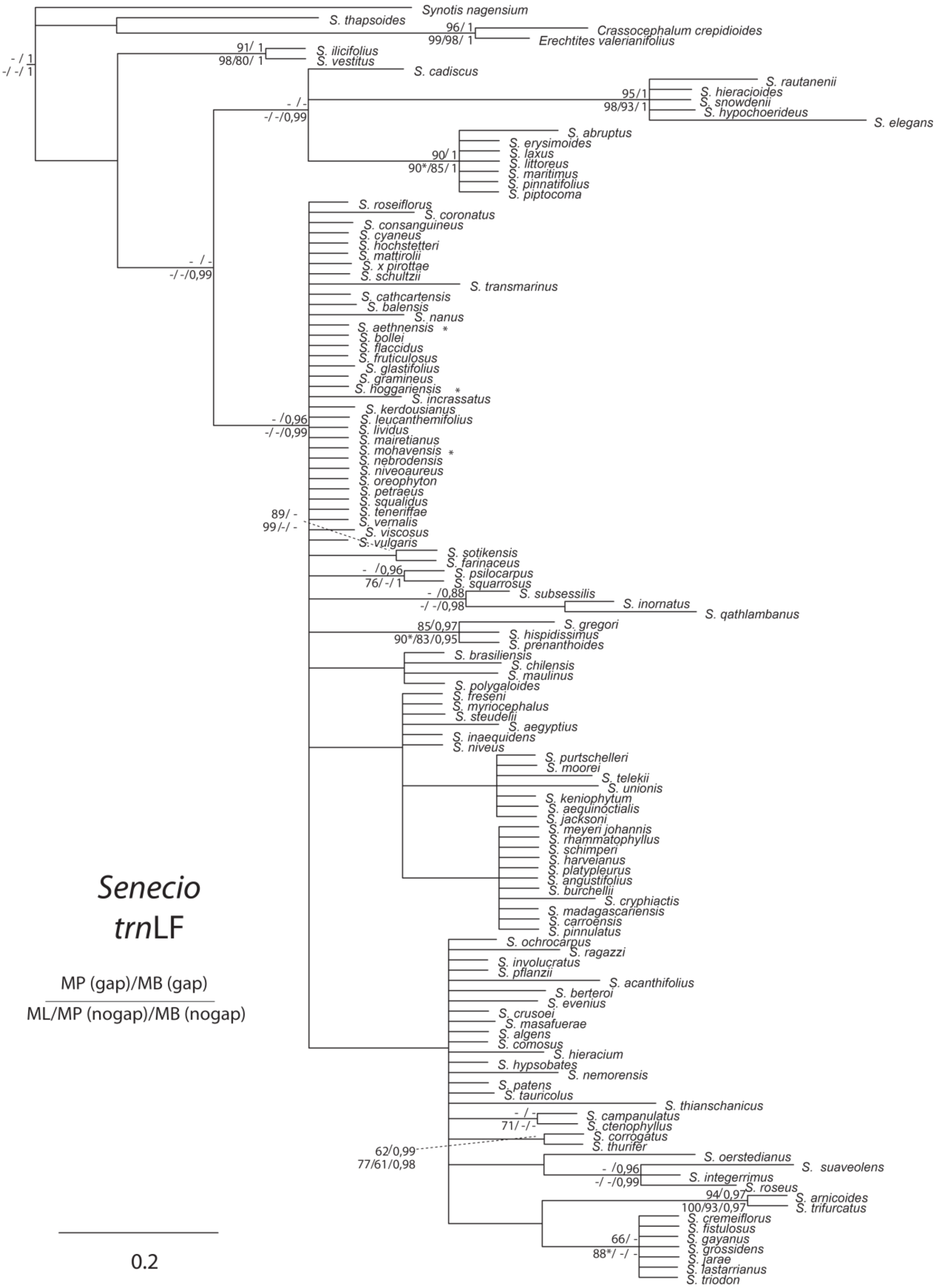


FIGURE S2.4: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON *TRN*LF MAJORITY RULE CONSENSUS TREE, CALCULATED WITH MRBAYES. SUPPORT VALUES FOR MAXIMUM PARSIMONY (MP; >65) AND BAYESIAN STATISTICS USING MRBAYES (MB; >0.95) WITH GAP CODING ARE SHOWN ABOVE AND VALUES FOR MAXIMUM LIKELIHOOD (ML; >70), MP AND MB WITHOUT GAP CODING BELOW BRANCHES. ASTERISKS MARK MINOR DIFFERENCES BETWEEN SUPPORT VALUES INSIDE CLADES RESULTING FROM DIFFERENT ANALYSES.

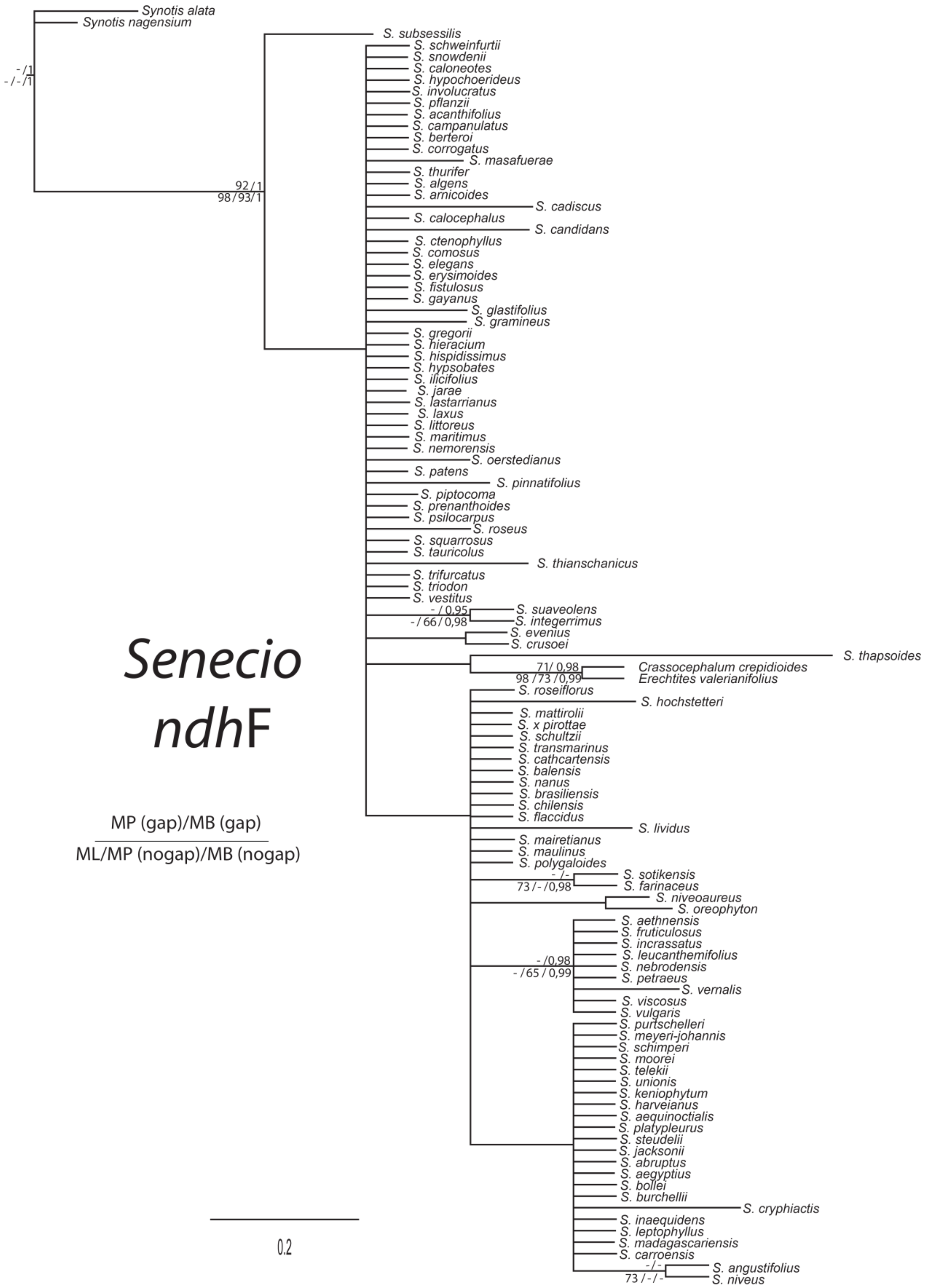


Figure S2.5: Phylogenetic reconstruction of *Senecio* based on *ndh*F majority rule consensus tree, calculated with MrBayes. Support values for Maximum Parsimony (MP; >65) and Bayesian statistics using MrBayes (MB; >0.95) with gap coding are shown above and values for Maximum Likelihood (ML; >70), MP and MB without gap coding below branches.

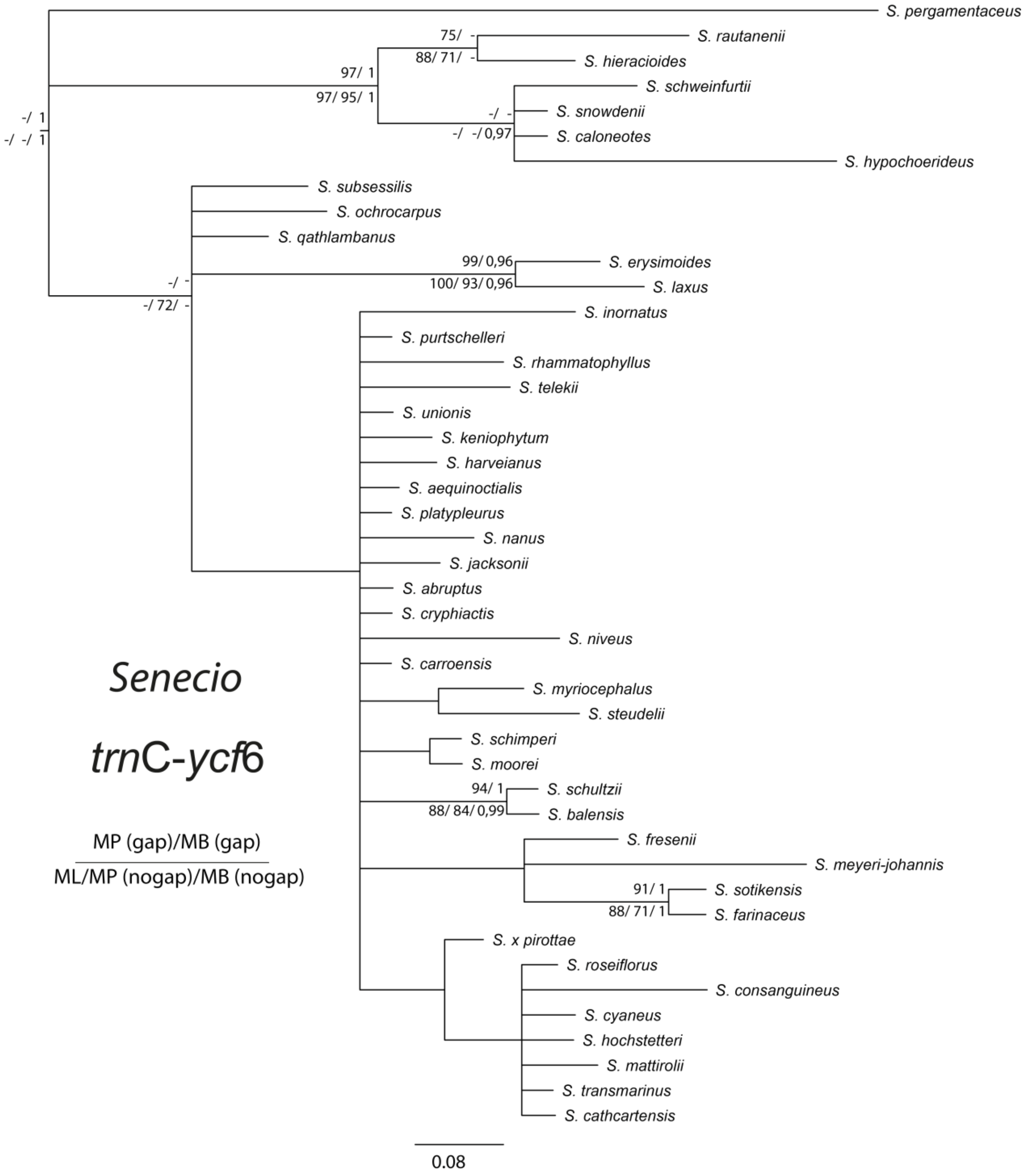


FIGURE S2.6: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON *TRN*C-*YCF*6 MAJORITY RULE CONSENSUS TREE, CALCULATED WITH MRBAYES. SUPPORT VALUES FOR MAXIMUM PARSIMONY (MP; >65) AND BAYESIAN STATISTICS USING MRBAYES (MB; >0.95) WITH GAP CODING ARE SHOWN ABOVE AND VALUES FOR MAXIMUM LIKELIHOOD (ML; >70), MP AND MB WITHOUT GAP CODING BELOW BRANCHES.

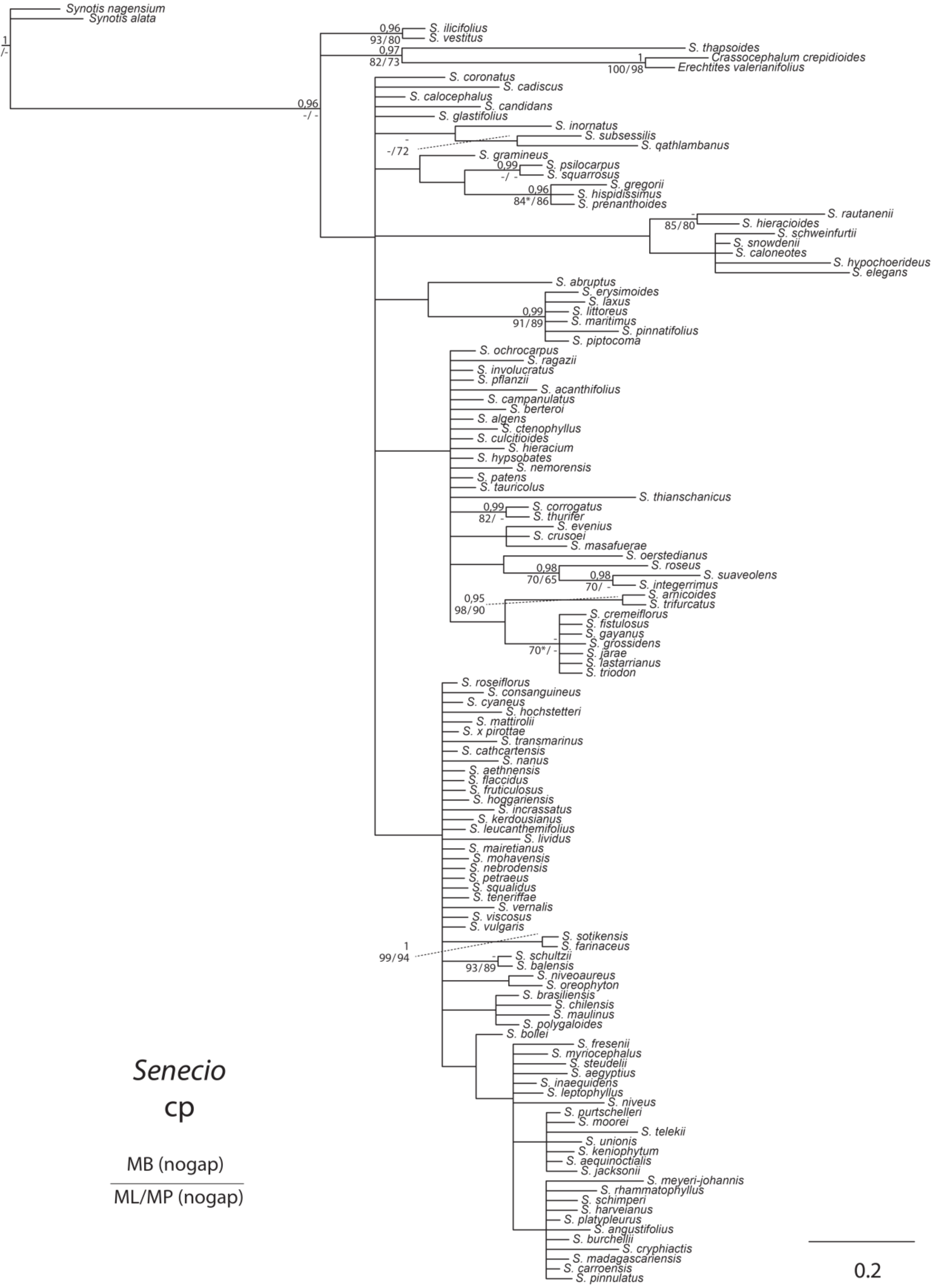


FIGURE S2.7: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON THE COMBINED CHLOROPLAST MAJORITY RULE CONSENSUS TREE, CALCULATED WITH MRBAYES. SUPPORT VALUES FOR MAXIMUM PARSIMONY (MP; >65) AND BAYESIAN STATISTICS USING MRBAYES (MB; >0.95) WITH GAP CODING ARE SHOWN ABOVE AND VALUES FOR MAXIMUM LIKELIHOOD (ML; >70), MP AND MB WITHOUT GAP CODING BELOW BRANCHES.

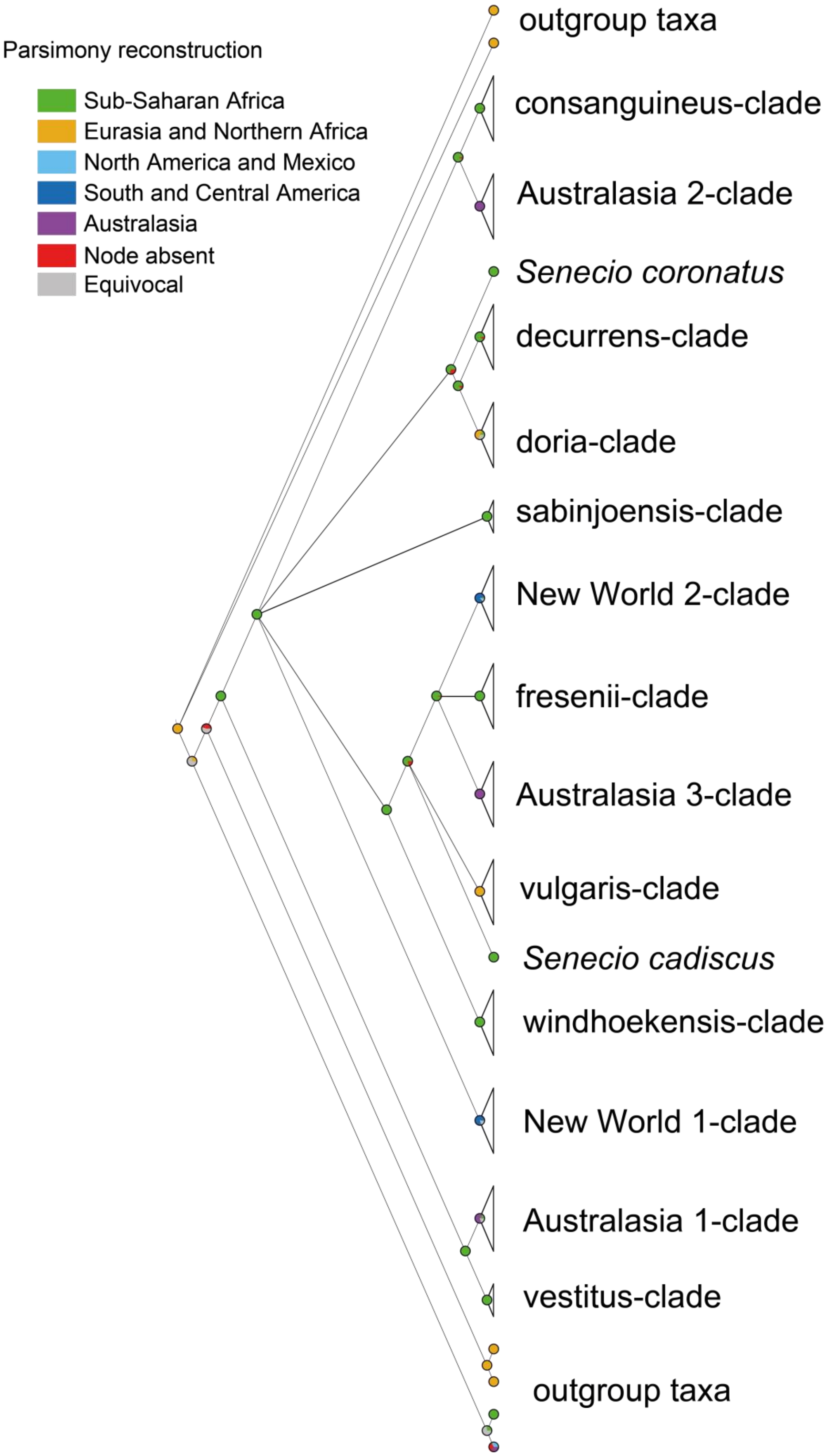


FIGURE S2.8: ANCESTRAL AREA RECONSTRUCTION MAPPED ONTO THE BAYESIAN ITS MAJORITY RULE CONSENSUS TREE OF *SENECIO* CALCULATED WITHOUT GAP CODING. RECONSTRUCTION IS BASED ON 1951 TREES OF THE MRBAYES ITS RECONSTRUCTION. FOR CLARITY ONLY MAJOR CLADES ARE SHOWN.

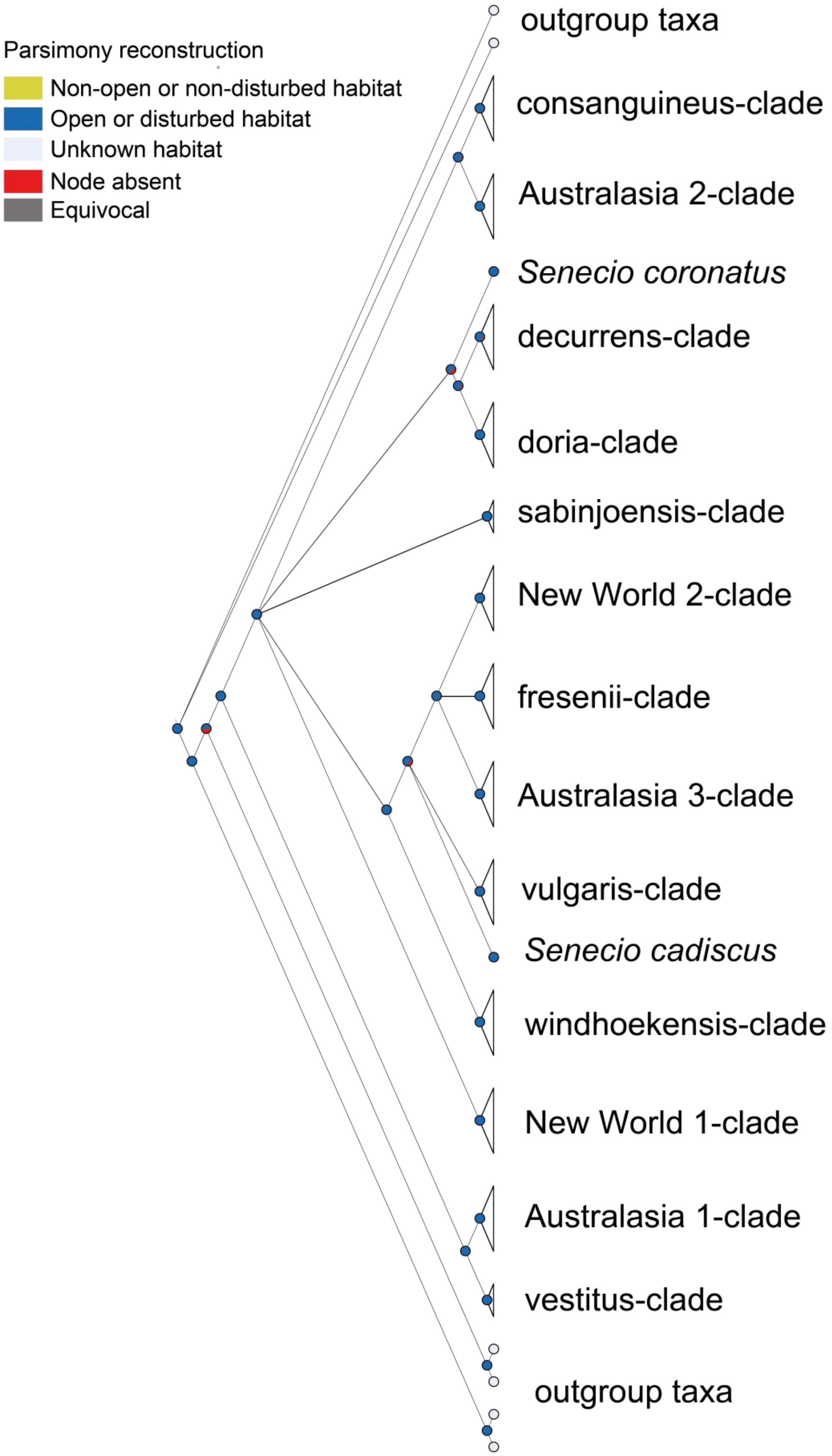


FIGURE S2.9: HABITAT RECONSTRUCTION MAPPED ONTO THE BAYESIAN ITS MAJORITY RULE CONSENSUS TREE CALCULATED WITHOUT GAP CODING OF *SENECIO*. RECONSTRUCTION IS BASED ON 1951 TREES OF THE MRBAYES ITS RECONSTRUCTION. FOR CLARITY ONLY MAJOR CLADES ARE SHOWN.

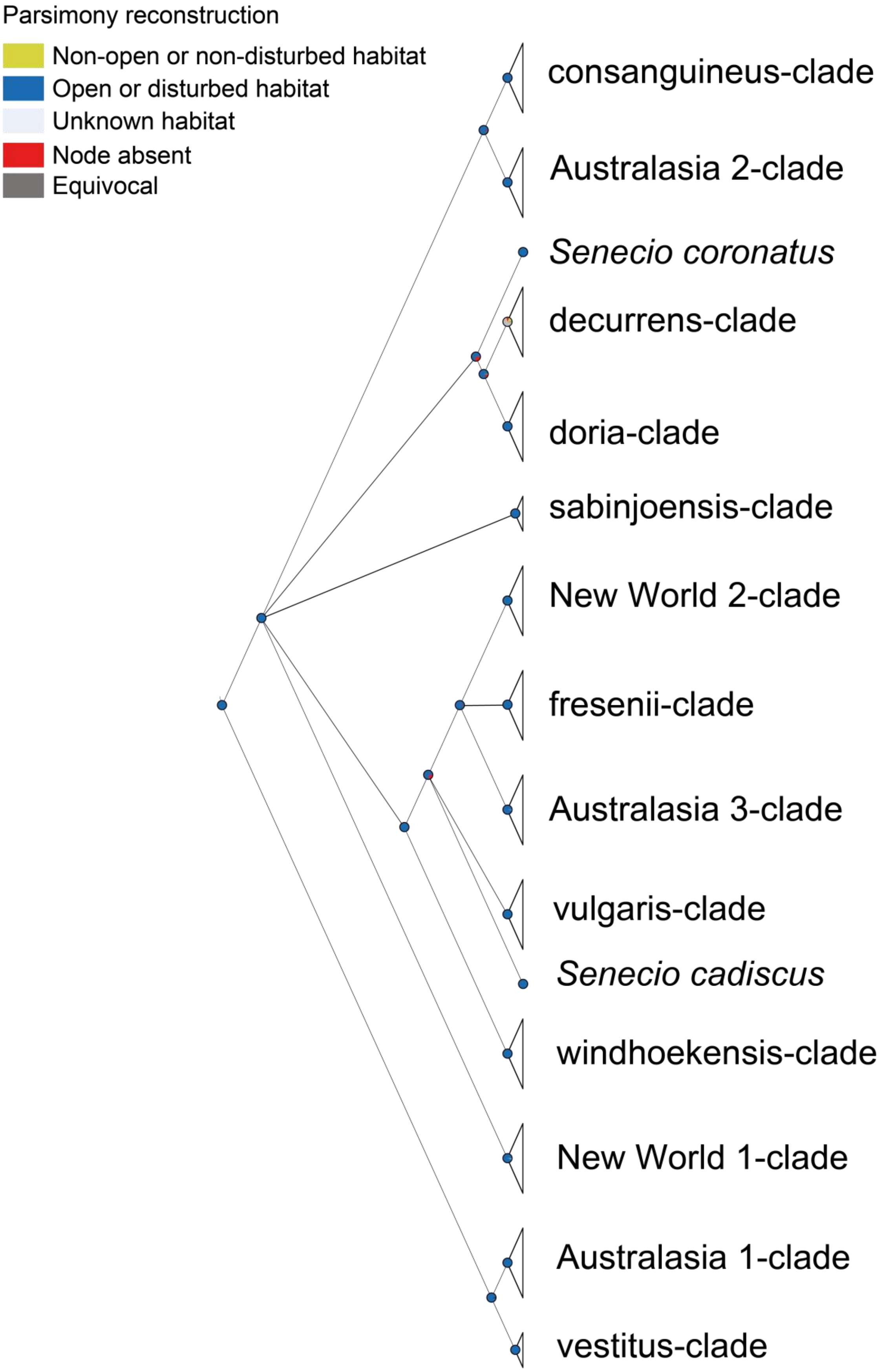


FIGURE S2.10: RESHUFFLED STATES OF HABITAT RECONSTRUCTION MAPPED ONTO THE BAYESIAN ITS MAJORITY RULE CONSENSUS TREE CALCULATED WITHOUT GAP CODING OF *SENECIO*. RECONSTRUCTION IS BASED ON 1951 TREES OF THE MRBAYES ITS RECONSTRUCTION. FOR CLARITY ONLY MAJOR CLADES ARE SHOWN.

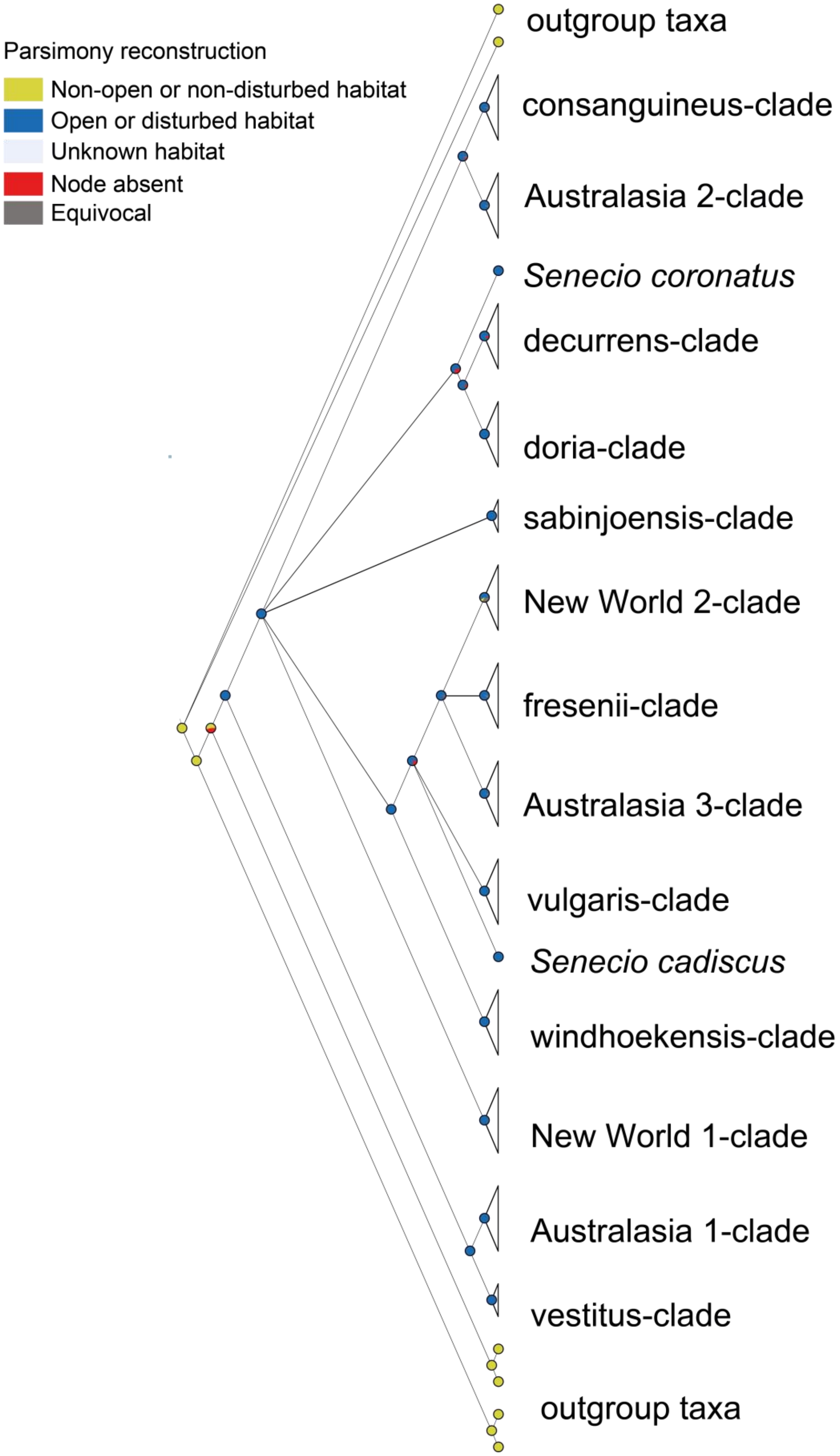


FIGURE S2.11: HABITAT RECONSTRUCTION WITH UNKNOWN HABITAT PREFERENCES CODED AS NON-OPEN/NON-DISTURBED MAPPED ONTO THE BAYESIAN ITS MAJORITY RULE CONSENSUS TREE CALCULATED WITHOUT GAP CODING OF *SENECIO*. RECONSTRUCTION IS BASED ON 1951 TREES OF THE MRBAYES ITS RECONSTRUCTION. FOR CLARITY ONLY MAJOR CLADES ARE SHOWN.

3. Colonization of the Palaearctic by *Senecio* from southern Africa: historical biogeography, ecology and life cycle evolution

Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Abstract

Aim Investigation of the origin of *Senecio* and the colonization of the Palaearctic including the relationship of ecology and life cycle in the source area and the colonized area.

Location Worldwide with a focus on the Afrotropic ecozone and the Palaearctic.

Methods Sampling focused on adding species from the Afrotropic to existing datasets of *Senecio*. Two nuclear markers (internal and external transcribed spacer) as well as three chloroplast markers (*trn*L, *trn*L-*trn*F and *trn*C-*ycf*6) were amplified and sequenced. Maximum Likelihood and Bayesian statistics were used to infer phylogeny, divergence times, biogeographic history and life cycle evolution.

Results *Senecio* originated most likely during the Mid to Late Miocene in western southern Africa (WSA). In the Palaearctic, *Senecio* seems to have established first in the Mediterranean winter rainfall or dry areas before colonizing other regions. Colonization of the Palaearctic probably took place via two different routes. One lineage of mostly annual lowland species seems to have dispersed directly from WSA, while the other lineage of perennial mountain species is more likely to have migrated to the Palaearctic via eastern sub-Saharan Africa.

Main conclusions *Senecio* evolved in arid or semi-arid regions in WSA during a period of ongoing aridification and broad scale biome changes at the onset of a winter rainfall regime in the Greater Cape Floristic Region. Differences in life cycle seem to be related to adaptation to different habitats in different parts of southern Africa, and probably enabled *Senecio* to colonize the Palaearctic via two different pathways.

Introduction

The southernmost tip of Africa, the so-called Cape Floristic region (CFR; Goldblatt, 1978), is known for its floristic diversity in terms of species numbers and endemism (Goldblatt & Manning, 2002; Linder, 2003; Manning & Goldblatt, 2012a). The concept of the CFR was expanded to the Greater Cape Floristic Region (GCFR), which comprises the entire winter rainfall region of southern Africa, i.e. the CFR and the Succulent Karoo (Born *et al.*, 2007; Snijman, 2013). The climate of this region can be considered as seasonal and temperate (Manning & Goldblatt, 2012a): The winters are mild and wet, while the summers are warm to hot and dry. This is different from the remaining parts of southern Africa, which mainly have a summer rainfall regime, so that the GCFR is ecologically distinct (Linder, 2003).

A large proportion of the species diversity in the CFR belongs to only a few lineages that are either part of the ‘largest Cape genera’ (LCG) and/or of the ‘Cape floral clades’ (CFC; Goldblatt & Manning, 2002; Linder, 2003). These two groups are partially overlapping. The CFC are lineages that originated in the CFR and have their highest species richness there. About 30 CFC account for 50 % of the species richness in the CFR (Linder, 2003), but contain only few species distributed elsewhere, especially in the mountainous Drakensberg area in the eastern part of southern Africa. Often only a few isolated species/populations of the CFC are distributed further north, mainly in the temperate regions of the East and West African mountains (Linder, 2003), and almost none contains species in the Northern Hemisphere. The LCG are the most species-rich genera of the CFR, and the 20 LCG account for about 30 % of all species of the CFR (Goldblatt & Manning, 2002; Manning & Goldblatt, 2012a). In contrast to the CFC, the LCG also contain groups that are more species-rich outside the CFR and contain species in the Northern Hemisphere (Manning & Goldblatt, 2012a). Only five of the LCG do not belong to the CFC.

The CFC and also the more widely distributed LCG have undergone fine scale niche evolution in the GCFR while showing niche conservatism at a broader scale by being mostly restricted to temperate regions or to winter rainfall areas (van der Niet & Johnson, 2009; Warren *et al.*, 2011; Schnitzler *et al.*, 2012). According to the hypothesis of niche conservatism, closely related species tend to occupy similar habitats because of non-lability of their inherited niche dimensions (Wiens, 2004). Donoghue (2008) summarized the typical response of lineages to changing environments, as ’it is easier to move than to evolve until it is not’. This phenomenon, if true, is probably explained by the fact that organisms find it difficult to simultaneously adapt to changes in too many dimensions of a niche especially when they never had contact with the new niche dimensions before (Edwards & Donoghue, 2013).

In general, colonization of the Palaearctic by southern African lineages has been suggested to have occurred through dispersal (Coleman *et al.*, 2003) or via two different migration corridors, i.e., a high altitude and an arid corridor (Balinsky, 1962; Verdcourt, 1969). Support for the high altitude corridor comes from distribution data of many taxa, such as *Protea* L. or *Moraea* Mill. that occur in the GCFR as well as throughout sub-Saharan Africa in cool montane environments (Carbutt & Edwards, 2001; Goldblatt *et al.*, 2002). Support for the arid corridor comes mostly from groups found in arid or winter rainfall areas in southern Africa and arid regions in northeast Africa (del Hoyo *et al.*, 2009; Bellstedt *et al.*, 2012).

Senecio L. (Asteraceae) is amongst the LCG (Goldblatt, 1978; Manning & Goldblatt, 2012a) even when considering that the genus is not monophyletic in its traditional circumscription (e.g. Pelser *et al.*, 2007). Our study focuses on *Senecio* (as defined by Pelser *et al.*, 2007), a genus with about 1000 species with an almost cosmopolitan distribution and with two diversity centres, sub-Saharan Africa and South America (Mabberley, 2008). In Africa, the genus is well represented in the GCFR and mountainous regions of South and East Africa (Hilliard, 1977; Cowling, 1999; Tadesse, 2004; Jeffrey & Beentje, 2005; Manning & Goldblatt, 2012b; Snijman, 2013), similar to many CFC, but is also present in North Africa and Eurasia. It has been shown that *Senecio* is of sub-Saharan origin (Pelser *et al.*, 2007). Timonin *et al.* (2015) proposed an origin in the arid regions of southern Africa, but without using formal methods of biogeographic reconstruction. Although *Senecio* is not a CFC sensu Linder (2003), as worldwide species richness is higher outside the CFR, the genus is well suited to study the floristic connections between the Afrotropic and Palaearctic (Fig. 1): *Senecio* is a species-rich genus in the CFR, occurs in the East African mountains, which constitutes a potential migration corridor to the Palaearctic, and is well represented in the Palaearctic, which was colonized twice independently according to Pelser *et al.* (2007).

Our aims were to identify the subregion of sub-Saharan Africa where *Senecio* originated and to infer the route(s) of colonization of the Palaearctic. We assessed whether Palaearctic lineages originated from the same or different regions, and whether the ecology of those lineages in the Palaearctic reflects their ecology in their source region(s). To address these questions we used phylogenetic inference methods based on extended sampling of nuclear ribosomal (nr) and chloroplast (cp) markers.

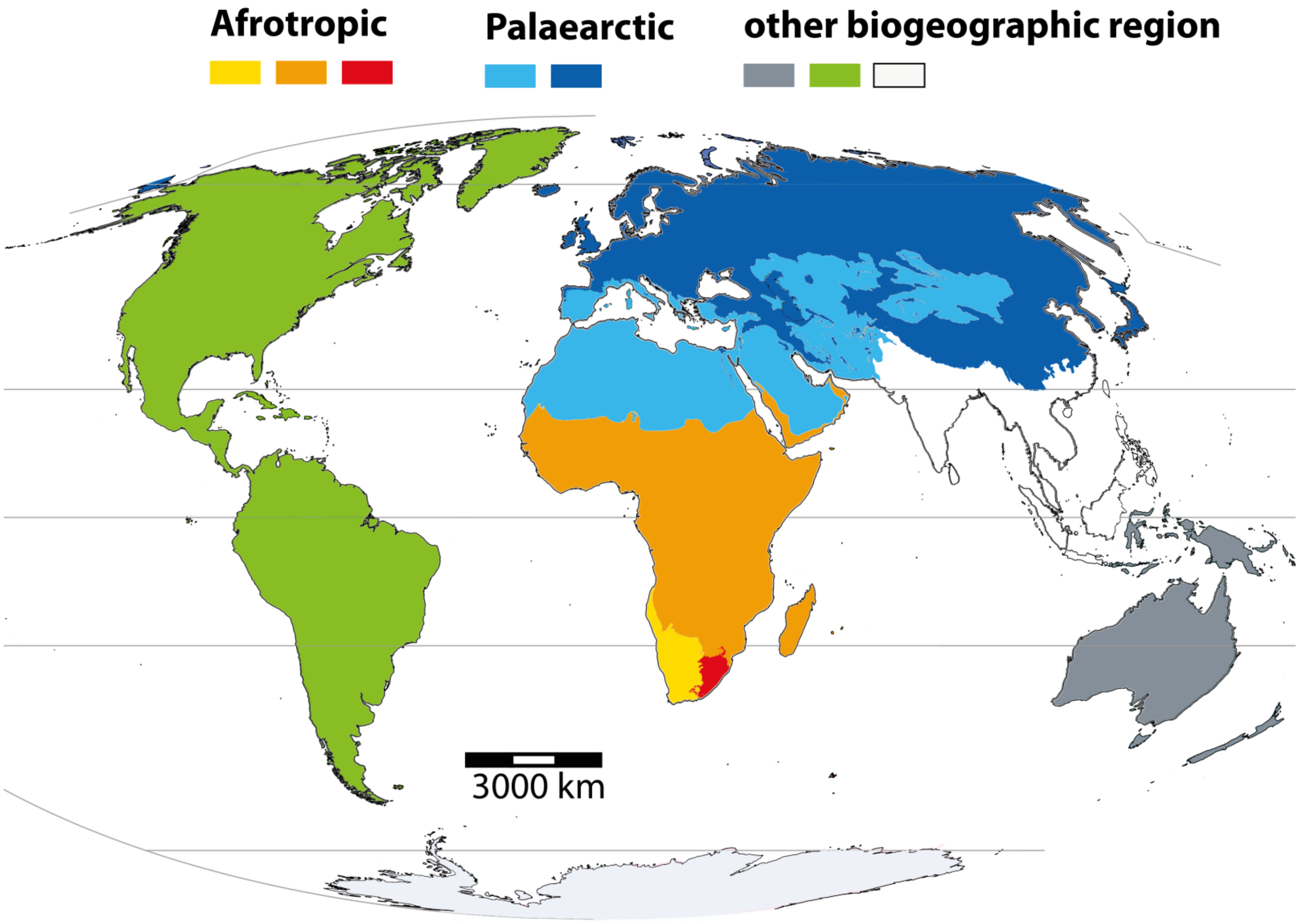


Figure 1: Biogeographical regions used in this study. Regions of the Afrotropic: orange – tropical and subtropical regions, yellow –dry and winterrainfall regions of western southern Africa (WSA), red – temperate montane areas of eastern southern Africa (ESA). Regions of the Palaearctic: dark blue – temperate and boreal regions, light blue – dry and winter rainfall areas. Other biogeographic regions: green – New World and grey – Australasia. No colour: no sample from the region included in the dataset.

Material and Methods

Taxon Sampling, DNA extraction, PCR amplification and sequencing

Previous sampling of *Senecio* focused either on sections of the genus (Calvo *et al.*, 2013) or on representing its entire distribution range (Pelser *et al.*, 2007). We focused on species from the Afrotropic ecozone (Fig. 1; sub-Saharan Africa including temperate southern Africa, southern and eastern fringes of the Arabian Peninsula and Madagascar) and the Palaearctic (Europe, Asia north of the Himalaya foothills, northern Africa, and the northern and central parts of the Arabian Peninsula). Mostly the species of one clade occur in a single ecozone, with the exception of a few species and South and North American species are placed together (Pelser *et al.*, 2007). We represented non-Afrotropic and non-Palaearctic clades with fewer placeholder species. In total, our sample includes 31 species occurring exclusively in eastern southern Africa (roughly the Drakensberg area), 24 from western southern Africa, 13 East African species, and 21 species occurring in at least two of these three regions (in total about 25 % of all sub-Saharan African species described as *Senecio*). Furthermore, 45 Palaearctic species are included, while Australasia is represented by six and the New World by 12 species only.

For newly sampled species, we extracted total genomic DNA from herbarium material (Appendix S1.1 in Supporting Information) and amplified the nr internal transcribed spacer (ITS) and external transcribed spacer (ETS) and the cp regions of *trn*LF (*trn*L intron and *trn*L-*trn*F spacer) and the *trn*C-*ycf*6 spacer (Appendix S1.1) using standard protocols for amplification and Sanger sequencing (for details Appendix S1.2). Previously published sequences of ITS, ETS and *trn*LF of *Senecio* species and close relatives were obtained from GenBank (Appendix S1.3). More cp markers are available in GenBank, but they did not contribute to phylogenetic resolution in the genus and were therefore not included in our analyses.

DNA sequence alignment and phylogenetic reconstruction

Two different datasets were created: 1) a *Senecio* dataset using the nr ITS and ETS regions with an emphasis on Afrotropic and Palaearctic species and 2) a *Senecio* dataset of cp markers (*trn*LF and *trn*C-*ycf*6). Individual gene trees were assessed manually for incidences of supported topological conflict (Bayesian Inference [BI] support: >0.95 Posterior Probability [PP]; Maximum Likelihood [ML]: >70 % bootstrap support [BS]). Our choice of outgroup, selection of substitution models and partitions as well as gap coding are described in Appendix S1.2.

Phylogenetic analyses were carried out on CIPRES (Miller *et al.*, 2010) using ML (RAxML v. 8.0.24 Blackbox implementation [Stamatakis, 2006]) and BI (MrBayes v. 3.2.1 [Ronquist *et al.*, 2012]). Under ML, the alignment was partitioned and substitution models were adjusted to the inferred best model (Appendix S2.1). Under BI, substitution models were adjusted to the inferred best model, running two independent runs, sampling every 1000th generation; with the length of the runs adapted to ensure that effective sampling sizes for parameters were >200 (estimated using TRACER v. 1.5; Rambaut & Drummond, 2007). After removing a burn-in of 10 %, the results of the two independent runs were combined.

Very few supported conflicts were identified between nr and cp phylogenies (Appendix S1.4). Combining the nr and cp datasets after removing those taxa resulted in a decrease of supported nodes found in the nr phylogeny. Therefore, we based further analyses on the better resolved and supported nr tree.

Ancestral area reconstruction

Ancestral area reconstruction was carried out using LAGRANGE v. 20130526 (Ree & Smith, 2008) as well as Bayesian Binary MCMC (BBM; modified from source code of MRBAYES 3.1.2 and implemented in RASP 3.02 [Yu *et al.*, 2015]). The reconstruction is based on a calibrated nr phylogeny, the dating methods are provided in Appendix S1.5. Geographical species distribution was scored according to Floras, previous publications and online resources (Appendix S1.6) as the sampling locality was often not specified for sequences from GenBank including the respective publications. The subdivision of the Afrotropic and Palaearctic (Fig. 1) is based on the biome distribution map by Olson *et al.* (2001). The Afrotropic biogeographic realm was divided into three regions: (1) dry and winter rainfall areas in western southern Africa (WSA), (2) eastern southern Africa including mostly temperate montane areas (ESA) and (3) tropical and subtropical Africa and Madagascar. The Palaearctic was divided into (1) dry and winter rainfall areas (including the Canary Islands) and (2) temperate and boreal regions. Furthermore, we coded Australasia (including Australia, Malesia, New Zealand and the Pacific) and the New World. Widespread species were coded as multistate. The outgroup taxa were scored as afrotropical on the basis of the reconstruction by Pelser *et al.* (2007).

In LAGRANGE, we used an iterative approach to test different assumptions by comparing the likelihood of two scenarios and using the model with the higher likelihood to test a new assumption (Tab. 1, matrices of the different assumption are provided in Appendix S1.8). In BBM the maximum area was set to two, the state frequencies were estimated and the other settings left as default.

Table 1: Tabular representation of the different assumptions that were compared for the biogeographic reconstruction in LAGRANGE. We compared two different assumptions and the one with the better likelihood was then compared to a new assumption. Ln(Likelihood)-values of the different assumptions are given at the end of each cell.

Constraint	Assumption 1	Assumption 2
Max area	Maximum polymorphic ancestral area is 3 (-310.9)	Maximum polymorphic ancestral area is 2 (-305.9)
Range	All ranges allowed (-305.9)	Ranges coupling two non-afrotropical areas is not allowed with the exception of the two Palaearctic regions (-298.7)
Dispersal	All dispersal equally likely (1.0; -298.7)	Dispersal within continents more likely (1.0) than between continents (0.5; -283.6)
Dispersal	Dispersal within continents more likely (1.0) than between (0.5; -283.6)	Dispersal between adjacent regions (tropical/ subtropical region to Palaearctic) is as likely as dispersal within a continent (1.0; -281.1)
Dispersal	Long distance dispersals are all equally likely (0.5; -281.1)	Dispersal from the Afrotropics to anywhere outside the Afrotropics is more likely (0.5) than dispersal between the other continents or from these to the Afrotropics (0.1; -272.2)

Altitudinal, substrate and life cycle information of sampled species

Altitudinal distribution, substrate preference and life cycle information for the sampled species was obtained from Floras, databases and other publications (Appendix S1.6). Altitudinal distributions and substrate preferences could not easily be assigned to distinct categories; we therefore discuss these factors without formal analysis instead. Evolution of life cycle (annual, biennial or perennial) was reconstructed using ML (1rate option) in MESQUITE 2.75 (Maddison & Maddison, 2011). To integrate phylogenetic uncertainty we used 1901 trees after burn-in of one of the MRBAYES tree files and mapped the results on the 50 % majority rule consensus tree. The known members of Australasia 2- and Australasia 3-clades (Pelser *et al.*, 2007) are both annual and perennial species. We accounted for this variability by representing each of these clades by two taxa, one annual and one perennial. As the life cycle of most New World species is unknown to us, we tested the effect of assigning an unknown state versus scoring some species as perennial and some as annual. Life cycle was not scored for the outgroup species.

Results

Alignment and Phylogeny

Both phylogenetic analysis methods (ML and BI) using ITS data only revealed a monophyletic *Senecio*, and support most major clades, but more limited support for relationships between and within those clades (Appendix S2.2). Most clades found in the ITS dataset were also present in the ETS phylogeny; however, fewer clades are supported, including the monophyly of the genus (Appendix S2.3). Comparison of the ITS and ETS phylogenies revealed supported incongruence in the position of *S. burchellii* DC. and *S. seminiveus* J.M.Wood & M.S.Evans, these sequences have been separated.

The combined nr phylogeny (Fig. 2; 3 & Appendix S2.4) revealed 11 clades (Australasia 1-, Australasia 2-, Australasia 3-, New World 1-, New World 2-, consanguineus-, doria-decurrens-, fresenii-, sabinjoensis-, vulgaris- and windhoekensis-clade) plus the western South African aquatic *S. cadiscus* B. Nord & Pelser in an unresolved position within a monophyletic *Senecio*. These groups are generally consistent with previous results by Pelser *et al*. (2007). Only the sabinjoensis-clade, which consists of two East African species, had not been identified previously. All clades were supported with PP of 0.97 or higher in the BI analysis with the exception of the Australasia 2-clade and the doria-decurrens-clade. In our analyses, the doria-clade is nested within the doria-decurrens-clade, while the doria-clade is supported as monophyletic sister to a monophyletic decurrens-clade in the BI analysis of the more sparsely sampled dataset in Pelser *et al.* (2007). The sister relationship of the Australasia 1-clade to the rest of *Senecio* as well as the branching order of the subclades within the core-Senecio-clade are supported. The ML analysis supported the same clades, except for the New World 1-clade and the sister relationship of Australasia 1 to all other clades. While the phylogenetic position of the Palaearctic vulgaris-clade is clearly resolved in both analysis methods, the phylogenetic position of the doria-clade did not receive support (Fig. 2). The cp data set contains relatively few informative characters (Appendix S2.1) and none of the cp markers supported the monophyly of the genus (Appendix S2.5 & S2.6). Comparison of the cp and nr phylogenies revealed incongruence in the position of some tips (Appendix S1.4, S2.4 & S2.7), which had already been detected and discussed by Pelser *et al.* (2010).

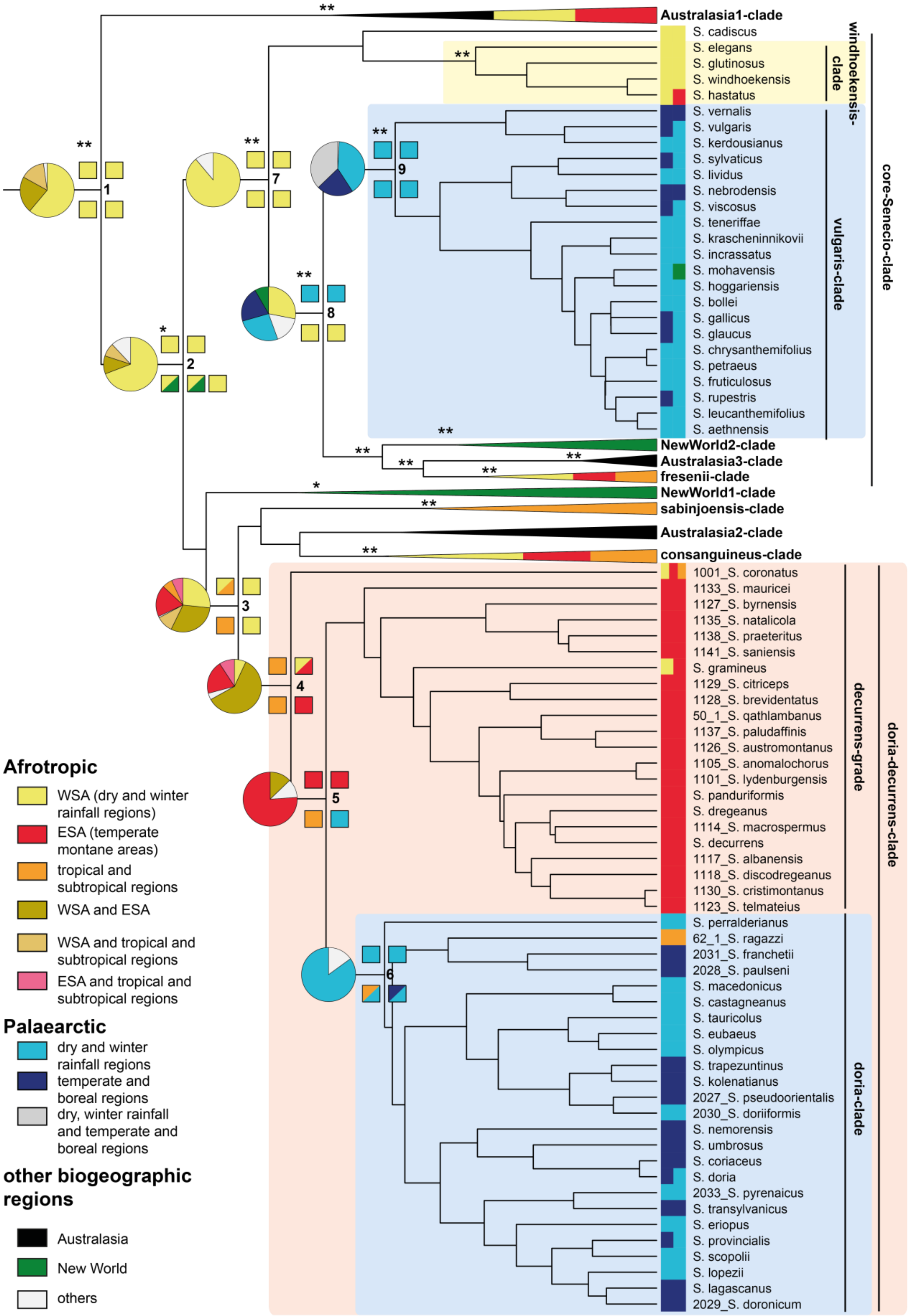


Figure 2: Caption see following page.

Figure 2 of page before: Phylogenetic reconstruction of *Senecio* (nr ITS and ETS maximum clade credibility tree generated in BEAST); only clades of interest are shown. Full representation of the phylogeny and detailed information of the reconstructions can be found in Appendix S1 and S2. Major clades supported by Bayesian Inference method (BI) and Maximum Likelihood are indicated by two asterisk, clades only supported by BI are marked with one asterisk. Nodes discussed are numbered. Distribution of species and of species of collapsed clades is shown at the tips/in the triangles of the tree and biogeographic reconstruction is shown along the branches. Here, pie charts show the result of the BBM method and boxes show the LAGRANGE results; the complex LAGRANGE model is shown at the left side of the branch and the simple model at the right side (boxes above the node represent the ancestral area of the branch above, and boxes below the node represent the ancestral area of the branch below). Two boxes at one node of a single analysis are only shown when the relative probability of the most likely reconstruction was less than 5% more than of the second most likely one (Appendix S2.9 for more details of the relative probabilities per node and region).

Molecular dating and ancestral area reconstruction

The dated nr phylogeny is congruent with earlier dating efforts (Pelser *et al*. 2010; Pelser *et al.*, 2012) and places the origin of the genus in the Mid to Late Miocene with most intercontinental colonizations at the Miocene-Pliocene boundary (Tab. 2).

Table 2: Results of the molecular dating analyses in million years including the 95% highest posterior density intervals of Asteraceae, Senecioneae (excl. *Doronicum*) and *Senecio* using BEAST (under a yule process)[3]. Abbreviations: 2°: secondary calibration.

Clade	**Posterior age estimates inferred with BEAST**	
	Fossil calibration	**2° calibration**
Asteraceae	53.24 (60.63-48.64)	
Senecioneae stem	25.14 (31.39-18.52)	
Senecioneae crown	21.75 (28.14-15.37)	
Senecio stem	11.44 (16.4-7.14)	10.58 (14.73-6.47)
Senecio crown	5.22 (9.56-1.85)	7.29 (10.93-4.06)
vulgaris-clade stem		4.38 (6.81-2.33)
vulgaris-clade crown		3.43 (5.44-1.74)
doria-clade stem		4.34 (6.74-2.32)
doria-clade crown		3.57 (5.59-1.85)

Of the biogeographic models that we tested using LAGRANGE, the most complex fits the data best (Tab. 1). This model involves a maximum number of polymorphic ancestral distribution areas (two), and only allowed widespread distributions of afrotropical species and within the Palaearctic regions; colonization between adjacent regions and within continents is more frequent than between continents, and colonization from the Afrotropics to anywhere is more frequent than colonization between the other continents or to the Afrotropics. We here describe the results of both, the simplest model (under the assumption that the maximum number of ancestral

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[3] Nachdem dieses Kapitel fertig geschrieben war und in einem internationalen Journal eingereicht wurde, wurde ein neues Fossil der Asteraceae publiziert das das Alter der Familie erheblich ändert. Dieses Fossil wurde in einer neuen Datierung berücksicht, deren Methoden und Ergebnisse in Appendix 3 zu finden sind. Das Alter der Asteraceae ist durch das neue Fossil deutlich älter geworden, das durchschnittliche Kronenalter von *Senecio* ist etwa 2 Millionen Jahre älter und die Kladen innerhalb von *Senecio* sind etwa 1 Millionen Jahre älter, als hier im Haupttext beschrieben. Die Altersangaben und die dazugehörige Diskussion in diesem Kapitel beruhen noch auf der Datierung ohne das viel ältere Fossil. Die neuen Ergebnisse werden im Review-Prozess für die Veröffentlichung in das Manuskript eingearbeitet.

polymorphic areas is two), and of the most complex model of the LAGRANGE analyses (simple and complex LAGRANGE), as well as the BBM results in order to illustrate the effects of the different assumptions and methods.

In general, all biogeographic analyses revealed a WSA origin of *Senecio* as most likely (Fig. 2), i.e. the dry or winter rainfall areas of southern Africa. The results of the different analyses differed in their probability values for the region of the most recent common ancestor (mrca) of *Senecio* and for the biogeographic assignment of some nodes within *Senecio* (cf. Appendix S2.9 for likelihood values and relative probabilities of the LAGRANGE analyses).

The two Palaearctic clades most likely arrived from two different ancestral areas in the Afrotropic (Fig. 2). The vulgaris-clade most likely arrived from WSA with some uncertainty dependent on colonization of the Palaearctic either by the mrca of the vulgaris- and its sister-clade (node 8; one of the likely BBM scenarios) or by a descendent of that mrca (along the branch between node 8 to 9). The colonization of the Palaearctic by an ancestor of the doria-clade (nodes 3-5) is not reconstructed with certainty. Depending on the method, different areas receive the best likelihood score, but WSA was never inferred as the most likely area. The colonization of the Palaearctic by an ancestor of the doria-clade occurred either via tropical/subtropical regions of the Afrotropics directly (along the branch between nodes 5 and 6; complex LAGRANGE) or from ESA directly (along the branch between nodes 5 and 6; simple LAGRANGE and BBM).

Both Palaearctic clades established most likely in the dry or winter rainfall areas of the Palaearctic (Fig. 2: nodes 9 and 6, Appendix S2.9) followed by colonization of cooler Palaearctic regions. Only the BBM analysis is less clear regarding the area of initial colonization by the mcra of the vulgaris-clade, which may also have been the temperate Palaearctic region or widespread in the Palaearctic.

Evolution/differentiation in preferred altitude range, substrate and life cycle

Changes in in altitudinal and substrate preferences and life cycle with regard to the Palaearctic clades seem to have occurred several times (Fig. 3 & Appendix S1.6).

The mrca of *Senecio* most likely was a perennial species and most species have a perennial life cycle. An annual life cycle probably evolved at least two times independently in *Senecio*, once in the consanguineus-clade and at least once in the core-Senecio-clade (Fig. 3 & Appendix S2.8). Generally, the reconstruction of life cycle is not much influenced by the different assignment of New World tips (Fig. 3 & Appendix S2.8; results of the non-coded New World tips not shown). Within the core-Senecio-clade, annual species are found in the windhoekensis-, vulgaris- and fresenii-clades. Thus, either an annual life cycle evolved several times independently within the core-Senecio-clade, or the mrca of that clade was an annual species and several transitions from an annual back to a perennial life cycle took place because several perennial species are also found in the core-Senecio-clade. Our reconstruction shows that the mrca of the windhoekensis- and the mrca of the vulgaris-clade were annual. As both contain perennial species, transitions from an annual to a perennial life cycle must have occurred. All species of the doria-decurrens-clade are perennial, and the mcra of them is unequivocally reconstructed as perennial (Fig. 3).

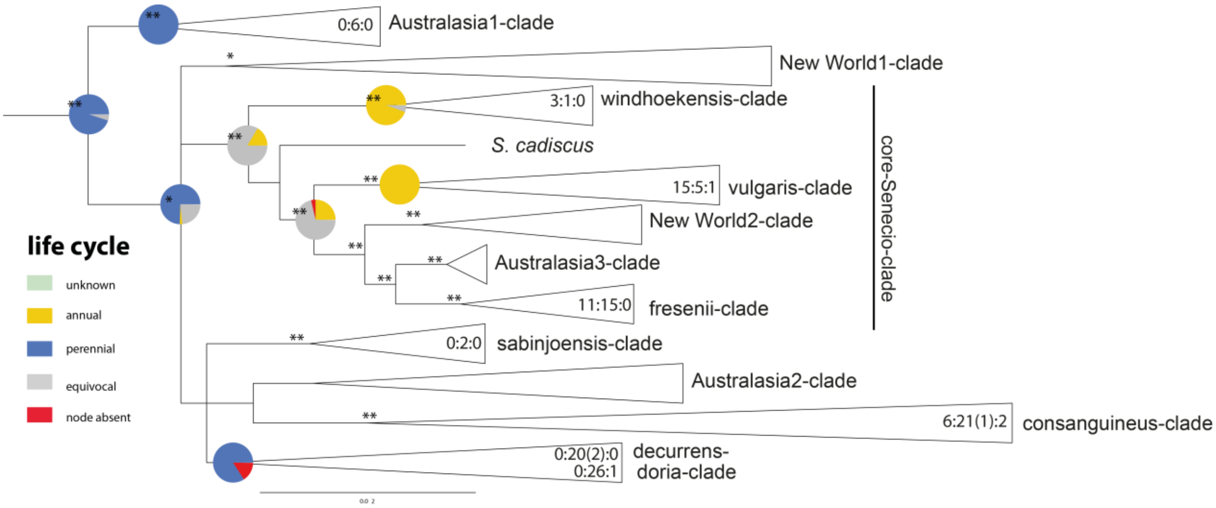

Figure 3: Phylogenetic reconstruction of *Senecio* based on the combined ITS and ETS majority rule consensus tree, calculated with MRBAYES. Results of the life cycle reconstruction is shown for nodes of interest. Clades for which no precise information was available or which were not fully sampled but contain perennial and annual species were coded as polymorphic. Numbers inside collapsed clades represent the number of species with an annual: perennial (biennial): unknown life cycle. Changes in life cycle within clades are only shown in Appendix S2.8. Major clades supported by Bayesian Inference and Maximum Likelihood methods are indicated by two asterisk, clades only supported by Bayesian Inference are marked with one asterisk.

Comparison of the altitudinal preferences of the Palaearctic clades and their sister lineages revealed differences. Most species of the doria-decurrens-clade (16 of 21 afrotropical species and 16 of 25 Palaearctic species) occur above 2000 m (Appendix S1.8). Additionally, a distribution map of sect. *Crociseris* (Calvo *et al.*, 2013; a large proportion of the doria-clade) shows that the majority of species occurs mostly in mountainous areas around the Mediterranean Basin. In contrast, species of the vulgaris-clade mostly occur near the coast of the Mediterranean Basin (Alexander, 1979), although this is apparently contradicted in part by wider elevational ranges reported for individual species (Appendix S1.8). The dissimilar distribution pattern of the two Palaearctic clades in the Mediterranean Basin is roughly reflected by their differential occurrence on sandy soils (Appendix S1.8). While sandy soil is specified as habitat information for 10 of 21 species of the vulgaris-clade, it is never indicated for species of the doria-decurrens-clade, which mostly occur in mountain areas. Furthermore, most species of the vulgaris-clade not occurring on sandy soil are weedy plants with generally broader distribution ranges.

Discussion

Origin of Senecio *in western southern Africa*

Our reconstructions show that *Senecio* most likely evolved in western southern Africa in the Mid to Late Miocene (Fig 2 & Tab. 2). This area today has an arid or winter rainfall climate. The estimated time of origin of the genus supports the hypothesis that *Senecio* evolved under arid or semi-arid conditions as the time of origin coincides with ongoing aridification in Africa. Climate reconstructions show that aridification, especially of southern Africa, started in the Mid Miocene and is associated with the establishment of the Benguela current (Cowling *et al*., 2009; Bonnefille, 2010; Dupont *et al.*, 2011), which led to changes from a more tropical climate and vegetation to a more seasonal and drier climate and temperate vegetation in the Late Miocene (Pound *et al.,* 2012). The strengthening of the Benguela current during the Pliocene led to the onset of the winter rainfall regime in the GCFR (Goldblatt & Manning, 2002). Through aridification and formation of grassland, fire activity increased and C4-photosynthesis started to become more abundant (Hoetzel *et al.*, 2013), both of which have been postulated to have triggered the rapid radiation of a number of GCFR-centred groups (*Phylica* L.: Richardson *et al*., 2001; *Ehrharta* Thunb.: Verboom *et al.*, 2003; core Ruschioideae: Klak *et al*., 2004). The origin of *Senecio* in WSA may not be completely unexpected as most afrotropical species of *Senecio* are indeed found in arid or montane regions of southern Africa (Harvey, 1865; Hilliard, 1977; Tadesse, 2004; Jeffrey & Beentje, 2005) and as Timonin *et al.* (2015) already hypothesised an arid southern African origin of *Senecio*. However, the genus has not commonly been described as a winter rainfall or dry-adapted group, despite the fact that the genus is among the LCG of the GCFR.

Two independent colonizations of the Palaearctic from southern Africa

The colonization of the Palaearctic seems to have taken place twice independently around 5 million years ago (Ma; highest posterior density interval [HPD]: 8.5-3.1) with first establishment in regions which are dry or have a winter rainfall climate today (Fig. 2 & Tab. 2). During this time, these parts of the Palaearctic experienced a period of extremely arid conditions, the ‘Messinian Salinity Crisis’ (5.96–5.33 Ma; Krijgsman *et al*., 1999). Diversification in both Palaearctic clades started around 4.4 Ma (HPD: 6.7-2.2), corresponding roughly to the onset of the Mediterranean climate (3.2–2.8 Ma; Suc, 1984), a climate similar to that of the CFR with hot and dry summers and cool and wet winters.

While both clades that reached the Palaearctic are likely to have established first in the dry or winter rainfall areas of the Palaearctic, the source areas in the Afrotropics are different according to our analyses (Fig. 2). The area of origin of the vulgaris-clade is most likely WSA, which indicates colonization either via the arid corridor (Verdcourt, 1969; del Hoyo *et al.*, 2009) or via long-distance dispersal to the Palaearctic (Coleman *et al.*, 2003). The source area of the doria-clade is less certain as the different reconstruction methods are more ambiguous. The results of the ancestral area reconstructions seem to depend partly on the position of *Senecio ragazii* Chiov., an Ethiopian high altitude species, which is nested within the doria-clade. According to our analyses, two scenarios for the colonization of the Palaearctic by an ancestor of the doria-clade are likely. 1) The mrca of the doria-decurrens-clade occurred in tropical/subtropical regions from where it colonized ESA and the Palaearctic; 2) an ancestor of the doria-clade occurred in ESA with colonization of the Palaearctic via tropical/subtropical African regions (high altitude corridor) or recolonization of tropical/subtropical Africa from the Palaearctic. The simple LAGRANGE model and BBM indicate that ESA (i.e. mostly the Drakensberg area) was the most likely source area (hypothesis 2). However, the complex LAGRANGE model indicates that a mcra in tropical/subtropical Africa is more likely (hypothesis 1).

Colonization of the Palaearctic from southern Africa via either the high altitude or the arid corridor has been suggested before based on plant and animal disjunctions (Balinsky, 1962; Verdcourt, 1969; Jürgens, 1997; Linder, 2014). Furthermore, our age estimate of the vulgaris- and doria-clades is similar to age estimates in other groups of similar distribution and which possibly took the same colonization routes (del Hoyo *et al.*, 2009; Devos *et al.*, 2010). Although colonizations from ESA, to the East African mountains and northern parts of the Afrotropic or to the Arabian peninsula have been shown before (Galley *et al,*. 2007; Devos *et al.*, 2010; Galbany-Casals *et al.*, 2014), further extension of distribution areas into the Palaearctic via the high altitude corridor has never been shown with confidence and cannot be shown with certainty in our analyses. With regard to the arid corridor, even though the disjunction between dry areas in the south and north has been thought to imply the past existence of an arid corridor, it is unclear whether this indeed was a physical connection, and, if yes, when it existed (Bellstedt *et al*., 2012).

Colonizations of the Palaearctic did not involve shifts in altitudinal range, substrate preference and life cycle

Despite inhabiting the same biome, the two Palaearctic clades show some differentiation in their preferred broad-scale niche. Species of the doria-decurrens-clade clearly prefer mountainous regions in the Palaearctic as well as in ESA (Fig. 2; Calvo *et al.*, 2013). By contrast, the vulgaris-clade occurs more commonly along or near the coast of the Mediterranean Basin (Alexander, 1979; see Results), where frequent occurrence on sandy soils indicates growth in unstable vegetation. This can be seen in the windhoekensis-clade, too (sister to a clade including the vulgaris-clade), but not in the doria-decurrens-clade.

Related to the above difference in distribution and ecology there exist differences in life cycle (Fig. 3). In the core-Senecio-clade there are at least two clades mainly comprising annual species: the windhoekensis- and the vulgaris-clades. It is unclear whether the annual life cycle in these two clades evolved independently or not (Fig. 3 & Appendix S2.8). Independent multiple origins of an annual life cycle in lineages that contain short- and long-lived species has been shown before (Evans *et al.*, 2005; Datson *et al*., 2008). On the other hand, our reconstruction indicates that reversals from an annual back to a perennial life cycle occurred in the windhoekensis- and vulgaris-clades (Fig. 3 & Appendix S2.8). The transition from annuality to perenniality is generally rare, and known only in its association with the evolution of other traits such as island woodiness, adaptation to montane habitats or polyploidisation (Böhle *et al.*, 1996; Drummond, 2008, Tank & Olmstead, 2008). Nevertheless, multiple cases have been described in Asteraceae (Baldwin, 2014), and this phenomenon is further apparent in the repeated life cycle changes during the evolution of *Senecio* inferred here (Appendix S2.8).

In arid or winter rainfall regions, a substantial proportion of species have an annual life cycle (15 % and more in most winter rainfall regions with exception of Australia and the CFR, Cowling *et al.*, 1996), and the evolution of annuality has been linked to climatic conditions in arid or winter rainfall regions (Fiz *et al.*, 2002; Verboom *et al.*, 2003; Datson *et al.*, 2008). Annuality is believed to be advantageous in seasonally dry environments for different reasons. With an annual life cycle, drought and heat stress can be avoided through survival as seeds. Successful seed formation will be increased when the life cycle is fast enough for seed set to be completed before the dry season starts, and seedling establishment will be favoured by generally more open vegetation (Goldblatt & Manning, 2002; Evans *et al*., 2005; Datson *et al*., 2008). Interestingly, an annual life cycle in *Senecio* seems to have first evolved after the origins of the winter rainfall regime in the GCFR and in the Mediterranean Basin, respectively. On the other hand, an annual life cycle is rare in mountainous habitats (Wang *et al*., 2002; Körner, 2003), and in some predominantly annual groups evolution of a perennial life cycle has been associated with the colonization of mountainous habitats (Drummond, 2008).

Acknowledgements

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Supporting Information

Colonization of the Palaearctic by *Senecio*
Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Appendix S1: Additional information for Material and Methods, including newly added material, GenBank accession numbers, detailed descriptions of laboratory work and alignments and information about the sampled species and the Lagrange *analyses.*

Table S1.1: Newly sequenced material used in this study. Lower case x indicates newly obtained sequences (GenBank number will be obtained during submission process); minus (-) indicates that no new sequences were obtained. Herbarium abbreviations: B – Botanischer Garten und Botanisches Museum Berlin-Dahlem/Germany; BR – Botanic Garden Meise/Belgium; C – Natural History Museum of Denmark/Copenhagen; E – Royal Botanic Garden Edinburgh/Scotland, UK; J – University of the Witwatersrand/South Africa; M – Botanische Staatssammlung München/Germany; MJG – Johannes Gutenberg-Universität Mainz/Germany; MSB – Ludwig-Maximilian-Universität München/Germany; S – Swedish Museum of Natural History/Stockholm; SIM – Staten Island Institute of Arts and Sciences/New York; UPS – University of Uppsala/Sweden. Lower case x: GenBank numbers have to be added during submission process. Minus (-) no new sequence obtained.

Species	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
Crassocephalum vitellinium (Benth.) S. Moore	H. Frankenhäuser 95/1990; RWA H61	MJG	2001	x	x	x	x
Senecio aegyptius L.	Soliman Sisi (s 12-19599)	S	34,1	x	x	x	x
Senecio aequinoctialis R.E.Fr.	O. Hedberg 1880	S	5,3	KM592486	x	KM592420	KM592407
Senecio affinis DC.	K. Balkwill & C. Kidger 7909	E	1124	x	x	x	x
Senecio albanensis DC.	Hilliard & Burtt 11057	E	1117	x		x	
Senecio anomalochorus Hilliard	K. Balkwill, S. Williamson & S. Smith 9888	E	1105	x	x	x	x
Senecio arniciflorus DC.	E. Esterhuysen 36083	E	1125	x		x	x
Senecio austromontanus Hilliard	J. K. Hoener 2119	E	1126	x	x	x	x
Senecio brevidentatus M.D.Hend.	Hilliard & Burtt 18844	E	1128	x	-	-	-
Senecio byrnensis Hilliard	Hilliard & Burtt 13895	E	1127	x	x	-	-
Senecio caloneotes Hilliard	Hilliard & Burtt 16426	S	42,1	KM592488	x	-	KM592403
Senecio cathcartensis O. Hoffm.	Hilliard & Burtt 19079	S	43,1	KM592489	x	KM592422	KM592404
Senecio chrysocoma Meerb.	K. Balkwill & M.J. Balkwill 4882	E	1110	x	x	x	x
Senecio citriceps Hilliard & B.L.Burtt	Hilliard & Burtt 18999	E	1129	x	x	x	x
Senecio consanguineus DC.	Dr. R. Seydel 3638	SIM	1026	KM592490	x	KM592423	KM592381
Senecio coronatus (Thunb.) Harv.	Hugo L. 1945 (BR0000013175160)	BR	1001	KM592491	x	KM592424	
Senecio cristimontanus Hilliard	Hilliard & Burtt 18646	E	1130	x	x	x	x
Senecio cryphiactis O.Hoffm.	Giess 10519	M	KAD259	-	-	-	KM592415
Senecio cyaneus O.Hoffm.	P.B. Phillipson 4870	C	17,3	KM592492	x	KM592425	KM592385

Species	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
Senecio discodregeanus Hilliard & B.L.Burtt	Hilliard & Burtt 17344	E	1118	x	x	-	-
Senecio doriiformis DC.	Thomas Gregor 6651 & Lenz Meierott	M	2030	x	-	-	-
Senecio doronicum (L.) L.	F. Schuhwerk 97/363	M	2029	x	-	-	-
Senecio erysimoides DC.	Cron & Goodman 685	J	626	-	-	-	KM592416
Senecio franchetii C. Winkl.	D. Podlech 21439	M	2031	x	-	-	-
Senecio fresenii Sch. Bip. ex Oliv. & Hiern	E. Westphal & J.M.C Westphal-Stevels 3139	C	16,4	KM592494	x	KM592427	KM592384
Senecio glanduloso-lanosus Thell.	Hilliard & Burtt 7662	E	1119	x	x	x	x
Senecio glanduloso-pilosus Volkens & Muschl.	K. Balkwill & R. A. Reddy 7202	E	1120	x	x	x	x
Senecio harveianus MacOwan	Hilliard & Burtt 6939	S	46,1	x	-	KM592428	-
Senecio harveianus MacOwan	James L. Sidey 3247	S	46,2	KM592495	x	-	KM592405
Senecio hieracioides DC.	Hannah I. Stevebs 474/Elemarie van der Watt	SIM	1025	KM592496	x	KM592429	KM592380
Senecio hirsutilobuss Hilliard	T. Edwards 1773	E	1113	x	-	-	-
Senecio hochstetteri Sch.Bip. ex A.Rich.	P.B. Phillipson 5080	C	19,3	KM592497	x	KM592430	KM592387
Senecio hypochoerideus DC.	Hilliard & Burtt 9613	S	47,1	KM592498	x	KM592431	KM592406
Senecio keniophytum R. E. Fr.	O. Hedberg 1730	S	4,5	KM592501	x	KM592434	KM592402
Senecio laxus DC.	Cron 669	J	628	-	-	-	KM592417
Senecio lydenburgensis Hutch. & Burtt Davy	K. Balkwill 9147	E	1101	x	x	x	x
Senecio macowanii Hilliard	Hilliard & Burtt 18884	E	1132	x	x	-	-
Senecio macrospermus DC.	T. Edwards 1770	E	1114	x	x	x	x
Senecio mauricei Hilliard & B.L.Burtt	Hilliard & Burtt 17920	E	1133	x	x	x	x
Senecio meyeri-johannis Engl.	Magnus Fries s.n. (s 12-19541)	S	22,2	KM592503	x	KM592436	KM592390
Senecio mooreanus Hutch. & Burtt Davy	Hilliard & Burtt 11962	E	1134	x	x	x	x
Senecio myriocephalus Sch.Bip. ex A.Rich.	Mesfin Tadesse, C. Puff & O. Ryding 7161	C	23,2	KM592505	x	KM592438	KM592391
Senecio natalicola Hilliard	J. Medley Wood 7285	E	1135	x	-	-	-
Senecio niveus (Thunb.) Willd.	W. Greuter 22177	B	630	-	-	-	KM592418
Senecio oederiafolius DC.	R.D.A. Bayliss BS 6860	SIM	1022	KM592508	x		
Senecio paludaffinis Hilliard	Hilliard & Burtt 18657	E	1137	x	x	x	x
Senecio paulsenii O. Hoffm. ex Pauls.	Don Bedunah 4	MSB	2028	x	-	-	-
Senecio polyodon DC.	G. V. Cron & K. Balkwill 460	E	1143	x	-	-	-
Senecio praeteritus Killick	Hilliard & Burtt 11753	E	1138	x	x	x	-
Senecio pseudoorientalis Schischk.	D. Podlech & Sh. Zarre 55287	MSB	2027	x	-	-	-
Senecio pyrenaicus L.	W. Dietrich 6055	M	2033	x	-	-	-

Species	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
Senecio qathlambanus Hilliard	Hilliard & Burtt 15321	S	50,1	KM592511	x	KM592443	KM592408
Senecio ragazzi Chiov.	Hedberg 5665	UPS	62,1	KM592512	x	KM592444	
Senecio rautanenii S Moore	Dr. R. Seydel 3525	SIM	1021	KM592513	x	KM592445	KM592379
Senecio reclinatus L.f.	R.D.A. Bayliss BS 4397	SIM	1020	KM592514	x	-	-
Senecio reptans Turcz.	Hilliard & Burtt 10666	E	1139	x	-	-	-
Senecio rhyncholaenus DC.	D.A. McCallum 872	E	1111	x	-	x	-
Senecio roseiflorus R.E.Fr.	O. Hedberg 1884	S	10,3	-	-	KM592447	-
Senecio rosmarinifolius L.f.	N.S. Pillans 10466	SIM	1030	KM592517	x	-	-
Senecio sabinjoensis Muschl.	Misimba, Muzinga Matamba 1 (BR0000013175146)	BR	1004	KM592518	-	-	-
Senecio sandersonii Harv.	K. Balkwill & M.J. Balkwill 10721	E	1112	x	-	x	-
Senecio saniensis Hilliard & B.L.Burtt	Hilliard & Burtt 16247	E	1141	x	-	-	-
Senecio schimperi Sch.Bip. ex A.Rich.	I. Friis, Sally Bidgood, Melaku Wondefrash & Ermias Getachew 10534	C	28,4	KM592519	x	KM592448	KM592394
Senecio seminiveus J.M. Wood & M.S. Evans	Hilliard & Burtt 3776	S	51,1	KM592522	x	-	-
Senecio snowdenii Hutch.	Ake Strid 3579	S	30,1	KM592523	x	KM592450	KM592397
Senecio telekii (Schweinf.) O. Hoffm.	O. Hedberg 2290	S	31,2	KM592527		KM592454	KM592398
Senecio telmateius Hilliard	Hilliard & Burtt 16793	E	1123	x	x	x	x
Senecio unionis Sch.Bip. ex A.Rich.	Arne Anderberg 1709	S	33,1	KM592529	x	KM592456	KM592400
Senecio urundensis S. Moore	S. Lisowski 93978 (BR0000013175139)	BR	1005	KM592530	x	-	-

S1.2: DETAILED DESCRIPTION OF LABORATORY WORK AND ALIGNMENTS.

DNA was extracted using DNeasy Plant Kit (Qiagen GmbH, Hilden, Germany) according to the manufacturer's MiniProtocol with minor changes. Samples were incubated for 30 min instead of 10 min after adding the lysis buffer and the DNA elution step was done twice using 50 µl respectively and incubated for 20 min. For most material we were able to amplify the entire ITS region (ITS-1, 5.8S, ITS-2) using external primers 'ITS 18S' (5′-CCT TMT CAT YTA GAG GAA GGA G -3′) and 'ITS 28S' (5′-CCG CTT ATT KAT ATG CTT AAA-3′; Muir & Schlötterer, [1999]). For some material ITS-1 and ITS-2 were amplified separately, using primers 'ITS A' (5′-GGA AGG AGA AGT CGT AAC AAG G-3′), 'ITS C' (5′-GCA ATT CAC ACC AAG TAT CGC-3′), 'ITS-B' (5′-CTT TTC CTC CGC TTA TTG ATA TG-3′) and 'ITS-D' (5′-CTC TCG GCA ACG GAT ATC TCG-3′; Blattner, [1999]). Amplifications were performed in 20 µl volumes containing 12.86 µl ddH$_2$O, 2 µl buffer, 1 µl 50 mM MgCl$_2$, 0.4 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase (all reaction liquids from NewEngland BioLabs Inc, Ipswich, USA) and 2 µl genomic DNA. Cycling conditions were: 94°C 1 min, 30x (94°C 0.2 min; 52°C 0.3 min; 72°C 1 min), 94°C 0.2 min, 52°C 1.2 min. ETS was amplified using "ETS2" (5′-CAA CTT CCA CCT GGC ATA CCT CCT CA-3′; Bayer *et al.,* 2002) and "18S ETS" (5′-ACT TAC ACA TGC ATG GCT TAA TCT-3′; Baldwin & Markos, 1998). Amplification was performed in 20 µl volumes containing 12.86 µl ddH2O, 2 µl Buffer, 1 µl 50mM MgCl$_2$, 0.4 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl taq-Polymerase (reaction liquids from NewEngland BioLabs Inc, Ipswich, USA, for some sequences we used a taq-Polymerase from Sigma Aldrich, St. Louis, USA) and 2 µl genomic DNA. Sometimes 0.2 µl of 10mg/ml BSA and/or 0.8 µl of DMSO has been added. Cycling conditions were the one described in Pelser *et al*. (2012). The *trn*L intron and *trn*L-*trn*F intergenic spacer were amplified together using 'tab C' (5′-CGA AAT CGG TAG ACG CTA CG-3′) and 'tab F' (5′-ATT TGA ACT GGT GAC ACG AG-3′; Taberlet *et al.,* [1991]). For some material we were only able to amplify the *trn*L-*trn*F intergenic spacer using 'tab E' (5′- GGT TCA AGT CCC TCT ATC CC-3′; Taberlet *et al.,* [1991]) and 'tabF'. Amplifications were performed in 20 µl volumes containing 13.38 µl ddH$_2$O, 2 µl buffer, 0.48 µl 50 mM MgCl$_2$, 0.8µl DMSO, 0.2 µl of 10 mg/ml BSA, 0.8 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase and 1 µl genomic DNA. Cycling conditions were those described by Shaw *et al.* (2005) for *rpl*16. *Trn*C-*ycf*6 was amplified using '*trn*C(GCA)F' (5′-CCA GTT CRA ATC YGGGTG-3′) and '*ycf*6' (5′-GCC CAA GCR AGA CTT ACT ATA TCC-3′; Shaw *et al.,* 2005). Amplifications were performed in 20 µl volumes containing 12.38 µl ddH$_2$O, 2 µl buffer, 0.48 µl 50mM MgCl$_2$, 0.8 µl DMSO, 0.2 µl of 10 mg/ml BSA, 0.4 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase and 2 µl genomic DNA. Cycling conditions were those described in Shaw *et al.* (2005) for *rpl*16.

PCR products were purified using ExoSAP-IT PCR Clean-Up (Affymetrix, Santa Clara, USA) following the recommended protocol. Cycle sequencing reactions were carried out with BigDye Terminator 3.1 (Applied Biosystems, Foster City, California, U.S.A.) following the recommended protocol with minor modifications (1 µl of BigDye Terminator instead of 2 µl) using the same primers as used for amplification and purified with Sephadex (GE Healthcare, Waukesha, USA). The sequencing of both strands was done on a 'GA3130XL' Genetic Analyser (Applied Biosystems, Carlsbad, USA; Hitachi Ltd., Tokyo, Japan) at Johannes Gutenberg-University Mainz (Germany). SEQUENCHER v.4.1.4 (Gene Codes Corporation, Ann Arbor, MI, U.S.A.) was used for file editing. The sequenced regions were checked by eye and adjusted prior to alignment when necessary. *Trn*LF showed double bands in some taxa. In those cases both bands were cut out, purified (Macherey-Nagel) and re-sequenced as described above.

As outgroup close relatives of *Senecio* were chosen according to Pelser *et al.* (2007): *Crassocephalum crepidioides* (Benth.) S. Moore, *C. vitellinium* (Benth.) S. Moore, *C. montuosum* (S. Moore) Milne-Redh., *Dendrocacalia crepidifolia* (Nakai) Nakai, *Erechtites valerianifolius* (Link ex Spreng.) DC., *Senecio thapsoides* DC. and *Synotis nagensium* (C.B. Clarke) C. Jeffrey & Y.L. Chen. The phylogenies were rooted with *Synotis nagensium*, except for the *trn*C-*ycf*6 phylogeny, where only *Crassocephalum vitellinium* was available as close relative. The analysis of the ETS dataset had problems with the convergence of the chain, which was solved by reducing the outgroup to *Crassocephalum vitellinium*. Alignments were made with MAFFT v7 (Katoh & Standley, 2013) and adjusted by hand with MACCLADE v. 4.08 (Maddison & Maddison, 2005). Missing data were coded as question marks. Substitution models and partitions were identified prior to analyses with PARTITIONFINDER v. 1.1.1 (Lanfear *et al.*, 2012) relying on the Bayesian information criterion. Combining the ITS and ETS data and using the proposed substitution model of PARTITIONFINDER (Appendix S2.1) resulted in non-convergence of the chains. The proposed substitution model for the combined nr dataset was a single substitution model for both regions. Instead, we used the separate substitution models as identified by PARTITIONFINDER for the individual markers, which resulted in convergence. The simple coding method by Simmons & Ochoterena (2000) as implemented in SEQSTATE 1.4.1 (Müller, 2005) was used to code insertions and deletions as binary data (presence/absence). These were only coded in the MRBAYES analyses and phylogenies with and without gap coding were checked for phylogenetic conflicts. However, adding indel characters did not result in higher support values and was therefore abandoned in further analyses.

Table S1.3: Sequences obtained from GenBank. Taxa used for molecular dating of the Asteraceae phylogeny are marked with a lower case x; minus (-) indicates that no sequence was taken from GenBank.

Taxon	**ITS**	**ETS**	***trn*LF**	***rbc*L**	***ndh*F**
x *Abrotanella emarginata* (Gaudich.) Cass.	-	-	EF538089		AJ012679
x *Acicarpha spathulata* R. Br.	-	-	EU385031	EU384939	EU385125
x *Boopis anthemoides* Juss.	-	-	EU547627	L13860	L39384
x Carduoideae sp Cass. ex Sweet	-	-	JQ303111	JQ303118	JQ303120
x *Carthamus oxyacanthus* M. Bieb.	-	-	HM002884	KC589814	KC589940
x *Cnicothamnus lorentzii* Griseb.	-	-	EU385054	EU384961	AF233823
x *Corymbium glabrum* L.	-	-	EU385055	EU384962	EU385148
x *Crassocephalum crepidioides* (Benth.) S. Moore	-	-	EF028722	GU817753	EF53795
x *Dasyphyllum* Kunth	-	-	EU841077	L13863	L39392
x *Doronicum pardalianches* L.	-	-	EF538098		AY723254
x *Erechtites valerianifolius* (Link ex Spreng.) DC.	EF538199	-	EF538100	EF537965	EF537965
x *Famatinanthus decussatus* (Hieron.) Ariza & S.E. Freire	-	-	KM191904	KM192092	KM192103
x *Gymnarrhena micrantha* Desf.	-	-	EU385076	EU384983	EU385170
x *Hecastocleis shockleyi* A. Gray	-	-	EU385077	EU384984	EU385171
x *Helianthus tuberosus* L.	-	-	GU818008	GU817765	GU817867
x *Hirpicium gazanioides* (Harv.) Roessler	-	-	AY504808		
x *Jacobaea vulgaris* Gaertn.	-	-	EF028725	GU817769	AB530940
x *Linzia* Sch. Bip. ex Walp.	-	-	EF155880		EF177479
x *Packera eurycephala* (Torr. & A. Gray) W.A. Weber & Á. Löve	-	-	EF538113	GU817778	EF537982
x *Pertya scandens* (Thunb. ex Murray) Sch. Bip.	-	-	EU385101	EU385008	AB288546
S. aethnensis Jan ex DC.	AJ400779	JN789726	EU195499	-	-
S. angustifolius (Thunb.) Willd.	JN789735	JN789687	JN789961	-	-
S. arenarius M. Bieb.	AF457421	-	-	-	-
S. asirensis Boulos & J.R.I.Wood	KC751413	-	-	-	-
S. asperulus DC.	EF538300	-	-	-	-
S. bollei Sunding & G.Kunkel	JN789736	JN789688	JN789962	-	-
S. brasiliensis (Spreng.) Less.	GU818641	GU818252	GU818061	-	-
x *S. burchellii* DC.	EF538309	FM173146	JN789963	AM234911	JN790015
S. cadiscus B.Nord. & Pelser	GU818506	GU818128	GU817980	-	-
S. calocephalus Poepp. & Endl.	HM050325	HM050321	-	-	-
S. campanulatus Sch.Bip. ex Klatt	EF538149	HM050324	HM050374	-	-
S. candidans DC.	HM050326	HM050322	-	-	-
S. carroensis DC.	JN789741	JN789690	JN790001	-	-
S. castagneanus DC.	JX895508	-	-	-	-
S. chilensis Less.	EF538313	GU818254	EF538122	-	-
S. chrysanthemifolius Poir.	AJ400780	-	-	-	-
S. coriaceus Aiton	EF538317	-	-	-	-
S. corrugatus (Philippi) Pelser	EF028708; EF028715	HM050319	HM050371	-	-
S. cryphiactis O. Hoffm.	JN789742	JN789691	JN789969	-	-
S. decurrens DC.	EF538324	-	-	-	-

Taxon	**ITS**	**ETS**	***trn*LF**	***rbc*L**	***ndh*F**
S. doria L.	AF459946	-	-	-	-
S. dregeanus DC.	EF538331	-	-	-	-
S. eenii (S. Moore) Merxm.	AF457425	-	-	-	-
S. elegans L.	GU818642	-	GU818064	-	-
S. eriopus Willk.	JX895291	-	-	-	-
S. erysimoides DC.	JN789743	JN789692	JN789970	-	-
S. eubaeus Boiss. & Heldr.	JX895245	-	-	-	-
S. flaccidus Less.	EF538336	GU818259	GU818066	-	-
S. fruticulosus Sibth. & Sm.	JN789744	JN789693	JN789971	-	-
S. gallicus Chaix	AJ400783	-	-	-	-
S. giessii Merxm.	AF457418	-	-	-	-
S. glastifolius L. f.	EF538340	JN789694	JN789972	-	-
S. glaucus L.	JN789745	-	-	-	-
S. glutinosus Thunb.	AF457427	-	-	-	-
S. gramineus Harv.	GU818650	GU818262	GU818068	-	-
S. gregorii F.Muell.	GU818651	GU818263	GU818069	-	-
S. hastatus L.	EF538345	-	-	-	-
S. hispidissimus I. Thomps.	GU818657	GU818266	GU818071	-	-
S. hoggariensis Batt. & Trab.	DQ208190	-	JN789978	-	-
S. hypsobates Wedd.	EF538348	GU818268	-	-	-
x *S. ilicifolius* L.	GU818662	GU818269	GU818074	-	-
S. inaequidens DC.	AF459943	JN789703	JN789979	-	-
S. incrassatus Lowe	JN789807	-	JN789983	-	-
S. kerdousianus Gómiz & Llamas	JN789808	JN789705	JN789984	-	-
S. kolenatianus C.A. Mey.	JX895252	-	-	-	-
S. krascheninnikovii Schischk.	AF457437	-	-	-	-
S. lagascanus DC.	JX895354	-	-	-	-
S. lautus (Willd.) G. Forst. ex Willd.	EU812814	KC695942	-	-	-
S. laxus DC.	JN789809	JN789706	JN789985	-	-
S. leptophyllus DC.	JN789810	JN789707	-	-	-
S. leucanthemifolius Poir.	JN789811	JN789709	JN789988	-	-
S. littoreus Thunb.	JN789812	JN789710	JN789989	-	-
S. lividus L.	AJ400795	JN789711	JN789990	-	-
S. lopezii Boiss.	JX895264	-	-	-	-
S. macedonicus Griseb.	JX895510	-	-	-	-
S. madagascariensis Poir.	GQ478106	JN789712	JN789991	-	-
S. mairetianus DC.	EF538359	GU818275	EF538128	-	-
S. maritimus L. f.	JN789816	JN789713	JN789992	-	-
S. mohavensis A. Gray	AF457435	JN789719	JN789998	-	-
S. nebrodensis L.	JN789902	JN789720	JN789999	-	-
S. nemorensis L.	AF459937	GU818278	EF028730	-	-
S. niveus (Thunb.) Willd.	JN789903	JN789721	JN790000	-	-
S. olympicus Boiss.	JX895511	-	-	-	-
S. panduriformis Hilliard	EF538364	-	-	-	-
S. perralderianus Coss.	EF538365	-	-	-	-
S. petraeus Boiss. & Reut.	JN789906	-	JN790003	-	-
S. pinnatifolius A. Rich	GU81867	GU818287	GU818081	-	-
S. pinnulatus Thunb.	JN789907	JN789724	JN790004	-	-

Taxon	ITS	ETS	*trn*LF	*rbc*L	*ndh*F
S. piptocoma O. Hoffm. ex Schinz	JN789908	JN789725	JN790005	-	-
S. polygaloides Phil.	EF538367	GU818288	GU818082	-	-
S. prenanthoides A. Rich.	GU818681	-	GU818083	-	-
S. provincialis (L.) Druce	JX895383	-	-	-	-
S. psilocarpus Belcher & Albr.	GU818692	GU818290	GU818084	-	-
S. pubiger L.	EF538368	-	-	-	-
S. purpureus L.	EF538370	-	-	-	-
S. roseus Sch. Bip.	EF538373	GU818292	GU818085	-	-
S. rupestris Waldst. & Kit.	JN789909	JN789727	JN790007	-	-
S. scopolii Hoppe & Hornsch. ex Bluff & Fingerh.	JX895513	-	-	-	-
S. sisymbriifolius DC.	EF538381	-	-	-	-
S. suaveolens (L.) Ell.	EF538222	GU818298	EF538102	-	-
S. sylvaticus L.	AF459928	JN789729	-	-	-
S. tauricolus V. A. Matthews	GU817570.	-	GU818087	-	-
S. teneriffae Sch. Bip.	JN789910	JN789731	JN790010	-	-
S. thapsoides DC.	-	-	EF538137	-	-
S. transsylvanicus Boiss.	JX895306	-	-	-	-
S. trapezuntinus Boiss.	JX895514	-	-	-	-
S. umbrosus Waldst. & Kit.	JX895447	-	-	-	-
S. vernalis Waldst. & Kit.	AJ400806	JN789708	JN789987	-	-
S. vestitus P.J. Bergius	GU818708	GU818305	GU818089	-	-
S. viscosus L.	AF459925	GU818306	EF028734	-	-
x *S. vulgaris* L.	AJ400811	AF319755	EF538139; JQ041866	HM850347	EF538017
S. windhoekensis Merxm.	AF457426	-	-	-	-
x *Schlechtendalia luzulaefolia* Less.	-	-	EU841085	AY874431	L39395
x *Stifftia* J.C. Mikan	-	-	JF920298	EU385020	L39399
x *Synotis nagensium* (C.B. Clarke) C. Jeffrey & Y.L. Chen	AF459922	-	EF028735		EF538018
x *Trixis* P. Browne	-	-	EU385120	EU385025	L39406
x *Wunderlichia mirabilis* Riedel ex Baker	-	-	EU385122	EU385028	EU385217

S1.4: INCONGRUENCES BETWEEN GENOMES

Initially, we combined the nr and cp datasets after either removing taxa with incongruent placements with significant support (Bayesian Inference [BI] support: >0.95 Posterior Probability; Maximum Likelihood [ML]: >70 % Bootstrap support) or including them twice with nr and cp data separately in the combined analyses (Pirie *et al.*, 2009). However, both methods led to the collapse of nodes that were well supported in the nr analyses. Incongruences between nr and cp gene trees in Senecioneae have been reported previously (Pelser *et al.*, 2007; Pelser *et al.*, 2010; Pelser *et al.*, 2012; Calvo *et al.*, 2013). The large number of gene tree conflicts was inferred to be the result of both incomplete lineage sorting and hybridisation in *Senecio* (Pelser *et al.*, 2010; Pelser *et al.*, 2012). Hybridisation seems to contribute significantly to speciation in the group, and, in support of this, crossability between species seems to be generally high (Alexander, 1979; Calvo *et al.*, 2013). Furthermore, the cp dataset only has relatively few parsimony informative characters (Appendix S2.1), and the resolution and branch support within the phylogeny is quite low. Therefore, further analyses are based on the nr dataset only as this dataset resulted in a much better resolved and supported tree.

S1.5: MOLECULAR DATING

We used a recently discovered fossil that suggests that Asteraceae are older than previously thought and that has been placed after the split between the newly described subfamily Famatinanthoideae (Panero *et al.*, 2014) and the rest of Asteraceae with a minimum age of 47.5 Million years ago (Ma; Barreda *et al.*, 2010). Other dating approaches of *Senecio*/Senecioneae were based on secondary root calibration and island ages as calibration points (Pelser *et al.*, 2010) or only based on ITS substitution rates (Pelser *et al*., 2012). To use the fossil we constructed an Asteraceae phylogeny including all described subfamilies and some representatives of the tribe Senecioneae using cp *trn*LF, *ndh*F and *rbc*L. Most sequences were available in GenBank (Appendix S1.1), *ndh*F amplification for *Senecio roseiflorus* R.E.Fr. was carried out as described by Pelser *et al.* (2007; GenBank accession: KM592459). In an initial analysis, the Asteraceae dataset did not resolve the phylogeny as shown by Panero & Funk (2008) that was based on much more species and sequence data. We therefore constrained the tree topology accordingly. For dating, we first used BEAST v 1.8 (Drummond *et al.*, 2012; run on CIPRES [Miller *et al.*, 2010]) on the Asteraceae tree. We chose an exponential distribution as prior for the fossil calibration, partitioning and substitution model according to the results of PARTITIONFINDER (Appendix S2.1), an uncorrelated lognormal relaxed clock (ULRC), and a yule speciation process as tree prior. The age of the root of the tree was calibrated with a uniform distribution of 48-101 Myr (maximum age of Asterales according to Beaulieu *et al*., 2013). Two independent runs were conducted and combined excluding burn-in of 10% using LOGCOMBINER v. 1.7.2 and TREEANNOTATER v. 1.7.2 (Drummond & Rambaut, 2007) when the effective sample size was above 200 as checked with TRACER (Rambaut & Drummond, 2007).

The stem age of *Senecio* as estimated in BEAST from the Asteraceae cp matrix was then used as a secondary calibration point to date the nr *Senecio* matrix. The mean of the highest posterior density (HPD) values of the stem age of *Senecio* was used as calibration point with a standard deviation of two using a normal distribution and the same priors as above. Results are presented in Tab. 2 in the main text.

A new fossil was published in the meantime, the results are not yet incorporated into the manuscript, but are presented in Appendix S3.

Table S1.6: Distribution, altitude, habitat and life cycle information for the Palaearctic and Afrotropic species. Species are ordered by clade affiliation. The delimitation of bioregions is described in the method section Ancestral area reconstruction. Abbreviation of delimited bioregions: WSA – western southern Africa, ESA – eastern southern Africa, trop – tropical and subtropical Africa and Madagascar, Med – Mediterranean and dry areas of the Palaearctic; EuAs – temperate and boreal regions of the Palaearctic. Information of the South African distribution of species is further divided into the provinces they occur in (CP – Cape Province, EC – Eastern Cape, FS – Free State, G – Gauteng, KZN – KwaZulu-Natal, Lim – Limpopo, M – Mpumalanga, NC – Northern Cape, NW – North West Province, TVL – Transvaal, WC – Western Cape). Coding of life cycle: a – annual; b – biennial; p - perennial. Information obtained from the same resources as for the habitat and altitude information. Minus indicates that no data was available. Resources of habitat and altitude information are given in superscripted letters: a – African Plant Database, 2012; b – Nordenstam *et al.*, 2009; c – Goldblatt & Manning, 2000; d – Manning & Goldblatt, 2012; e – POSA Flora, 2007; f – Harvey, 1865; g – Hilliard, 1977; h – Hilliard & Burtt, 1987; i – Jeffrey & Beentje, 2005; k – Manning & Bruyns, 2013; l – Tadesse, 2004; m – Agnew & Agnew, 1994; n – Matthews, 1975; o – Calvo *et al.*, 2015; p – Hegi *et al.*, 1987; q – Chater & Walters, 2010; r – Jeffrey & Chen Yi-Ling, 1984; s – Shishkin, 1995; t – Chen *et al.*, 2011; u – Lotfi *et al.*, 2010; w – Carbutt & Edwards, 2006; x – Pooley, 2003; y – Pitart *et al.*, 1909; z – Brennan *et al.*, 2009; A – Jahn & Schönfelder, 1995; B – Alexander, 1979; C – Gómiz & Llamas, 2005; D – Sociedade Portuguesa de Botânica, 2014; E – Barkley, 2006; F – Gilmer & Kadereit, 1989; G – Merxmüller, 1967.

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
		No clade affiliation			
S. cadiscus	WSA	WC	105-260[a]	Seasonal ponds or vernal pools[b]	a
		Australasia 1-clade			
S. arniciflorus	WSA	WC	10-300[a]	Sandy coastal flats and lower slopes[c]	p
S. ilicifolius	ESA, WSA	EC, WC	5-700[a]	Clay flats and slopes[d]	p
S. oederiafolius	WSA	EC, WC	15-990[a]	Damp grassland[e]	p
S. pubiger	WSA	WC	5-1585[e]	Dry stony clay, often disturbed sites[d]	p
S. rosmarinifolius	ESA, WSA	EC, NC, WC	5-1350[a]	Sandy and stony slopes[d]	p
S. vestitus	WSA	NC, WC	700-1690[a]	Rocky sandstone slopes[d]	p
		Consanguineus-clade			
S. arenarius	WSA	Namibia, NC, WC	10-1340[a]	Sandy and gravelly flats and washes[f, d]	a
S. asperulus	ESA, WSA	Lesotho, EC, FS, G, KZN, M, NC, WC	515-2590[a]	Grows socially in poor stony soil, weed along roadside[g]	p
S. caloneotes	ESA	Lesotho, EC, KZN	2700-3300[a]	Boggy ground near streams or lakes, may grow close to snow line or glacier lakes in shelter of rocks; disturbed soils beside glaciers and streams[g, h]	p
S. cathcartensis	ESA	Lesotho, EC, FS, KZN	1480-2440[a], 1800-2700[h]	Grassland, damp or even wet places[g]	p
S. chrysocoma	ESA, WSA	EC, KZN, WC	60-900[a]	Common along road sides, disturbed grassland[g]; grassy slopes, forest margins[d]	b
S. consanguineus	ESA, WSA	Botswana, Namibia, FS, G, KZN, LIM, NC, NW	915-2000[a]	Favours river banks[g]	a
S. cyaneus	Trop	Tanzania	2300-3350[i]	Upland grassland and heath zone, less often in forest margin[i]	p
S. eenii	WSA	Botswana, Namibia, NC	245-1650[a]		a

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
S. giessii	WSA	South Namibia, NC		Sandy and gravelly flats[k]	a
S. glanduloso-lanosus	ESA	EC, KZN	1115-2075[a]	Found in rank growth on forest margins[g]	p
S. glanduloso-pilosus	ESA	FS, G, KZN, LIM, M, NW	915-1295[a]	Open grassland[g]	p
S. glastifolius	WSA	EC, WC	60-1090[e]	Forest margins[c]	p
S. hieracioides	ESA	Lesotho, EC, FS, G, KZN, M, NW	1450-1800[g], 1000-3050[e]	Socially in poor grasslands, among rocks often becoming a weed along roadsides[g]	p
S. hirsutiloides	ESA	EC, KZN	1200-1700[g]	Grows in grassland, often on steep slopes and adjacent to forest patches[g]	p
S. hochstetteri	Trop	From Sierra Leone to Cameroon, Uganda, Kenya, Tanzania, DR Congo, Rwanda, Burundi, Sudan, Ethiopia, Malawi, Zimbabwe, LIM	900-2800-(3350)[i]	Grassland, occasionally in forest margins or wooded grassland[i]; open bushland[l]	p
S. hypochoerideus	ESA	Lesotho, EC, FS, KZN,	2400-3200[g], 1800-3200[h]	Grows socially on rocky, grassy mountain slopes[g]	p
S. macowanii	ESA	EC, KZN	1675-2745[a]	Moist grassy slopes[h]	p
S. mooreanus	ESA, WSA	FS, KZN, LIM, M, NW	1435-2200[a]	Grows in open grassland, damp situations[g]	p
S. polyodon	ESA, trop	Swaziland, Lesotho, Zimbabwe, EC, FS, G, KZN, M,	600-3000[g], 230-3100[a], 1800-3000[h]	Found along marshy stream sides, in marshes or seasonally waterlogged grasslands[g, h]	p
S. purpureus	ESA, trop	Angola, DR Congo, Malawi, Tanzania, Zambia, Zimbabwe, EC, KZN, WC	(1200-)1500-2700; 5-1830[i, a]	Marshy ground by streams or in swamp edges, in ruderal sites such as road-sides and cultivation[i]; moist slopes, esp. after fire[d]	p
S. rautanenii	WSA	Botswana, Namibia, NC	245-1650[a]	-	a
S. reclinatus	ESA, WSA	-	-	-	-
S. reptans	ESA, WSA	EC, FS, NC, NW	915-1615[a]	-	p
S. rhyncholaenus	ESA	Swaziland, EC, KZN	90-1525[a]	Grows socially in grassland, particularly among rock outcrops on hillslopes[g]	p
S. sandersonii	ESA	KZN	?-1675[a]	Grows in grassland; often near forest margins[g]	p
S. seminiveus	ESA	Lesotho, EC, FS, KZN,	1600-3355[a], 2100-3200[h]	Grows in rounded clumps on cliff faces or sprawled over rock sheets or in the crevices of rock sheets[g]	p
S. sisymbriifolius	WSA	Namibia, NC	195-1405[e]	Shaded places among rocks[k]	a
S. snowdenii	Trop	Kenya, Uganda	2700-4250[i]	Clearings in the bamboo zone almost to the summit, in grassland or Afroalpine bushlands[i]; moorland[m]	p
			Decurrens-grade		
S. albanensis	ESA	Lesotho, Swaziland, FS, G, LIM, M, EC, KZN, WC	915-2130[a]	Open grassland[g]	p

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
S. anomalochorus	ESA	FS, G, KZN, M	1050-2420[a]	Grassland, often among rocky outcrops or in the crevices of rock sheets[g]	p
S. austromontanus	ESA	Lesotho, EC, KZN	2350-2670[a]	Seepage over rock sheets and damp grassland[h]	p
S. brevidentatus	ESA	EC, FS, KZN	600-2250[a]	Grows socially in damps grassy mountain slopes or on soil hummocks in marshes[g]	p
S. byrnensis	ESA	EC, KZN	1370-1435[a]		p
S. citriceps	ESA	EC, KZN	1800-2335[a]	Grows scattered in grasslands[g]	p
S. coronatus	ESA, WSA, Trop	Angola, Botswana, Lesotho, Malawi, Swaziland, Tanzania, Zambia, Zimbabwe, EC, FS, G, KZN, LIM, M, NW, WC	1800-2400[h]	In dry ground, often most noticeable in burnt areas, marshy grassland[i]; shallow rocky soils in grassland [h]	p
S. cristimontanus	ESA	KZN	1950-2435[a]	Short dry stony grassland and steep S-facing sandstone ridges of Little 'Berg[w]; steep broken grass and rock slopes and rock crevices[h]	p
S. decurrens	ESA	Lesotho, EC, KZN, M	305-2350[a]	Grows in open grassland, marshy ground[g, h]	b
S. discodregeanus	ESA	Lesotho, Swaziland, EC, FS, G, KZN, M	50-2375[a]	Growing socially in grassland[g]	p
S. dregeanus	ESA	EC, KZN	765-1340[a]	Open grassland[g]	p
S. gramineus	ESA, WSA	Lesotho, EC, KZN, WC	1400-3275[a]	Grows in short turf and in crevices of rock sheets; grassland; mainly on the summit, around margins of rock sheets and stony ridges[g, d, x]	p
S. lydenburgensis	ESA	FS, G, KZN, M, NW	365-1850[a]	Grassland[g]	p
S. macrospermus	ESA	Lesotho, EC, KZN	2500-3000[g]	At the heads of mountain passes, steep damp mountain slopes, either grass or scree, often in large colonies[h]	p
S. mauricei	ESA	KZN	1675-2440[a]	Steep moist grass slopes often below Cave sandstone cliffs[h]	p
S. natalicola	ESA	EC, KZN	275-365[a]	Grows in grassland, sometimes rather marshy places[g]	p
S. paludaffinis	ESA	Swaziland, KZN	1370-2440[a]	Always in marshy places and streambanks[g, h]	p
S. panduriformis	ESA	Swaziland, EC, KZN, LIM, M	600-1600[g]	Grows in scrubs on forest margins[g]	b
S. praeteritus	ESA	EC, KZN	650-2250[a]	Growing socially on grassy streamsides or in moist grassy gullies down the mountain slopes[g]	p
S. qathlambanus	ESA	Lesotho, EC, KZN	2300-3200[h]	Damp subalpine and alpine grassland, on steep slopes and along watercourses[w]	p
S. saniensis	ESA	Lesotho, KZN	2865-3135[a], 2375-2865[h]	Grows in rich black turf along the foot of a cliff at the summit of the pass[g]; grassy places at foot of moist basalt cliffs[h]	p
S. telmateius	ESA	Lesotho, KZN	2195-2440[a]	Marshy ground[h]	p

Species	**Bio-region**	**Distribution**	**Altitude**	**Habitat**	**Life cycle**
			Doria-clade		
S. castagneanus	Med	East Turkey, mainly western Anatolia	1250-2100[o]	rocky slopes, forest clearings; subalpine meadows, woods of *Quercus*, *Pinus*, unless on siliceous soils[n, o]	p
S. coriaceus	EuAs	-	-	-	-
S. doria	Med, EuAs	Bulgaria, central Czechoslovakia, East France, south-central Russia to south Spain, Sicily,	Lowland[p]	Damp meadows and woods, open woodland and scrubs, marshes[q]	p
S. doriiformis	Med	Israel, Iran?, Iraq, Lebanon, Palestine, Syria, Turkey	1800-2700[n], 1000-2500[o]	Streamsides[n]; rocky places, woods of *Cedrus*; on calcareous soils[o]	p
S. doronicum	EuAs	Austria, Bosnia-Herzegovina, Croatia, France, Germany, Italy, Spain, Switzerland; mountains of central and southern Europe	1690-2930[p], 800-2600[o]	Alpine meadows, montane pastures, rocky slopes, screes, edge of woods of *Abies*, *Fagus*, *Picea*, *Pinus*, calcareous and siliceous soil[o, q]	p
S. eriopus	Med	Mountains in south-west Spain; northern Morocco	300-1450[o, q]	Shrublands *with Chamaerops, Pistacia, Quercus*; open woods of *Pinus, Quercus*; rocky places[o, q]	p
S. eubaeus	Med	Greece, mountains of Euboea Islands	600-1550[o]	Mountain rocks, rocky slopes, open formations of *Abies*, on calcareous soils[o, q]	p
S. franchetii	EuAs	Afghanistan, Kyrgyzstan, Tajikistan, Uzbekistan	750-3850[o]	Rocky slopes, clay slopes, steppe meadows, shrubs with *Juniperus* and *Pistacia*[o]	p
S. kolenatianus	EuAs	Georgia, Russia, Turkey	1200-3050[o]	Subalpine and alpine damp meadows, screes, thickets of *Rhododendron*, woods of *Abies*, *Picea*, *Fagus*, on granitic and calcareous soils[o]	p
S. lagascanus	EuAs	France, Portugal, Spain; mountains of north and east Spain	240-1650[o]	Shrublands, meadows, woods of *Quercus*, *Pinus* (sometimes of *Fagus*), on calcareous or siliceous soils[o]	p
S. lopezii	Med	southern Portugal, southern Spain	110-470[o]	Woods of *Quercus*, *Arbutus*, *Castanea*, on siliceous soils[o]; shady places[q]	p
S. macedonicus	Med	Bulgaria, Greece, Macedonia	900-1800[o]	Grassy subalpine meadows, rocky outcrops, woods of *Quercus*, *Pinus*, *Fagus*, on calcareous soils, rarely siliceous[o]	p
S. nemorensis	EuAs	much of Europe, much absent from Mediterranean	700-3000[r]	Coniferous and birch aspen forests, their edges, in pine woodlands, scrubs, mountains ascending almost to the upper treeline; open places in forests, streamsides[s]; damp meadows woods[t]	p
S. olympicus	Med	Turkey (endemic of western Anatolia)	1600-2550[o]	Subalpine meadows, rocky slopes[o]	p

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
S. paulsenii	EuAs	Afghanistan, Iran, Pakistan, Tajikistan, Turkmenistan	1400-3000, 2400-4300[o]	Rocky slopes, screes, steppes, grassy open slopes and clay slopes, dry places, steppes, serpentine rocks, unless on calcareous soils[o]	p
S. perralderianus	Med	Algeria, Morocco	700-2100[o]	Woods *of Cedrus, Quercus*, shady rocky places, on calcareous soils[o]	p
S. provincialis	Med, EuAs	France, Spain	175-1800[o]	Camephytic meadows, exposed rocky places, shrublands, and open woods of *Pinus*, *Quercus*; calacareous soils[o]	p
S. pseudoorientalis	EuAs	Armenia, Azerbaijan, Iran, Iraq,Turkey	2200-2800[u], 1400-2850[o]	Grassy slopes, damp places[n]; subalpine and alpine meadows, streamsides, banks of marshes, steppes, on calcareous and volcanic soils[o]	p
S. pyrenaicus	Med	southern France, Spain, Portugal; mountains of SW Europe	1700-2000[q], 1000-2750[o]	Rocky outcrops, subalpine meadows, sometimes in woods of *Pinus*, usually on siliceous soils, less common on calcareous soils[o]	p
S. ragazzi	Trop	Ethiopia	2700-3900[l]	Montane grassland on sloping ground, *Erica -Hagenia* forest, bamboo thicket[l]	p
S. scopolii	Med	Albania, Bosnia-Herzegovina, Croatia, Greece, Italy, Macedonia, Montenegro, Serbia, Slovenia	1100-2400[o], 330-2800[q, o]	Montane to alpine meadows, rocky slopes, edge of woods of *Fagus* and *Carpinus*, on calcareous soils[o]; dry places[q]	p
S. tauricolus	Med	Turkey, endemic of southern-central Anatolia; Taurus mountains	1200-2200[o], 1450-2500[n]	Steppe, rocky slopes, scrub[n]; rocky slopes, steppes, forest of *Quercus*, *Juniperus*; on calcareous soils[o]	p
S. transylvanicus	EuAs	Bulgaria, Greece, Macedonia, Montenegro, Romania	2000-2700[o]	Rocky places (granite, slate, schist, serpentine), alpine grasslands, on siliceous soils[o]	p
S. trapezuntinus	EuAs	Turkey	200[o]	rocky places[n, o]	p
S. umbrosus	EuAs	Czechoslovakia to Bulgaria and Slovakia	mountains[p]	Forest edges in river valleys[s]	p
Fresenii-clade					
S. aegyptius	Trop, Med	Egypt, Ethiopia, Sudan	1700-2500[l]	River bed, roadside ditches; banks of River Nile and associated waterways, desert oases[l]	a
S. aequinoctialis	Trop	southern Ethiopia, Kenya	3000-4250[i], 1900-2200[l]	Moist sited in Afroalpine grasslands, shallow soil over rocks[i]	p
S. affinis	ESA	Lesotho, EC, FS, G, KZN, LIM, M, NW	155-2250[a]	Grows socially in open grassland, often poor stony soil[g]	p
S. angustifolius	ESA, WSA	EC, NC, WC	10-1020[a]	Stony flats and slopes[d]	p
S. asirensis	Med	Saudi Arabia, Yemen	-	-	p
S. burchellii	ESA, WSA	EC, NC, WC	5-1750[a]	Sandy and stony slopes[d]	p
S. carroensis	WSA	WC	10-790[a]	Stony, rocky places[f]	a
S. cryphiactis	WSA	Botswana, Namibia	-	-	a
S. erysimoides	WSA	NC, WC	210-915[a]	-	a

Species	**Bio-region**	**Distribution**	**Altitude**	**Habitat**	**Life cycle**
S. fresenii	Trop	Ethiopia	1500-4300[l]	*Juniperus* forest at high altitudes, *Erica arborea* bushland, well drained grassy slopes in Afro-alpine meadow[l]	p
S. harveianus	ESA, WSA	Lesotho, EC, FS, G, KZN, LIM, M, NW	760-2500[g], 1800-3000[h]	On rocky outcrops, bare places on mountains[x]	p
S. inaequidens	ESA, WSA	Lesotho, Swaziland, EC, FS, G, KZN, LIM, M, NC, NW	1000-2850[a]	Among rock outcrops on steep, moist, grassy mountain slopes and along rocky watercourses, weed along roadside, disturbed areas[g]	p
S. keniophytum	Trop	Kenya	(3700-)4050-4500(-5000)[i]	Wet rocky places, damp ground around rock sheets and other bare areas[i, m]	p
S. laxus	WSA	NC, WC	75-915[e]	Waste ground[f]; sandy slopes[c]	a
S. leptophyllus	ESA, WSA	EC, NC, WC	550-1830[a]	Dry stony karroid slopes[e]	p
S. littoreus	WSA	WC	10-100[a]	Sandy ground and near cultivations[f]; mainly coastal sands[c]	a
S. madagascariensis	ESA, WSA, Trop	Kenya, Madagascar	+/- 2400[i]		a
S. maritimus	WSA	WC	2-15[e]	Sea shores[f]; coastal dunes and slopes[c]	a
S. meyeri-johannis	Trop	Tanzania	2650-4500[i]	Moist peaty soil in upper moorlands, Afroalpine grasslands, seepage areas[i]	p
S. myriocephalus	Trop	Ethiopia	2250-3300-(3900)[l]	Margins of *Hagenia-Schefflera* forest, *Podocarpus* forest, usually in forest clearings[l]	p
S. niveus	WSA	Namibia, EC, NC, WC	365-1650[e]	Stony slopes, dry river banks[k]	p
S. pinnulatus	WSA	NC, WC	15-1890[a]	Moist sandy slopes[d]	a(p)
S. piptocoma	WSA	Namibia, NC, WC	5-1400[a]		a
S. schimperi	Trop	Congo, Eritrea, Ethiopia	1600-3300[l]	Riverine forest, *Juniperus-Olea* forest, *Juniperus-Podocarpus* forest, low open scrub, grassland, roadside ditches, arable land, waste or fallow fields[l]	a
S. telekii	Trop	Tanzania	(3350-)3600-5400[i]	Dry stony slopes, scree, stony gravel, in rock crevices, in the lower part of its range in open giant heath, in the upper part of its range in the shelter of rocks, or even next to glacier[i]	p
S. unionis	Trop	Ethiopia	3170-4050[l]	Open slopes in *Erica arborea* scrubland, rocky places in the Afroalpine[l]	p
			Sabinjoensis-clade		
S. sabinjoensis	Trop	DR Congo, Rwanda, Uganda	2900-3950[i]	Heath zone, mossy crevice on bare lava slope[i]	p
S. urundensis	Trop	Burundi, DR Congo, Malawi, Rwanda, Tanzania, Zambia	1500-2700[i]	Grassland and sparsely wooded grassland, esp. where burned[i]	p

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
Vulgaris-clade					
S. aethnensis	Med	Sicily; Mount Etna	>1000^{q}	Lava slopes^{q}	p
S. bollei	Med	Canaries		Zone maritime^{y}	-
S. chrysanthemifolius	Med	Sicily, Mount Etna	?-1000^{z}	Volcanic soils^{z}	p
S. fruticulosus	Med	Crete	Mountains^{q}, (1000-) 1400-2400^{A}	Thorny Mediterranean heathland and scree slopes^{A}	p
S. gallicus	Med, EuAs	southern Europe to central France, Sicily, Algeria, Alboran Island	0-1000^{B}	Sand dunes, sandy fields, and *Pinus* forests, river banks, less commonly on schists and calcareous soils^{B}	a
S. glaucus	Med, EuAs	Asia, northern Africa, China, Spain, Turkey	0-2370^{B}	Maritime sand and sandy places not far from the sea; river banks, stony and rocky slopes and deserts^{B}	a
S. hoggariensis	NA	Sinai and Egypt, Hoggar mountains, Tibesti mountains	1400-2500^{B}	Montane sandy river beds and fallow fields^{B}	a
S. incrassatus	Med	Canaries	-	-	a
S. kerdousianus	Med	Morocco; Anti-Atlas	1050-1250^{C}	Growing in the shadiest and wettest parts of a road-side ditch, areas below fallen rocks and at the base of vertical rocks, and on terraces above the road^{C}	a
S. krascheninnikovii	Med	Western and central Mediterranean region; Afghanistan Turkistan, Pakistan, Kashmir	2000-3500^{B}	Mountain spruce forests, gravel beds of mountain streams, near rocks, stony sloped, rubbly talus and occasionally in lucerne crops, gravely slopes and sandy places, ruderal, shady places by streams and on cliffs $^{s, r, B}$	a
S. leucanthemifolius	Med	Western Mediterranean, Italy	0-2250^{B}	Maritime sands and rocks; agrestal and ruderal forest clearings, roadsides, hillsides, mostly calcareous soil, occasionally sandy soil, calcareous cliffs and rocky hillsides^{q}; rarely inland^{B}	a
S. lividus	Med	From Portugal to Turkey, North Africa	-	Under cover of pine trees, cork oaks and thickets, in acid soils, sometimes humid^{D}	a
S. mohavensis	Med, NW	South-west Asia	100-700^{E}	Sandy or rocky washes, desert flats ^{E}	a
S. nebrodensis	Med	Mountains of central and southern Spain	ca. 2000^{B}	Rocky places^{q}	p
S. petraeus	Med	South-west Spain	Mountains^{q}	Limestone rocks^{q}	a
S. rupestris	Med, EuAs	around Mediterranean and further north; mainly in the mountains	0-2200^{B}	Ruderal and open sandy and rocky places, wastegrounds, railway-sidings, cliffs and rocky hillsides on limestone, eroded banks, dry gulleys on marls, shales and schists, occasionally on calcareous rock, woodland and scrub, also on disturbed rocky ground$^{q, B}$	p

Species	Bio-region	Distribution	Altitude	Habitat	Life cycle
S. sylvaticus	Med, EuAs	Central Fennoscandia/ North-central Russia southwards to Central Portugal, Central Italy and Bulgaria	?-1800[p]	Forest-margins, disturbed ground, sandy soils[q]	a
S. teneriffae	Med	Tenerife	?-1000[F]	Roadsides, forest clearings[F]	a
S. vernalis	EuAs	East and central Europe	?-2800[p]	Sandy meadows, stony and calcareous slopes, logged areas, scrubs, railroad embankments, field borders[s]; open and sandy or stony habitats[q]	a, b
S. viscosus	Med, EuAs	From Netherlands, Russia to central Spain and Greece	?-2275[p]	Wasteground, railway-lines, other open sandy or gravelly places[q]	a
S. vulgaris	Med, EuAs	Throughout Europe	0-2000[B]	Cultivated land, waste places, maritime sands[q]	a
		Windhoekensis-clade			
S. elegans	WSA	EC, WC	5-200[e]	Sandy ground[f]	a
S. glutinosus	WSA	Namibia, EC, NC, WC	5-1920[e]	Rocky, mostly sandstone slopes[d]	a
S. hastatus	ESA, WSA	Lesotho, EC, FS, KZN, NC, WC	2000-2650[h]	Grows on rubble slopes, in the crevices of cliffs or under shelter of outcropping rocks; rocky streamsides, steep rocky grass slopes[h]	p
S. windhoekensis	WSA	Namibia, NC	900-1675[a]	Gravelly quartzitic soils, mica-schist and -slate, near dam, riverbed, common agricultural weed[G]	a

Table S1.7: Details of model assumptions and matrices for the different constraints of the biogeographic analyses in Lagrange described in the method section of the ancestral area reconstruction. Numbers from one to seven in the matrices correspond to delimited bioregions: 1 – western southern Africa, 2 – eastern southern Africa, 3 – tropical and subtropical regions of the Afrotropic, 4 – temperate and boreal regions of Palaearctic, 5 – New World, 6 – Australasia, 7 – Mediterranean and dry areas of Palaearctic.

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<tr><th>4</th><td>0.5</td><td>0.5</td><td>0.5</td><td>1.0</td><td>0.5</td><td>0.5</td><td>1.0</td></tr>
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<tr><th>6</th><td>0.5</td><td>0.5</td><td>0.5</td><td>0.5</td><td>0.5</td><td>1.0</td><td>0.5</td></tr>
<tr><th>7</th><td>0.5</td><td>0.5</td><td>0.5</td><td>1.0</td><td>0.5</td><td>0.5</td><td>1.0</td></tr>
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<tr><td>4</td><td>Dispersal constraint</td><td>Dispersal within continents more likely than between continents:
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</table></td><td>Dispersal between adjacent regions is as likely as within a continent:
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Comparison	Constraints	Assumptions															
5	Dispersal constraint	Dispersal between adjacent regions is as likely as within a continent:								Dispersal from the Afrotropic to somewhere is more likely than dispersal between the other continents or to the Afrotropic:							
			1	**2**	**3**	**4**	**5**	**6**	**7**		**1**	**2**	**3**	**4**	**5**	**6**	**7**
		1	1.0	1.0	1.0	0.5	0.5	0.5	0.5	**1**	1.0	1.0	1.0	0.5	0.5	0.5	0.5
		2	1.0	1.0	1.0	0.5	0.5	0.5	0.5	**2**	1.0	1.0	1.0	0.5	0.5	0.5	0.5
		3	1.0	1.0	1.0	1.0	0.5	0.5	1.0	**3**	1.0	1.0	1.0	1.0	0.5	0.5	1.0
		4	0.5	0.5	0.5	1.0	0.5	0.5	1.0	**4**	0.1	0.1	0.1	1.0	0.1	0.1	1.0
		5	0.5	0.5	0.5	0.5	1.0	0.5	0.5	**5**	0.1	0.1	0.1	0.1	1.0	0.1	0.1
		6	0.5	0.5	0.5	0.5	0.5	1.0	0.5	**6**	0.1	0.1	0.1	0.1	0.1	1.0	0.1
		7	0.5	0.5	0.5	1.0	0.5	0.5	1.0	**7**	0.1	0.1	0.1	1.0	0.1	0.1	1.0

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Appendix S2: Additional results regarding phylogenetic reconstructions, molecular dating, ancestral area and life cycle reconstructions.

Table S2.1: Alignment length, substitution models and informative characters of DNA regions.

Dataset	**Region**	**Substitution model**	**Partition scheme of combined analyses**	**# of sequenced species**	**Alignment length in bp (excl. bases)**	**# of variable positions/ informative characters**
Senecio (including outgroup)	ITS	SYM+I+G	Proposed: unpartitioned, GTR+G+I; Realized: partitioned in ITS and ETS	156	678	339/216
	ETS	GTR+G		96	412	189/100
	*trn*LF	GTR+G	Combined and reduced: unpartitioned - HKY+I+G	96	866	71/34
	*trn*C-*ycf*6	HKY+G		40	795 (29)	77/31
Asteraceae	*ndh*F	GTR+G	*ndh*F and *trn*L-*trn*F are one partition scheme: GTR+G, *rbc*L a second: K80+I+G	26	1720	246/91
	*trn*LF	GTR+G		28	824	188/68
	*rbc*L	K80+I+G		21	1432	196/75

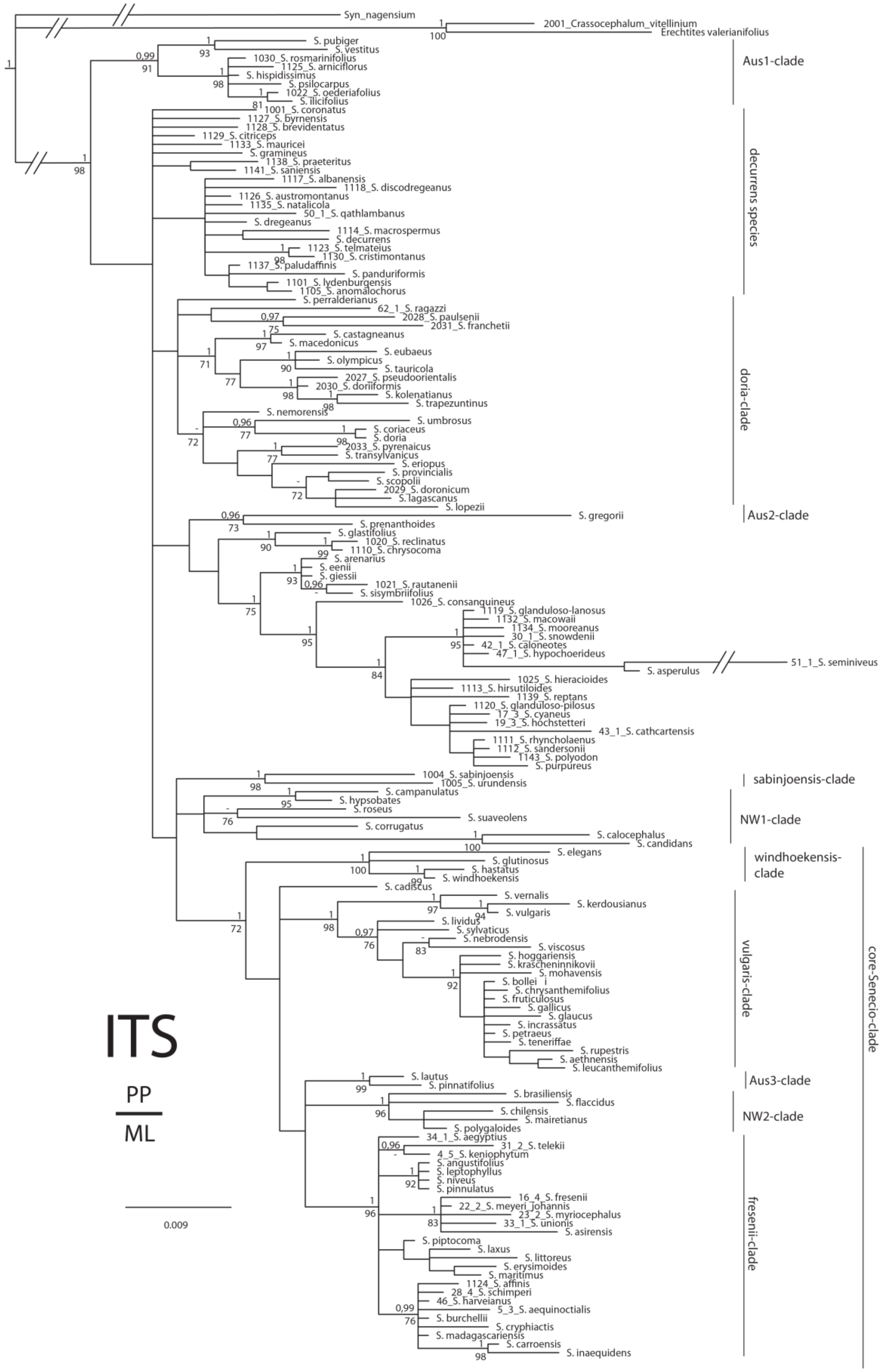

FIGURE S2.2: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON NR ITS MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES WITH BAYESIAN >0.95 (PP) SUPPORT VALUES AND MAXIMUM LIKELIHOOD >70 (ML) BOOTSTRAP VALUES

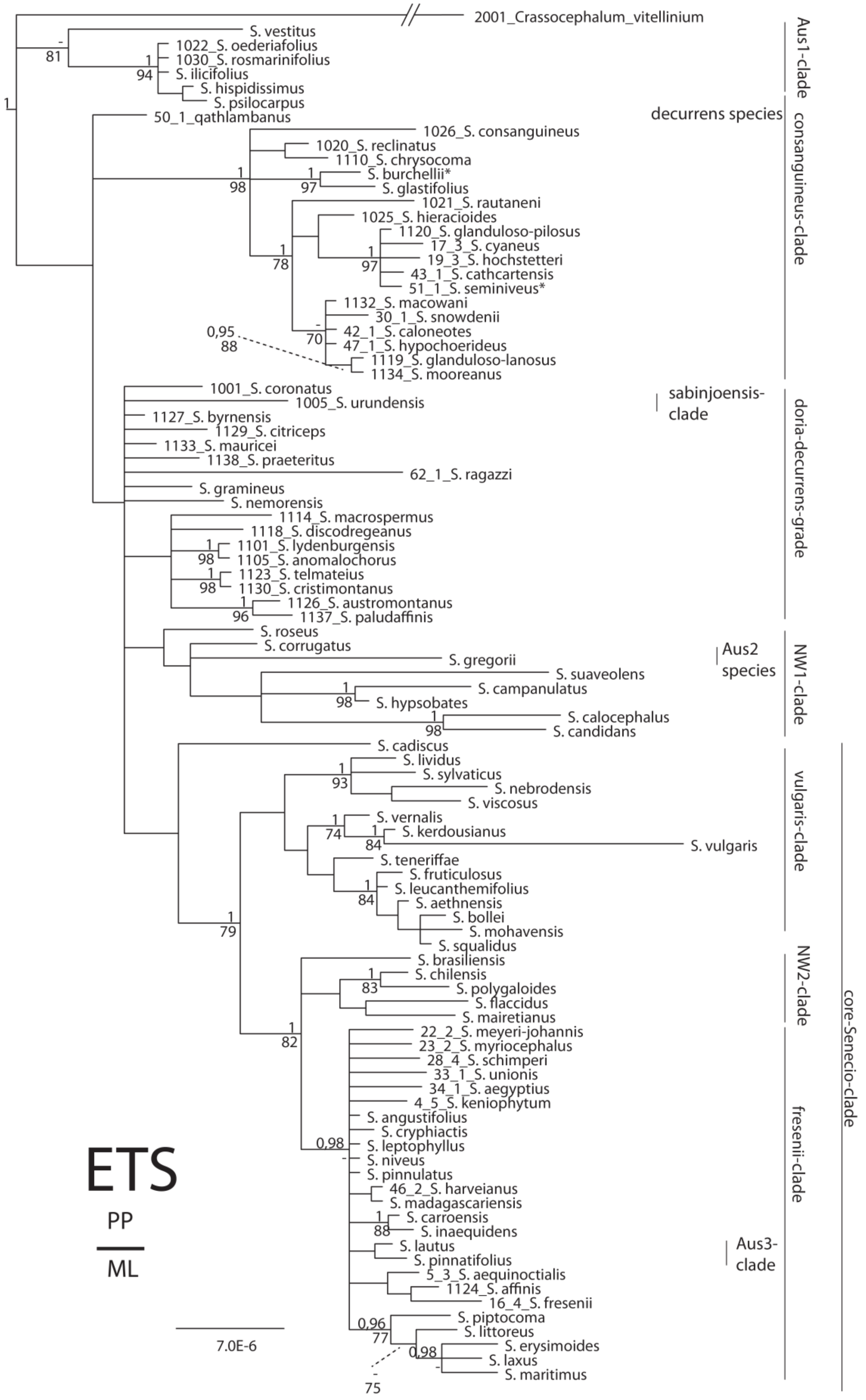

FIGURE S2.3: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON NR ETS MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES.

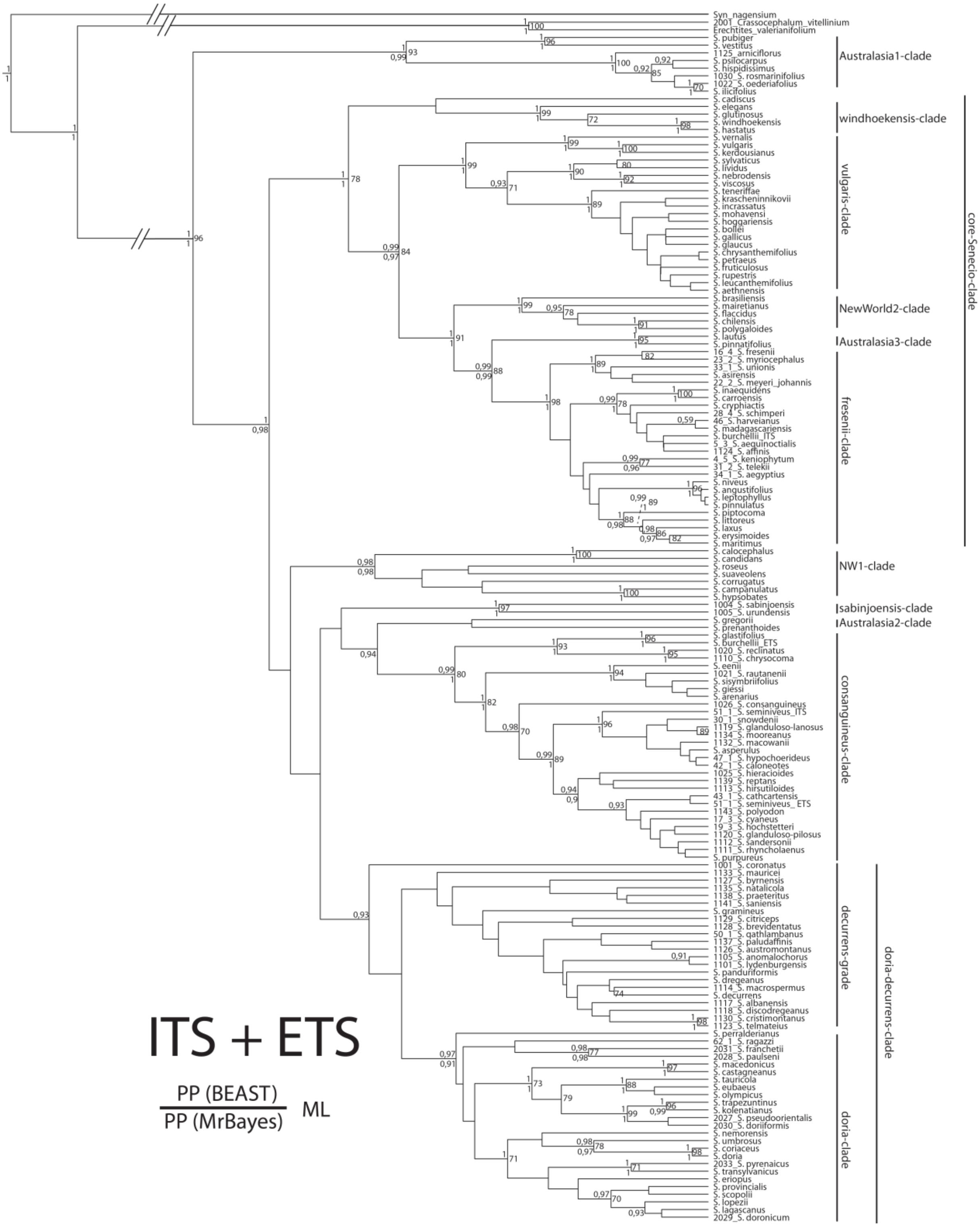

Figure S2.4: Phylogenetic reconstruction of *Senecio* based on the combined nr ITS and ETS majority rule consensus tree, calculated with BEAST. Support values for Bayesian Inference >0.95 posterior probability (PP) and for Maximum Likelihood (ML) bootstrap support values >70 are shown at the nodes.

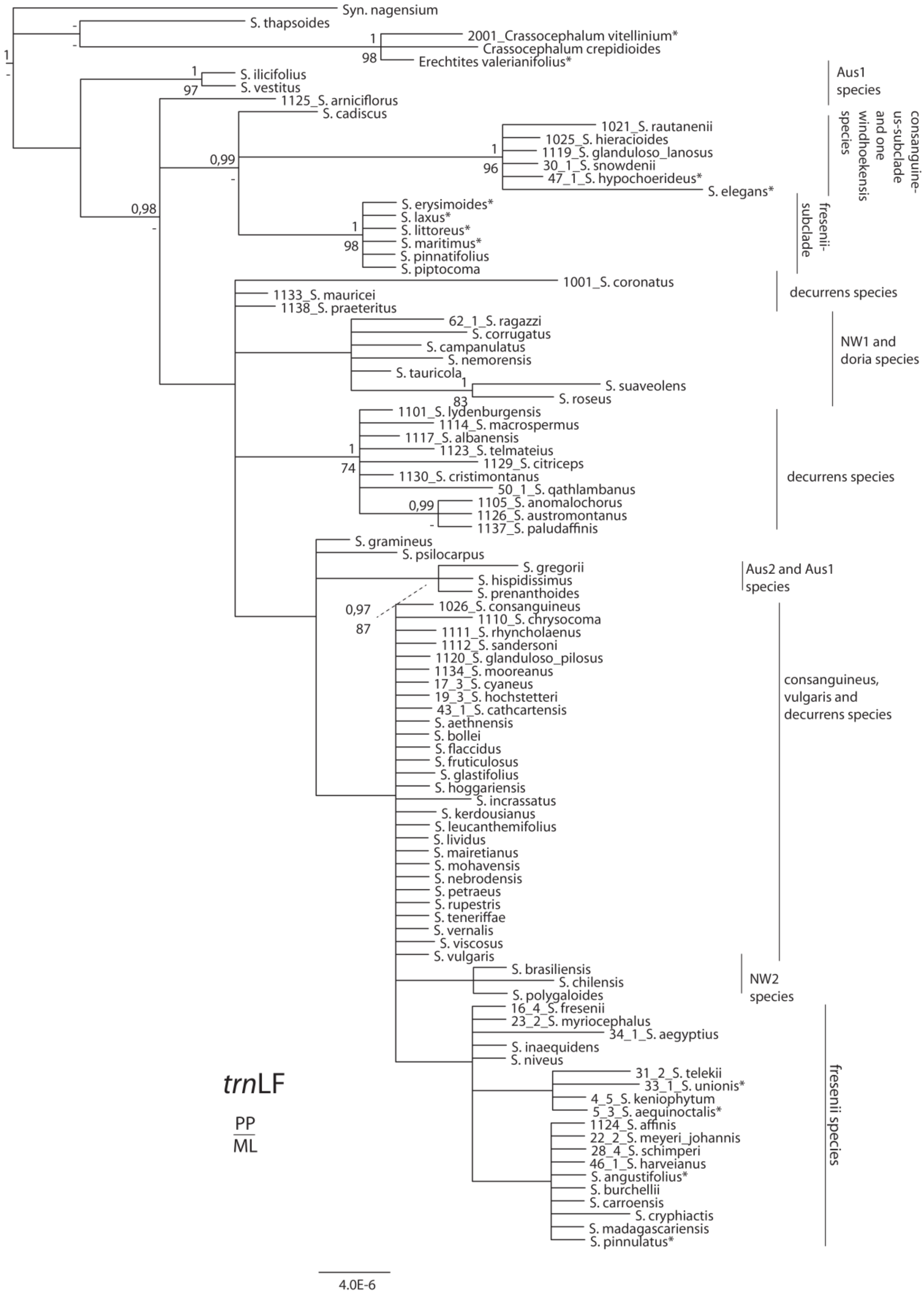

FIGURE S2.5: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON *TRN*LF MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES. ASTERISKS MARK MINOR DIFFERENCES BETWEEN SUPPORT VALUES INSIDE CLADES RESULTING FROM DIFFERENT ANALYSES.

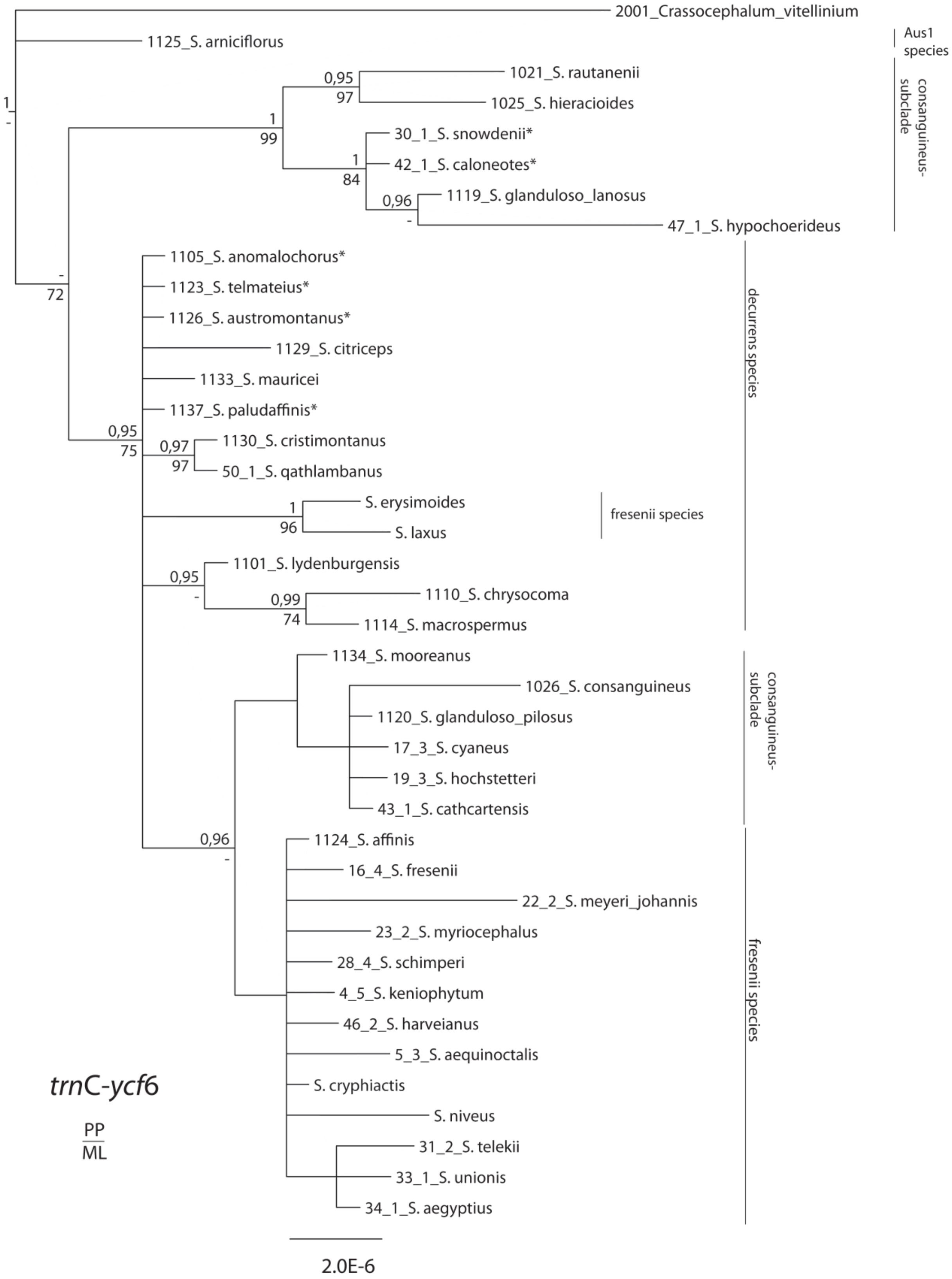

FIGURE S2.6: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON *TRN*C-*YCF*6 MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES. ASTERISKS MARK MINOR DIFFERENCES BETWEEN SUPPORT VALUES INSIDE CLADES RESULTING FROM DIFFERENT ANALYSES.

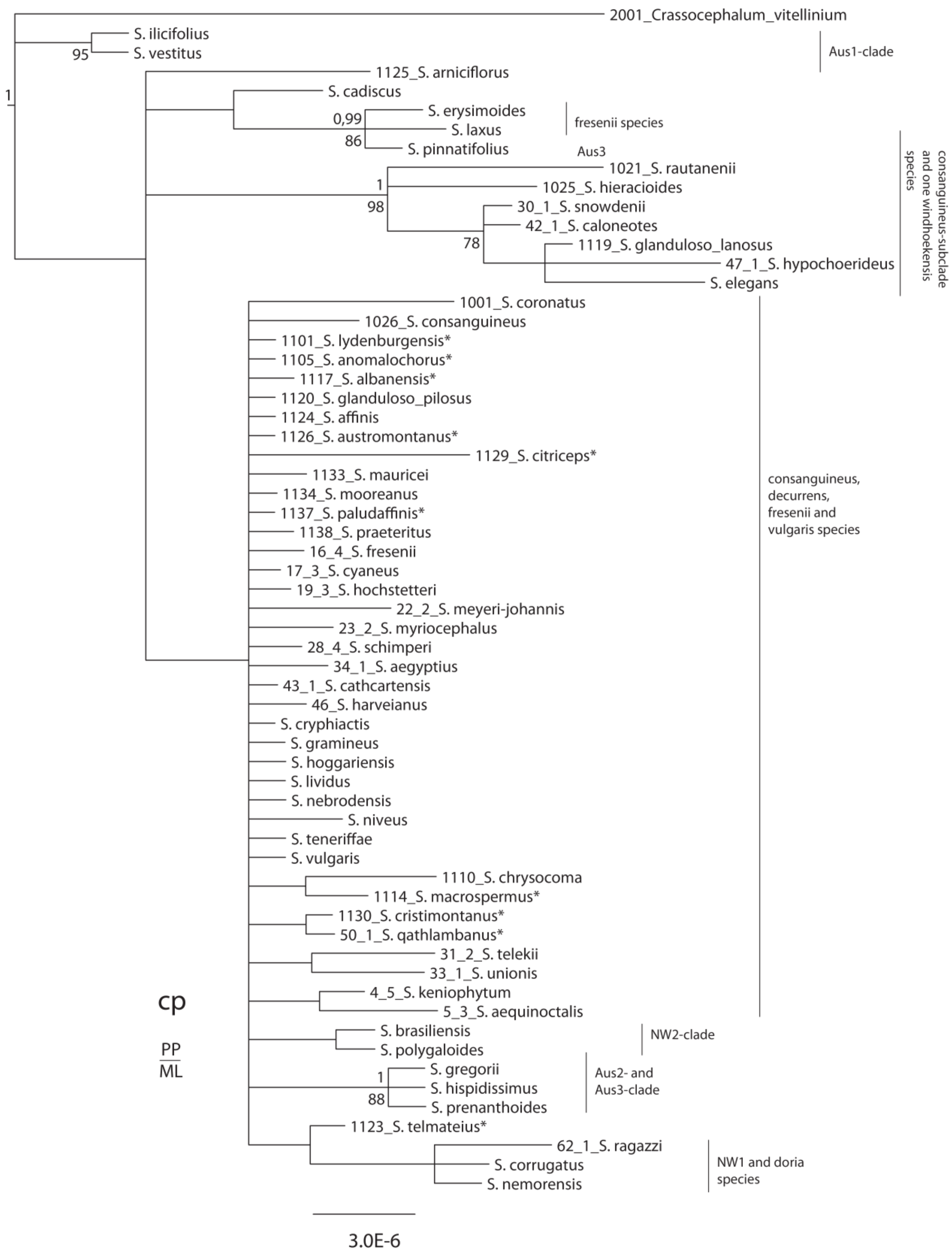

Figure S2.7: Phylogenetic reconstruction of *Senecio* based on the combined chloroplast majority rule consensus tree, calculated with Bayesian Inference (BI) method. Support values for BI >0.95 posterior probability (PP) and for Maximum Likelihood (ML) bootstrap support values >70 are shown at the nodes. Asterisks mark minor differences between support values inside clades resulting from different analyses.

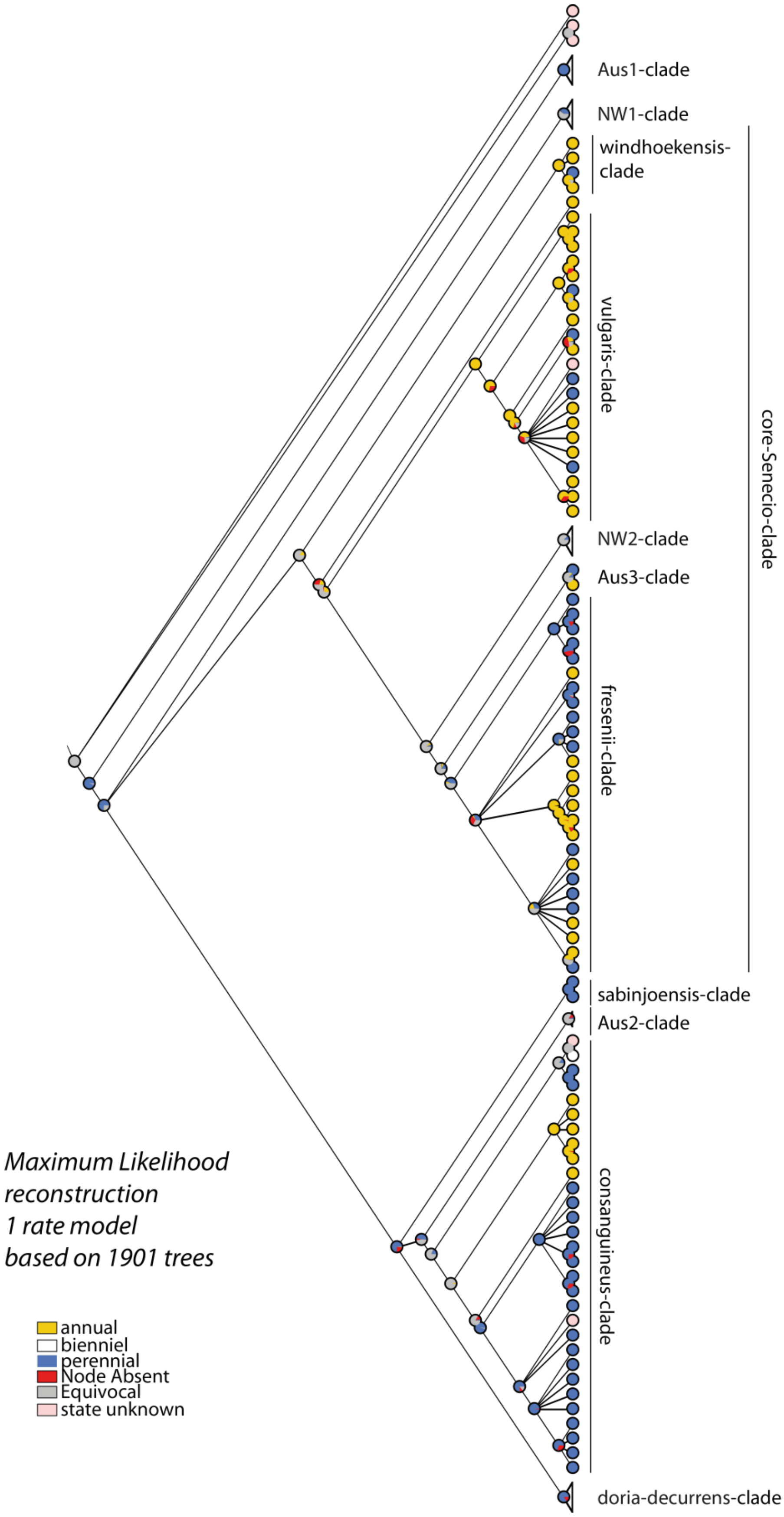

Figure S2.8: Life cycle reconstruction of *Senecio* based on 1901 trees after burn-in of one of the combined nr MrBayes tree files and mapped on the majority rule consensus tree. Reconstruction here is based on coded New World and Australasian nodes. For clarity, clades with only perennial species or equivocal reconstructions are shown as triangles.

Table S2.9: Results of the biogeographic Lagrange reconstruction. Results of the biogeographic reconstruction. Complex model: most likely Lagrange analysis; simple model: maximum number of allowed ancestral polymorphic areas is two in Lagarange. Reconstructed regions with their likelihood and relative probability are shown for major nodes. Upper and lower branch correspond to the branches as displayed in Figure 2 of the main text. Abbreviations for ancestral area reconstruction: WSA – western southern Africa, ESA – eastern southern Africa, trop – tropical and subtropical Africa and Madagascar, Med – Mediterranean and dry areas of the Palaearctic; EuAs – temperate and boreal regions of the Palaearctic, Aus – Australasia, NW – New World. Mathematical abbreviations: Log-Likelihood – lnL; relative probability – rel. Prop.

	Complex model				**Simple model**			
	Biogeographic region of				**Biogeographic region of**			
Node	**Upper branch**	**Lower branch**	**lnL**	**Rel.Prob.**	**Upper branch**	**Lower branch**	**lnL**	**Rel.Prob.**
1	WSA	WSA	-272.9	0.58	WSA	WSA	-306.4	0.59
	WSA	WSA+NW	-273.6	0.24	WSA	WSA+NW	-307.4	0.23
	WSA	WSA+Trop	-274.7	0.08	others			0.14
	WSA+Aus	WSA	-274.9	0.07				
	others			0.08				
2	WSA	WSA+NW	-273	0.45	WSA	WSA+NW	-306.9	0.35
	WSA	WSA	-273.5	0.28	WSA	WSA	-307	0.32
	WSA+Trop	Trop	-274.8	0.08	WSA+NW	NW	-308.6	0.07
	WSA	Trop	-275.2	0.05	others			0.21
	others			0.13				
3	WSA+Trop	Trop	-273.1	0.43	WSA	WSA	-306.8	0.42
	WSA	WSA	-273.8	0.21	WSA+Trop	Trop	-308	0.13
	Trop	Trop	-274.4	0.12	WSA+Trop	WSA	-308.6	0.07
	WSA+Trop	WSA	-275.2	0.05	ESA	ESA	-308.6	0.07
	others			0.19	Trop	Trop	-308.9	0.05
					others			0.22
4	Trop	Trop	-273.4	0.30	WSA+ESA	ESA	-306.8	0.38
	WSA+ESA	ESA	-274.3	0.13	ESA	ESA	-307.8	0.15
	ESA	ESA+Trop	-274.4	0.11	ESA+Trop	ESA	-308.4	0.08
	Trop	ESA+Trop	-274.5	0.10	Trop	Trop	-308.7	0.06
	WSA+Trop	Trop	-274.9	0.07	WSA	ESA	-308.8	0.05
	ESA	ESA	-275	0.06	others			0.18
	others			0.18				
5	ESA	Trop	-272.4	0.81	ESA	Med	-306.6	0.51
	ESA	Med	-274.4	0.12	ESA	EuAs	-307.2	0.28
	ESA	EuAs	-275	0.06	ESA	Trop	-307.9	0.13
					others			0.04
6	Med	Trop+Med	-272.5	0.79	Med	EuAs+Med	-306.6	0.50
	Med	EuAs+Med	-274.5	0.10	Med	Med	-307.4	0.22
	others			0.11	Med	Trop+Med	-307.8	0.15
					Med	EuAs	-308.6	0.07
					others			0.02

	Complex model				**Simple model**			
	Biogeographic region of				**Biogeographic region of**			
Node	**Upper branch**	**Lower branch**	**lnL**	**Rel.Prob.**	**Upper branch**	**Lower branch**	**lnL**	**Rel.Prob.**
7	WSA	WSA	-272.9	0.53	WSA	WSA	-306.8	0.41
	WSA	Trop	-273.7	0.24	WSA	NW	-307.7	0.17
	WSA	WSA+Med	-274	0.17	WSA	Med	-307.8	0.15
	WSA	WSA+EuAs	-275.2	0.05	WSA	WSA+Med	-308	0.12
					others			0.11
8	Med	WSA	-272.8	0.57	Med	WSA	-306.8	0.41
	Med	Trop	-273.9	0.19	Med	NW	-307.8	0.15
	EuAs	WSA	-274	0.17	EuAs	WSA	-308	0.13
	EuAs	Trop	-275.1	0.06	Med	Med	-308.8	0.05
					Med	Trop	-308.8	0.05
					others			0.16
9	Med	Med	-272.7	0.63	Med	Med	-306.4	0.63
	EuAs+Med	Med	-274.1	0.16	EuAs+Med	Med	-307.7	0.17
	EuAs	EuAs	-274.6	0.09	EuAs	EuAs	-308.4	0.08
	EuAs	EuAs+Med	-275.2	0.05	EuAs	EuAs+Med	-308.8	0.06
	others			0.05	others			0.02

Appendix S3: Method and Results of the molecular dating approach incorporating the newly published fossil.

S3.1: MOLECULAR DATING

We used two recently discovered fossils that suggests that Asteraceae are older than previously thought. One fossil has been placed after the split of the newly described subfamily Famatinanthoideae (Panero *et al.*, 2014) with a minimum age of 47.5 Million years ago (Ma; Barreda *et al.*, 2010). The second fossil was placed within the Barnadesioideae (Barreda *et al.*, 2015) with a minimum age of 72.1 Ma. Other dating approaches of *Senecio*/Senecioneae were based on secondary root calibration and island ages as calibration points (Pelser *et al.*, 2010) or only based on ITS substitution rates (Pelser *et al.*, 2012). To use the fossils we constructed an Asteraceae phylogeny including all described subfamilies and some representatives of the tribe Senecioneae using cp *trn*LF, *ndh*F and *rbc*L. All sequences were available in GenBank (Appendix S1.1). In an initial analysis, the Asteraceae dataset did not resolve the phylogeny as shown by Panero *et al.* (2014) that was based on much more sequence data and taxa. We therefore constrained the tree topology accordingly. For dating, we first used BEAST v 1.8.2 (Drummond *et al.*, 2012; run on CIPRES [Miller *et al.*, 2010]) on the Asteraceae tree. We chose an exponential distribution as prior for the fossil calibrations, partitioning and substitution model according to the results of PARTITIONFINDER (Appendix S2.1), an uncorrelated lognormal relaxed clock (ULRC), and a yule speciation process as tree prior. The age of the root of the tree was calibrated with a uniform distribution of 73-101 Myr (maximum age of Asterales according to Beaulieu *et al.*, 2013). Two independent runs were conducted and combined excluding burn-in of 10 % using LOGCOMBINER v. 1.8.2 and TREEANNOTATER v. 1.8.2 (Drummond *et al.*, 2012) when chains converged and the effective sample size was above 200 as checked with TRACER (Rambaut & Drummond, 2007). Results are presented in Appendix S3.2. The crown age of the *Synotis*-*Senecio*-clade as estimated in BEAST from the Asteraceae cp matrix was then used as a secondary calibration point to date the nr *Senecio* matrix. The mean of the highest posterior density (HPD) values of the crown age was used as calibration point with a standard deviation of two using a normal distribution and the same priors as above. Results of the secondary calibration are presented in Appendix S3.3.

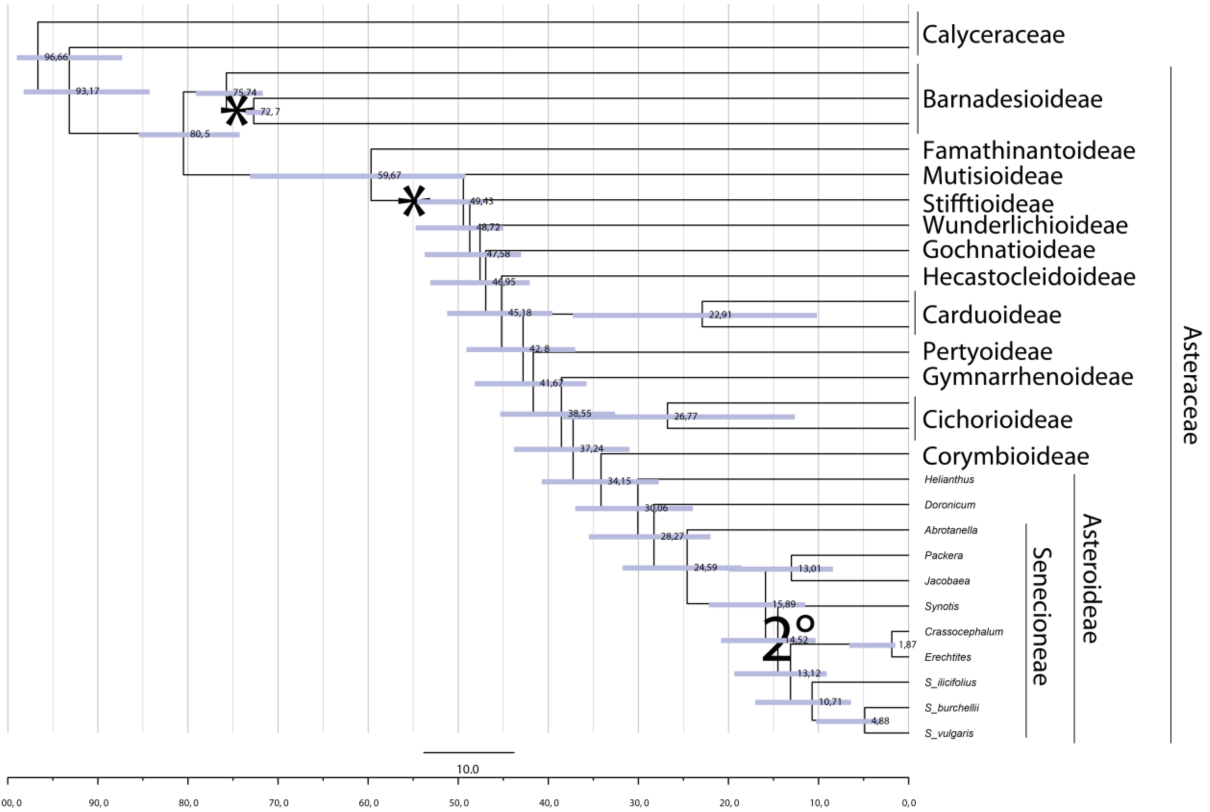

Figure S3.2: Maximum clade credibility tree of the dated Asteraceae cp phylogeny. Placement of fossil calibration points are indicated by an asterisk and the age estimate used for the secondary calibration point is indicated by 2°.

Table S3.3: Results of the molecular dating analyses in million years including the 95% highest posterior density intervals of Asteraceae, Senecioneae (excl. *Doronicum*) and *Senecio* using BEAST (under a yule process). Abbreviations: 2°: secondary calibration.

Clade	**Posterior age estimates inferred with BEAST**	
	Fossil calibration	**2° calibration**
Asteraceae crown	80.5 (86.99-75.41)	
Senecioneae stem	28.27 (35.3-21.35)	
Senecioneae crown	24.59 (31.45-17.76)	
Senecio stem	13.12 (18.62-8.00)	13.83 (17.80-9.75)
Senecio crown	10.71 (16.2-5.22)	9.21(13.57-5.47)
vulgaris-clade stem		5.42 (8.14-3.09)
vulgaris-clade crown		4.26 (6.58-2.38)
doria-clade stem		5.36 (8.09-3.08)
doria-clade crown		4.42 (6.64-2.42)

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4. Frequent colonization and little *in situ* speciation in *Senecio* L. in the tropical alpine-like islands of eastern Africa

Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Abstract

The high altitude areas of the eastern African high mountains, the so-called tropical Afroalpine, have climatic conditions very different from the surrounding lowlands and can thus be considered continental habitat islands. Floras of such continental habitat islands, like those of islands, originate mainly through colonization, which can be followed by *in situ* speciation. We here address the question of the relative importance of colonization and *in situ* diversification in those mountains using the most species-rich genus in the region, *Senecio*, as an example. For this purpose, we expanded earlier Senecioneae phylogenies by adding more tropical African species and analysed our phylogenetic tree biogeographically. The phylogeny shows that *Senecio* contains at least five clades with tropical African species, all of them containing tropical afroalpine species. Between five to 14 independent colonization events into the Afroalpine most likely from montane regions in southern Africa could be inferred, and relationships of afroalpine species to the Palaearctic and South America were found. Although some *in situ* diversification was found for *Senecio* in the tropical Afroalpine, the resulting number of species is low and never higher than seven species, depending on relationships of subclades. This contrasts strongly with the high amount of *in situ* diversification found in the Andes, another mountain range of comparable ecology. We briefly discuss possible explanations for the absence of large radiations in the tropical Afroalpine.

Introduction

Because of their geographical or ecological isolation, the floristic composition of islands is much influenced by colonization and *in situ* speciation (MacArthur & Wilson, 1967; Carlquist, 1974). The frequency of colonization depends on the degree of isolation (MacArthur & Wilson, 1967) and influences the degree of divergence between the source area and the islands. This divergence can be further enhanced by *in situ* evolution and speciation subsequent to colonization (Coyne & Orr, 2004; Clegg, 2010; Gillespie & Baldwin, 2010). The concept of island biogeography as proposed by McArthur and Wilson (1967) has been expanded to include continental habitats which are isolated from similar habitats by unfavourable terrain, so-called sky islands (Gorman, 1979). An example for such are alpine-like habitats on high mountains in tropical environments which can be considered climatically temperate islands in tropical environments (Hedberg, 1969, 1970; Sklenář *et al.*, 2014). Such alpine-like habitats, which can be found above the natural treeline, require certain plant properties, such as frost tolerance (Körner, 2003), which is not needed in tropical environments. Whereas most tropical alpine-like regions in South America (Andes) and in New Guinea are part of high elevation mountain ranges with a more or less continuous temperate zone, the high mountains in eastern Africa (EA) mostly are isolated volcanoes, with a smaller number of mountains being part of mountain ranges (Hedberg, 1951; Gehrke & Linder, 2014; Fig. 1).

With their plant species composition much different from the surrounding lowlands, the alpine-like regions in EA have been classified as an independent floristic region, the tropical Afroalpine (Hedberg, 1951; Hauman, 1955; White, 1983; Gehrke & Linder, 2014). However, not all African regions with alpine-like climatic conditions are considered tropical Afroalpine (Fig. 1). Mountains in Yemen share a number of taxa with the tropical Afroalpine but lack many tropical Afroalpine characteristics and are more seasonal and drier, and mountains in southern Africa (SA) such as the Drakensberg Mountains have some tropical alpine-like characteristics but are generally lower and more seasonal (Gehrke & Linder, 2014). The tropical Afroalpine, which is characterized by a diurnal climate, can be divided into subregions based on their floristic composition (Hedberg, 1965; White, 1983; Gehrke & Linder, 2014; Fig. 1). The EA Mountains have been divided into three subregions: Ethiopia, the eastern branch and the western branch of the Great Rift Valley (Gehrke & Linder, 2014). The only mountain in western Africa, which is high enough to support an alpine-like zone, Mt. Cameroon, has been considered a fourth subregion of the tropical Afroalpine. The orogeny of the EA mountains is closely linked to the genesis of the Greater Rift Valley, and although some EA mountains already existed before the

Miocene, many did not attain high elevations before the Pliocene (Chorowicz, 2005; Gehrke & Linder, 2014).

The affinity of the EA tropical Afroalpine flora to other temperate floras has been noted ever since research on the region was conducted (Engler, 1904; Hedberg, 1965; Goldblatt, 1978; Killick, 1978; Smith & Cleef, 1988; Rundel *et al.*, 1994), and such affinity has been confirmed by the few phylogenetic analyses available (Assefa *et al.*, 2007; Galley *et al.*, 2007; Popp *et al.*, 2008; Bergh & Linder, 2009; Gehrke & Linder, 2009; Galbany-Casals *et al.*, 2014). Considering the probable predominance of niche conservatism (Wiens, 2004; Donoghue, 2008), dispersal from temperate regions indeed seems more likely than adaptive evolution of lineages from surrounding tropical regions. Although, as described above, the mountains of Yemen and SA are not considered as tropical Afroalpine, they represent temperate patches in warmer surroundings and might have acted as stepping-stones in the colonization of the EA high altitude islands. Other source areas for the tropical Afroalpine seem to be the Northern Hemisphere and other temperate parts of southern Africa (Hedberg, 1965).

Here, we investigate the colonization of the EA tropical Afroalpine by *Senecio* L., the most species-rich genus in the region (Gehrke & Linder, 2014). *Senecio* belongs to Asteraceae, which contributes more species to the tropical Afroalpine than any other family (Gehrke & Linder, 2014). *Dendrosenecio* B. Nord., a very characteristic genus of the tropical Afroalpine, belongs to the same tribe as *Senecio*, but is only distantly related to it (Knox & Palmer, 1995a; Pelser *et al.*, 2007). Traditionally, *Senecio* had been considered to contain about 3000 species (Jeffrey *et al.*, 1977; Bremer, 1994), but more recently it has been shown not to be monophyletic (e.g. Knox & Palmer, 1995b; Pelser *et al.*, 2007; Calvo *et al.*, 2013). The genus has a nearly cosmopolitan distribution with major diversity centres in SA and South America (Bremer, 1994; Pelser *et al.*, 2007). Earlier molecular analyses and ancestral area reconstructions showed that the genus is likely to have originated in the dry or winter rainfall regions of WSA in the mid to late Miocene, from where it dispersed to other parts of Africa and to all other continents except Antarctica (Pelser *et al.*, 2007; Pelser *et al.*, 2010; Pelser *et al.*, 2012, Chapter 3).

We here expand existing molecular phylogenies of Senecioneae and *Senecio* by adding tropical African species, and analyse our phylogenetic tree in order to address the following questions: (1) Are the tropical afroalpine species derived from a single or from multiple colonization events? (2) Did the tropical afroalpine species originate from tropical lowland stock or from temperate species which colonized the tropical Afroalpine by dispersal? (3) What is the extent of *in situ* diversification in the tropical Afroalpine? (4) When did the tropical Afroalpine species evolve?

Finally, we will compare our results for *Senecio* in the tropical Afroalpine with studies of tropical alpine-like regions in other parts of the world.

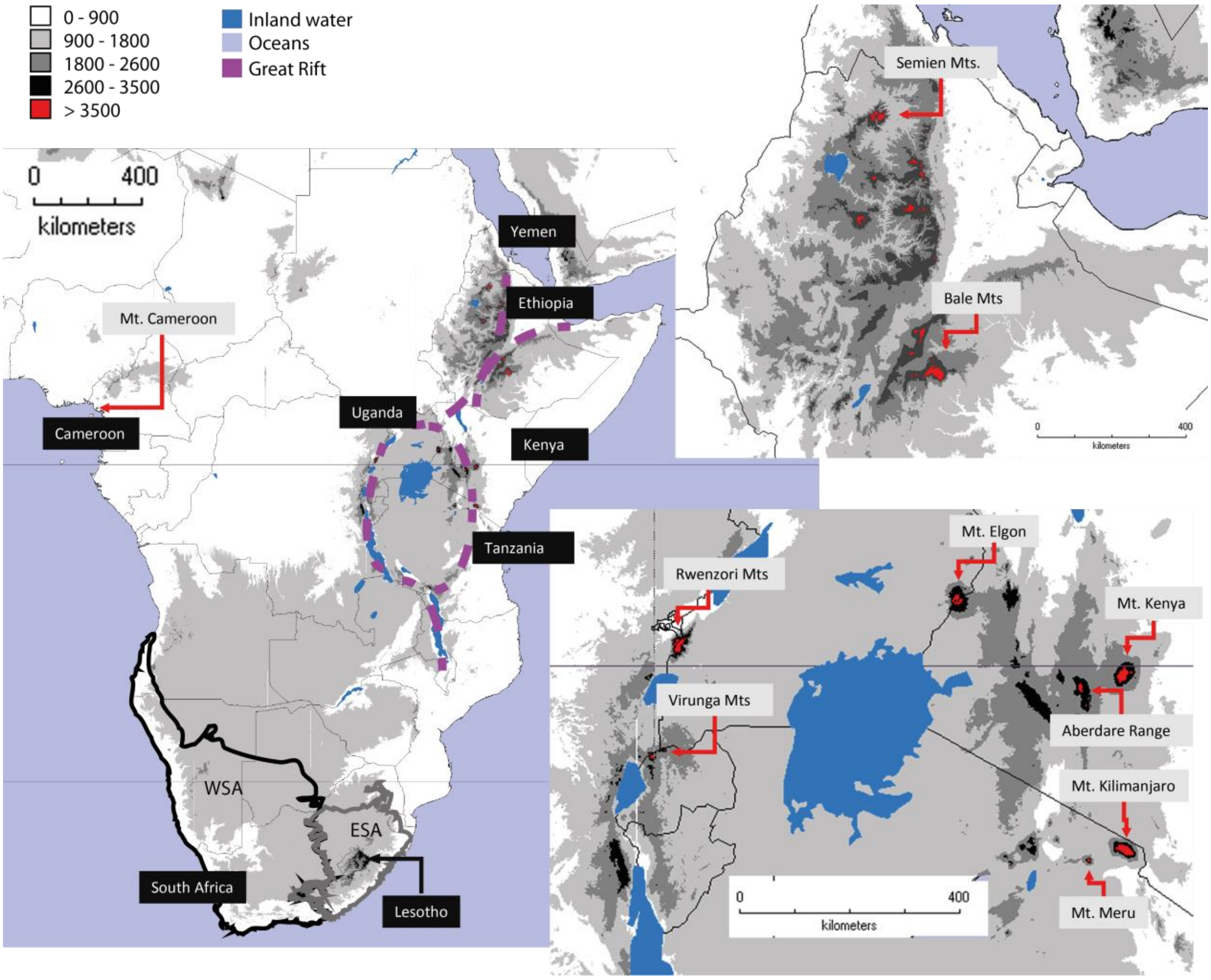

Figure 1: Sub-Saharan Africa with East Africa and Ethiopia enlarged (insets). Country names of importance, elevation and names of major mountain systems are given. Grey scale and red colours indicate elevation, blue colours indicate water and purple lines indicate the East African Great Rift.

Material and Methods

Taxon Sampling, DNA extraction, PCR amplification and sequencing

After removing intraspecific taxa, synonyms and species which now are known not to be part of *Senecio* as circumscribed by Pelser *et al.* (2007), the African Plant Database (2012) lists 144 *Senecio* species in tropical Africa and 260 species occurring exclusively in SA. According to the Flora of Tropical East Africa (Jeffrey & Beentje, 2005) and the Flora of Ethiopia and Eritrea (Tadesse, 2004a), there are 87 species native to Ethiopia, Eritrea, Kenya, Tanzania and Uganda. According to other tropical African Floras, the rest of tropical Africa harbours only a small number of *Senecio* species (Oliver & Hiern, 1877; Lisowski, 1989; Hutschinson & Dalziel, 2014). Many species described as *Senecio* might not be part of *Senecio* as newly defined (Pelser *et al.*, 2007). To identify whether the species sampled for this study belong to *Senecio* or not, we included a selection of other genera of Senecioneae in our analyses (Pelser *et al.*, 2007). Within *Senecio*, most species from EA are nested in sub-Saharan African clades (Chapter 2 & 3) which were therefore sampled as completely as possible. All other clades of the genus in which no tropical African species are found were represented by a small number of placeholder species only. In total, we included 52 (36 %) tropical African and 84 (32 %) exclusively SA species in our analyses. The 52 tropical African species include 24 of the 26 EA high altitude species. Of the two missing species, one, *Senecio hedbergii* C. Jeffrey, is rare and occurs at elevations below 3650 m, and the second, *S. polyadenus* Hedb., is only known from the Virunga Mts. Our sampling comprises publicly available sequences of 294 species (Appendix S1.1 in the Supporting Information) and 42 species were newly sequenced (Appendix S1.2). We amplified the nuclear ribosomal (nr) internal transcribed spacer (ITS) and external transcribed spacer (ETS), and the plastid (cp) *ycf*6-*trn*C and *trn*L-*trn*F intergenetic spacer and the *trn*L intron. Extraction, amplification and sequencing followed standard protocols as described in Chapter 3 (see also Appendix S1.3).

DNA sequence alignment and phylogenetic reconstruction

Different nr datasets were used: The Senecioneae dataset of ITS sequences includes major lineages of Senecioneae, with only few representatives of *Senecio*, and *Doronicum* L. as outgroup. This dataset was used to determine whether a given species belonged to *Senecio* or to another genus of the tribe. The *Senecio* dataset of ITS and ETS comprises all available accessions of clades containing sub-Saharan African species and a subsample of taxa for the other clades, and *Crassocephalum* Moench as outgroup. The ITS and ETS data were combined after removing multiple accessions of species (in order to reduce missing data). Sequences of taxa for which topologies of individual markers were conflicting (>0.95 Bayesian posterior probability [PP]; >70 % Maximum Likelihood bootstrap support [BS]) were not concatenated but treated as independent accessions. The cp dataset consists only of *Senecio* species with *Crassocephalum* as outgroup. Substitution model and best partitioning scheme were inferred using PARTITIONFINDER v.1.1.1 (Lanfear *et al.,* 2012). Phylogenetic relationships were reconstructed using nrDNA and cpDNA separately, accounting for a high degree of incongruence between the cp and nr data described earlier (Pelser *et al.,* 2007; Pelser *et al.,* 2010; Pelser *et al.,* 2012; Calvo *et al.,* 2013; Chapter 3). Indels were coded for the cp data only (Appendix S1.3). Phylogenetic analyses were carried out using Maximum Likelihood (ML; RAXML v. 8.0.24 [Stamatakis, 2006; http://embnet.vital-it.ch/raxml-bb/]) and Bayesian Inference (BI; MRBAYES v. 3.2.1 [Ronquist *et al.,* 2012]). Under ML, standard settings were applied, multiple markers of one genome were treated as one partition and rate heterogeneity was accounted for where necessary (Appendix S2.1). Under BI, multiple markers of one genome were treated as one partition and substitution models were adjusted according to the results of PARTITIONFINDER (Appendix S2.1). Two independent runs were conducted with sampling every 1000th generation. Length of the runs was between ten and twenty million to ensure that effective sampling sizes for parameters were >200 (estimated using TRACER v. 1.5; Rambaut & Drummond, 2007). After removing a burn-in of 10 %, the results of the two independent runs were combined.

Age estimate of tropical afroalpine Senecio *species*

To identify the time period when *Senecio* colonized the tropical Afroalpine, we examined the dated *Senecio* phylogeny of Chapter 3 which includes all clades containing tropical afroalpine species. As no supported relationships within clades with afroalpine species were found (cf. Fig. 3), we will only refer to the crown ages of the supported subclades including tropical afroalpine species.

Ancestral area reconstruction and character optimisation

Information about distribution and altitude was collected for all tropical African *Senecio* species (sampled and non-sampled species) as well as all sampled SA species using Floras, earlier publications and online resources (Appendix S1.4-S1.6). Ancestral area and altitudinal distribution reconstructions were performed for clades including tropical afroalpine species and showing sufficient resolution (only the consanguineus-clade) using LAGRANGE v. 20130526 (Ree & Smith, 2008) with standard settings. For this, the clade of interest was taken from the Bayesian nr *Senecio* phylogeny and polytomies were arbitrarily bifurcated using the ape-package in R (Paradis *et al.*, 2004; R Core Team, 2013). For the other clades including tropical afroalpine species but lacking resolution, we discuss possible area relationships without formal analysis.

Geographical distribution of species was scored as: (1) tropical Africa; (2) western southern Africa (WSA); (3) eastern southern Africa (ESA); (4) Palaearctic (Europe, Asia north of the Himalayan foothills, northern Africa, and the northern and central parts of the Arabian Peninsula), (5) Australasia (including Australia, Malesia, New Zealand and the Pacific); (6) America (Fig. 1). Widespread species were coded as multiple states. We scored species according to overall distribution instead of sampling locality because in most cases we did not sample their entire distribution ranges.

Altitudinal distribution was scored as 1) lowland, 2) montane and 3) alpine-like using altitudinal information in combination with distribution range (details can be found in Appendix S1.4-S1.5). As the delimitation of these categories depends on latitude, climate, water availability and further parameters (Körner, 2003), their limits in meters above sea level is different in different regions. Depending on mountain, its location, climatic conditions, etc., the tropical Afroalpine is located around a seasonal mean ground temperature of about 5 to 6 °C (Körner, 2003; Körner & Paulsen, 2004), which can be found from 3500 to 4000 m above sea level (Hedberg, 1951). We chose 3500 m as limit to classify species as tropical Afroalpine. Species occurring from 1800-3500 m in EA were coded as montane, and those occurring below 1800 m as lowland. Species in SA were scored differently to account for the effect of latitude: lowland: 0-900 m; montane: 900-2600 m and alpine-like: >2600 m. Since we wanted to score the major range of species, they were allowed to occur up to 100 m above or below the limits as defined. For example, an EA species found between 3420 to 4310 m was scored as alpine-like (min. elevation 3500 m), and a species found between 3390 to 4310 m was scored as alpine-like and montane. Non-African species were not scored for altitudinal distribution.

Results

Phylogenetic relationships

Of the 46 newly sampled African species, 18 do not belong to *Senecio,* including nine species occurring in tropical Africa (Fig. 2). These species all group within Senecioneae subtribe Senecioninae, and most occur in lowland or montane areas (Tab. 1). However, four of the SA species which do not belong to *Senecio* also occur in alpine-like areas in SA (Appendix S1.5).

The ITS phylogeny revealed a monophyletic *Senecio* with seven supported and four unsupported clades and *Senecio cadiscus* B.Nord. & Pelser in an unresolved position (Appendix S2.2). The ETS phylogeny recovered most of the clades present in the ITS phylogeny, but fewer of them were supported (Appendix S2.3). Comparison of the ITS and ETS phylogenies showed supported incongruence in the positions of *S. seminiveus* J.M. Wood & M.S. Evans, *S. sabinjoensis* Muschl. and *S. x pirottae* Chiov. (Appendix S2.5). These species are represented twice in the nr phylogeny, once with only the ITS and once with only the ETS sequence (Fig. 3). The combined ITS and ETS phylogeny (Fig. 3) revealed 11 clades, all supported by 0.97 PP or higher in the BI analyses, except for the doria-decurrens (0.9) and Australasia 2-clade (0.77). ML bootstrap support higher than 75 was found in all clades except for the New World 1-, Australasia 2- and the doria-decurrens-clades. These findings are consistent with previous results by Pelser *et al.* (2007) and Chapter 3.

Most species of *Senecio* occur at least in montane regions (>1800 m) in tropical Africa. The only tropical African *Senecio* species found as low as 900 m is *S. hochstetteri* Sch.Bip. ex A.Rich, a widespread species also occurring in western and southern Africa. Four more species are found as low as 1500 m in tropical Africa (Tab. 1 & Appendix S1.4). In total, we lack phylogenetic information for 93 species described as *Senecio* and which occur in tropical Africa (Tab. 1 & Appendix S1.6). We did not find any altitudinal information for 26 of those, and of the remaining species 21 were coded as purely lowland. Overall, seven species have been recorded to occur below 900 m, but these species are also found in SA and the altitudinal information was taken from SA publications or databases (Appendix S1.6). All other species recorded to occur in tropical Africa occur exclusively above 900 m.

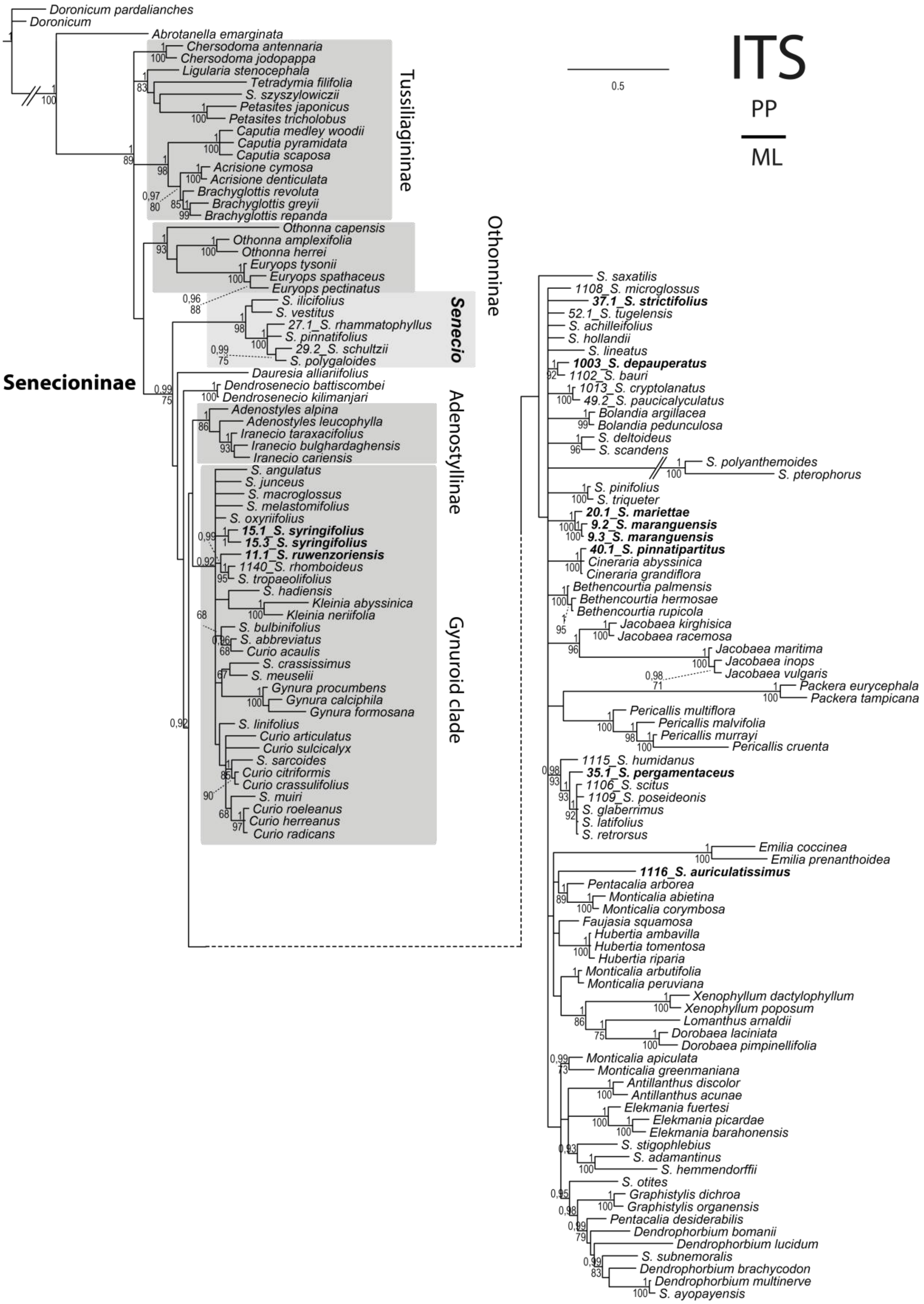

Figure 2: Phylogenetic reconstruction of Senecioneae based on the ITS majority rule consensus tree, calculated with Bayesian Inference (BI) method. Species names in bold are newly added tropical African species which do not belong to *Senecio*. Species not obtained from GenBank are indicated by their extraction number before the name. Support values for BI >0.9 posterior probability (PP) and for Maximum Likelihood (ML) bootstrap support values >75 are shown at the nodes.

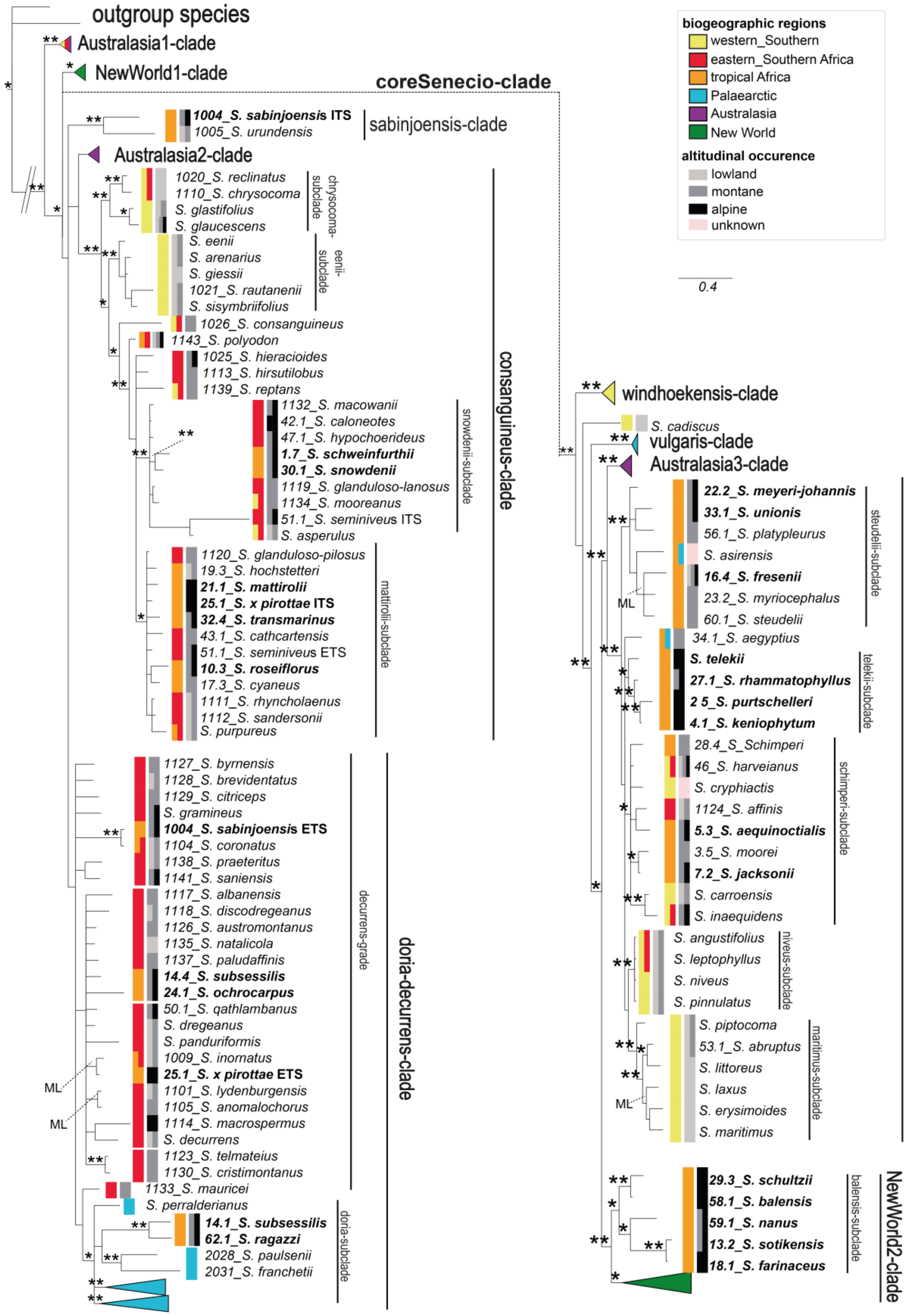

Figure 3: Phylogenetic reconstruction of *Senecio* based on the combined nr ITS and ETS majority rule consensus tree, calculated with Bayesian Inference (BI) method. Species written in bold italic are tropical afroalpine species. Species not obtained from GenBank are indicated by their extraction number before the name. Clades supported by BI >0.95 and ML >75, respectively, are indicated by two asterisk, clades only supported by BI >0.95 are marked with one asterisk and clades only supported by ML >75 are indicated with the abbreviation ML. Ancestral reconstruction of the consanguineus-clade can be found in Supporting Information S2.6 and S2.7.

Table 1: Species listed as *Senecio* in the African Plant Database (excluding species already known not to belong to *Senecio* before this study) as occurring in tropical Africa, arranged according to our generic results and their altitudinal distribution.

generic affiliation	#	unknown altitude	low	low and montane	montane	montane and alpine-like	alpine-like	all altitudes
Senecio	39	1	0	5	7	17	8	1
Non-*Senecio*	14	1	0	6	7	0	0	0
unknown	93	26	21	18	24	1	1	1
total	146	28	21	29	38	18	9	2

Age of tropical afroalpine Senecio *species*

The crown ages of subclades including tropical afroalpine species ranged from 6.64 to 0.31 Million years ago (Ma; considering the highest posterior density intervals; Tab. 2).

Table 2: Ages (with highest posterior density intervals) in Million years of clades including tropical afroalpine *Senecio* species based on the dated phylogeny of Chapter 3[4].

Clade	Subclade	Stem age	Crown age
Consanguineus		5.8 (8.77-3.31-)	4.43 (6.86-2.47)
	snowdenii		1.83 (3.01-0.88)
	mattirolii		1.41 (2.39-0.66)
Doria-decurrens		6.5 (9.66-3.73)	5.96 (9.09-3.49)
	doria		4.42 (6.64-2.42)
	decurrens		-
Fresenii		3.79 (6.73-2.08)	2.76 (4.36-1.54)
	steudelii		1.96 (3.25-0.96)
	telekii		1.20 (2.37-0.31)
	schimperi		1.59 (2.61-0.74)
New World 2		4.45 (6.73-2.44)	3.25 (5.22-1.67)
	balensis		-
sabinjoensis	-	6.5 (9.66-3.73)	3.64 (6.39-1.41)

Tropical afroalpine Senecio *species and their source area*

Several independent colonizations of the mountains of EA took place in *Senecio*. However, the source areas of these tropical afroalpine species could not be inferred unambiguously (Fig. 3 & Tab. 3). We found five clades containing tropical afroalpine species (Fig. 3), i.e., the consanguineus-, doria-decurrens-, fresenii-, New World 2- and sabinjoensis-clades, with, dependent on how relationships are resolved, between five to 14 independent colonization events (Tab. 3). In all clades more than one subregion of the tropical Afroalpine was colonized, and all

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[4] Diese Altersangaben beziehen sich auf die Datierung, die das neue Fossil berücksichtigt (Kapitel 3: Appendix 3).

contain montane species (Fig. 3 & Tab. 3). The number of independent colonization events into the mountains of EA would be four if colonization of montane regions were included (Fig. 3).

All afroalpine species are either single mountain endemics or endemic to only a few mountains in close proximity within one EA tropical Afroalpine subregion, except for the montane and alpine-like *S. subsessilis* Oliv. & Hiern. (Appendix S1.4). *Senecio subsessilis* is widespread in eastern and central Africa, but is not monophyletic in our analyses. In general, montane species occurring only in tropical Africa are confined either to Ethiopia or to the western branch of the Rift Valley, while tropical montane species that also occur in SA are generally more widespread in EA (Appendix S1.4).

Consanguineus-clade

The nr phylogeny revealed four well-supported subclades and five unplaced species in the consanguineus-clade. This was the only clade with enough supported resolution to perform an ancestral area reconstruction (Fig. 3, Appendix S2.6 & S2.7). In total, the clade contains five tropical afroalpine species (plus one tropical afroalpine species that shows phylogenetic conflict between ITS and ETS), two in the snowdenii-subclade and three in the mattirolii-subclade. All tropical afroalpine species of the clade occur in the western and eastern branches of the Rift Valley (Fig. 3 & Tab. 3).

The relationships of the snowdenii-subclade differ between the cp and nr phylogenies but without support in the cp phylogeny (Fig. 3 & Appendix S2.4). The relationships of the mattirolli-subclade are congruent between the two data sets, but the subclade contains two species with conflicting ITS and ETS sequences (one tropical afroalpine species and one SA species). The ITS sequence of *Senecio x pirottae* placed this species, which had been described as a hybrid between *S. transmarinus* S. Moore and *S. mattirolli* Chiov., both endemic to the western branch of the Rift Valley (Jeffrey & Beentje, 2005), in the same subclade as its putative parents. The ETS sequence of *S. x pirottae* placed the species with high support outside the consanguineus-clade (i.e., in the unsupported decurrens-grade). *Senecio seminiveus*, which occurs in the Drakensberg area of SA, is placed in the snowdenii-subclade with the ITS sequence data and in the mattirolli-subclade with the ETS data.

According to our LAGRANGE analyses (Appendix S2.7 & S2.6), the most likely geographical scenario is dispersal from the lowlands in WSA to montane ESA to montane and alpine-like regions in EA. However, the number of independent colonization events of the EA high mountains is ambiguous. Either the most recent common ancestor (mrca) of the two subclades containing tropical afroalpine species colonized EA (either montane or alpine-like regions) with back-colonization of SA, or the EA mountains were colonized up to four times independently if afroalpine species of the mattirolli-subclade do not form a monophyletic lineage; Fig. 3 & Tab. 3). This count does not consider the tropical afroalpine species with incongruent positions in the ITS and ETS datasets.

Doria-decurrens-clade

The unsupported nr doria-decurrens-clade consists mostly of ESA and Palaearctic species, of which the Palaearctic plus two tropical alpine-like species form the supported doria-subclade (Fig. 3) which is nested within the decurrens-grade. In the cp phylogeny, the doria-subclade is unsupported but all except five species of the nr decurrens-grade form a well supported clade (Appendix S2.4).

In total, there are four tropical afroalpine species always placed in the doria-decurrens-clade plus two species which are placed here only with their ETS sequences (Fig. 3 & Tab. 3). The tropical afroalpine species occur in Ethiopia and the western branch of the Rift only, while the non-afroalpine species occur in tropical Africa and in ESA. In the decurrens-grade, relationships between ESA and tropical African species are unresolved. Similar to the doria-subclade, two tropical African species occur in montane and alpine-like regions, but their relationships to the Palaearctic species are unclear. One species, *Senecio ragazzi* Chiov., occurs only in Ethiopia, while the other species, *S. subsessilis*, is widely distributed in tropical Africa but not monophyletic in our analyses. Two accessions of *S. subsessilis* sampled in the Aberdares/Kenya are sister to *S. ragazzi* (Fig. 3 & Tab. S1.2), while the third accession, collected on Mt. Kilimanjaro/Tanzania, is placed in the decurrens-grade. We conclude that there were one to three independent colonization events of the tropical Afroalpine in the doria-decurrens-clade (Fig. 3 & Tab. 3). Either one or two from ESA with one onward dispersal to the Palaearctic, or one or two from ESA and one from the Palaearctic. This does not consider species with incongruent positions of ITS and ETS.

Fresenii-clade

The nr phylogeny revealed five supported subclades plus *S. aegyptius* L. in an unresolved position in the fresenii-clade. The maritimus- and niveus-subclades include predominantly species from SA lowlands. The other three subclades mostly consist of EA species occurring in montane and alpine-like regions in Ethiopia and the western branch of the Rift Valley. In total, there are nine afroalpine species in the fresenii-clade. In two of the subclades *in situ* speciation seems likely. The four species of the telekii-subclade occur only in montane and alpine-like regions of East Africa and are supported as a monophyletic lineage and the supported steudelii-subclade consists only of montane and alpine-like Ethiopian species, plus one species from Yemen and Saudi Arabia, *S. asirensis* Boulos & J.R.I.Wood. There are three afroalpine species in this subclade, but relationships are unsupported. The third subclade, the schimperi-subclade, consists of EA and SA species and contains two afroalpine species. *Senecio platypleurus* Cuford (sampled from Ethiopia), which has been considered a heterotypic synonym of *S. aequinoctialis* R.E.Fr. (Tadesse, 2004a), is here placed in the steudelii-subclade, while *S. aequinoctialis* (sampled from Kenya*)* is found in the schimperi-subclade.

Depending on relationships among the three subclades including afroalpine species there could have been two to six independent colonization events (Fig. 3 & Tab. 3). However, poor support within the whole clade makes it impossible to reconstruct the exact number and geographic and altitudinal origin of the colonizing lineages, but a sub-Saharan African ancestry of the entire clade is most likely.

New World 2-clade

The New World 2-clade of the nr phylogeny shows that a supported subclade of five montane and afroalpine EA species, the balensis-subclade, is sister to a subclade of New World species (Fig. 3). The balensis-subclade comprises four Ethiopian afroalpine endemics and one montane and alpine-like Mt. Elgon endemic species, S. *sotikensis* S. Moore. Within this clade, there was one colonization event of the tropical Afroalpine with subsequent *in situ* speciation (Tab. 3). The source area is either the New World or there was a colonization of the Afroalpine from somewhere else, most likely sub-Saharan Africa, and the New World was colonized from the tropical Afroalpine.

Sabinjoensis-clade

This clade consists only of *S. sabinjoensis* and *S. urundensis* S. Moore (Fig. 3). *Senecio urundensis* is widespread in EA and occurs in lowland and montane regions, while *S. sabinjoensis* is restricted to montane and alpine-like habitats in the Virunga Mts (Appendix S1.4). There is a phylogenetic conflict between the ITS and ETS sequences of *S. sabinjoensis*, and the ETS sequence places the species in the decurrens-grade, where it forms a well supported clade with *S. coronatus*, a species widespread in sub-Saharan Africa but not known to occur on the Virunga Mts. The source region as well as the altitudinal origin of the mrca of this clade is unclear as the position of this clade in the phylogeny is unresolved (Fig. 3).

Table 3: List of clades that contain tropical afroalpine *Senecio* species. Information about the distribution of the clades in the different subregions, the most likely source area of the EA species, as well as the most likely altitude in the source area and EA are given. Number of independent colonization events of tropical afroalpine lineages within subclades are given without counting tropical afroalpine species where phylogenetic conflict was discovered. Asterisks (*) mark clades with tropical afroalpine species showing phylogenetic conflict. For subregions see Fig. 1. Abbreviations for subregions: EEA – eastern branch of the Great Rift; ESA – eastern southern Africa; ETH – Ethiopia; EuAs – Palaearctic; trop – tropical African regions, excluding EEA, WEA, ETH; WEA – western branch of the Great Rift; WSA – western southern Africa. Abbreviation for altitudinal zonation: a – alpine-like; l – lowland; m – montane.

Clade	**Subclade**	**Occurrence in subregion**	**# of tropical/ tropical afroalpine species**	**# of colonization events into the tropical afroalpine**	**Area and altitudinal occurrence of species from the possible source areas**
Consanguineus			8/5*	1-4	
	snowdenii	EEA, WEA, ESA, WSA	2/2	1	ESA, WSA; (l), m, a
	mattirolii	EEA, WEA, trop, ETH, ESA	6/3*	1-3	ESA, trop, EEA, WEA, ETH; l, m, a
Doria-decurrens			6/4**	1-3	
	doria	ETH, EEA, WEA, trop, EuAs	2/2	1	EuAs, ESA; ?
	decurrens	EEA, WEA, ETH, trop, ESA	4/2**	1-2	ESA (EEA, WEA, ETH, trop); l, m, a
Fresenii			15/9	2-6	
	steudelii	ETH, Arabian Peninsula	7/3	1-3	?; ?
	telekii	EEA, ETH, EuAs	4/4	1	?; ?
	schimperi	EEA, ETH, ESA, WSA	4/2	1-2	WSA, ESA, trop, EEA, ETH; (l), m, a
New World 2			5/5	1	
	balensis	ETH, EEA	5/5	1	?; ?
Sabinjoensis	-	EEA, WEA trop	2/*	0	?; ?

Discussion

Tropical African and tropical Afroalpine Senecioneae

All tropical alpine-like species included in our study belong to *Senecio*, and most *Senecio* species from tropical Africa occur at least in montane regions. In contrast to this, most species from lowland or lowland and montane regions of tropical Africa analysed here do not belong to *Senecio* (Fig. 2 & Tab. 1). We identified only five *Senecio* species that occur in lowland areas of tropical Africa (0-1800 m), of which four have not been recorded below 1500 m and one not below 900 m in tropical Africa (Tab. 2 & Appendix S1.4). Only 33 of the 65 unsampled tropical African species, for which generic identity is unknown but information about altitudinal distribution is available, occur in the lowlands or in lowland and montane regions, i.e., at least partly below 1800 m (Appendix S1.6). In conclusion, of the 130 tropical African species described as *Senecio* (excluding those that have been shown not to belong to *Senecio*), only one quarter occurs in lowlands and for most of them we do not know their generic identity. Of the 12 non-*Senecio* genera of Senecioneae listed in EA Floras, only four are represented in the tropical Afroalpine (Tadesse, 2004b; Beentje *et al.*, 2005). The only genus of Senecioneae apart from *Senecio* with more than three species in the tropical Afroalpine is *Dendrosenecio* (Knox & Palmer, 1995a; Beentje *et al.*, 2005).This clearly shows that whereas Senecioneae, excluding *Dendrosenecio*, are frequent in tropical parts of Africa, *Senecio* itself is predominantly distributed in non-tropical and only rarely in tropical climates. Such conclusion had been anticipated by Cabrera (1999) who observed that the highest diversity of *Senecio* species (where *Senecio* was defined more traditionally) is found in mountainous regions of America, Asia and Africa. Furthermore, despite different assumptions about the relationships of *Senecio* in Asteraceae, already Small (1919) anticipated that the migration of *Senecio* took place along the mountains.

Multiple independent colonizations of the tropical Afroalpine and their source areas

All tropical afroalpine *Senecio* species are derived from five to 14 independent colonization events (Tab. 3). It has been shown for other plant lineages that colonization of the high mountains in EA took place more than once independently both from the Palaearctic (*Carex* L., *Ranunculus* L. and *Arabis alpina* L. [Assefa *et al.*, 2007; Gehrke & Linder, 2009]) and from southern Africa (*Pentaschistis* [Nees] Spach and *Helichrysum* Mill. [Ahmed, 2013; Galbany-Casals *et al.*, 2014]). Independent colonization events in these groups range from two to a maximum of 14, with the highest number reported for *Carex* from the Palaearctic (9-14 events; Gehrke & Linder, 2009). The high number of independent colonizations of the tropical Afroalpine by *Senecio* reported here fits this pattern well and shows once more that understanding of the floristic affinities of the tropical Afroalpine requires phylogenetic analyses and can not be fully understood based on taxonomic data only.

The area of origin of *Senecio* is WSA (Chapter 3), and based on our phylogeny it seems most likely that most colonizations of alpine-like regions of EA by *Senecio* occurred from the montane Drakensberg region, either directly or after establishment in montane regions of EA (Tab. 3). Overall, there is increasing support for a substantial contribution of southern Africa, especially the Drakensberg region, to the Afroalpine flora (Galley & Linder, 2006; Galley *et al.*, 2007; Devos *et al.*, 2010; Ahmed, 2013; Galbany-Casals *et al.*, 2014). Although the importance of northern hemispheric relationships of the tropical Afroalpine flora had been emphasized by Linder (2014), our results support the Cape to Cairo migration hypothesis of a recent northward migration from SA via the Drakensberg to the tropical Afroalpine (Linder, 1994; Galley *et al.*, 2007).

The Drakensberg range probably acted as a stepping-stone area, where species most likely from WSA (the area of origin of *Senecio*) preadapted to montane and alpine-like environments, before the tropical Afroalpine was colonized. A mountainous source area for tropical afroalpine species in turn implies that these colonizing *Senecio* lineages retained their broad scale niche. Expansion of distribution range without changes in broad scale niche had already been shown for two Palaearctic lineages of *Senecio* originating from SA (Fig. 3 & Chapter 3). Discussion of preadaptation before colonization of the mountains of EA assumes that montane or alpine-like environments in EA were already present at the time of colonization. According to the dating analysis of Chapter 3 (see also Tab. 2), diversification of the major clades containing tropical afroalpine species mostly started around the Pliocene-Pleistocene boundary (crown age estimates of subclades; Tab. 2), a time period which has also been inferred for the colonization of the tropical Afroalpine from SA by some other plant groups (*Stoebe* L.: 3.5-2.0 Ma [Bergh & Linder, 2009]; *Hypericum* L.: Mid-Miocene to Pliocene [Meseguer *et al.*, 2014]). However, other colonizations seem to be older (Giant Lobelias and dantonioid grasses; Antonelli, 2009; Linder *et al.*, 2013). As we only referred to the crown ages of clades containing tropical afroalpine species, we are more likely to overestimate than to underestimate ages. Accordingly, afroalpine species may have originated even more recently. The mountains in EA had reached heights that were able to support alpine-like conditions in the Pliocene (Chorowicz, 2005), and it has been postulated that at least some of the mountains of EA have continuously supported tropical afroalpine vegetation independent of Pleistocene climatic oscillations (Harmsen *et al.,* 1991). If true, suitable alpine-like habitats available to preadapted alpine-like species would have been present continuously since at least the Pliocene.

We have some evidence in *Senecio* for dispersal between different mountains and subregions (Fig. 3 & Appendix S1.4). As documented by pollen fossils, vegetation belts in EA were depressed during colder periods of the Pleistocene (Coetzee, 1964; Hamilton & Taylor, 1991; Harmsen *et al.*, 1991). While the alpine-like belts probably never came into direct contact, it has been suggested that montane forest belts formed a contact zone. All clades including tropical afroalpine species also contain species that are not confined to the alpine-like regions, which might have facilitated inter-mountain exchange of species occurring in montane regions (Hedberg, 1969). Furthermore, it has been reported that species occurring in montane regions in EA show less geographic structuring (according to AFLP and cp data) than species restricted to the tropical Afroalpine (Assefa *et al.*, 2007; Ehrich *et al.,* 2007; Gizaw *et al.*, 2013; Masao *et al.,* 2013), and indeed endemism increases with altitude (Hedberg, 1969). This supports the hypothesis of more frequent dispersal between different EA mountains by montane than by tropical afroalpine species. *Senecio* fits this pattern well: montane species are often more widespread and tropical afroalpine species are mostly restricted to single or geographically close mountains. However, there are also some purely tropical afroalpine species which occur on more than a single mountain. In summary, the discontinuous distribution of temperate areas in sub-Saharan Africa does not prevent migration and/or dispersal between the different subregions and mountains, an observation typical for many other tropical Afroalpine species (Gehrke & Linder, 2014).

Apart from relationships to SA we also found relationships of tropical afroalpine *Senecio* species to the Palaearctic and the New World. Within the unresolved doria-decurrens-clade, two different colonization scenarios are conceivable. One possible scenario is that a Palaearctic lineage gave rise to tropical afroalpine species in the doria-subclade, which had been shown before for otherwise predominantly northern temperate groups (Assefa *et al.*, 2007; Gehrke *et al.*, 2008; Gehrke & Linder, 2009; Pimentel *et al.,* 2013). The other is that there was one colonization from ESA to the Palaearctic via EA by a mrca of the doria-clade as hypothesized but never unambiguously demonstrated for other disjunct northern temperate/Mediterranean – SA genera (Galley *et al.,* 2007; Devos *et al.,* 2010; Galbany-Casals *et al.,* 2014, Chapter 3). In this latter alternative, the tropical Afroalpine would have been source area of a Palaearctic lineage. Different colonization scenarios are also possible for the New World 2-clade, where a group of tropical afroalpine species, the balensis-subclade, is sister to a purely American clade.

Considering that the core-Senecio-clade, which includes the New World 2-clade, is of WSA origin (Chapter 3), and that only very few *Senecio* species occur in West Africa of which none can be found in West African tropical alpine-like regions (Hutschinson & Dalziel, 2014), it seems likely that the New World was colonized from the EA Afroalpine. We have been unable to find other examples for the colonization of America from EA or the other way round that have been investigated in detail although this type of disjunction is known from several plant groups (Renner, 2004). All unambiguously reconstructed southern hemisphere colonizations of sub-Saharan Africa seem to have involved either the west coast of Africa or Australasia (Renner, 2004; Sanmartín & Ronquist, 2004; Queiroz, 2005).

Comparison of the role of in situ *speciation in tropical alpine-like areas in Africa, South America and Malaysia*

The tropical Afroalpine harbours 27 *Senecio* species derived from five to 14 colonizations. Although *in situ* diversification was found in some tropical afroalpine *Senecio* clades, the amount of *in situ* speciation is low, and a maximum number of seven extant high altitude species might have evolved from one common ancestor in the fresenii-clade (Fig. 3 & Tab. 3). As all afroalpine *Senecio*-clades are of roughly the same age (Tab. 3), age differences are unlikely to be responsible for these differences in *in situ* diversification (comparing species numbers and ages; see Tab. 2 & 3), and we can think of no morphological characters which might have allowed some clades to diversify in the tropical Afroalpine.

Speciation in the tropical Afroalpine has been reported for some lineages (e.g. African *Alchemilla* L.. *Carex*, *Dendrosenecio*, *Euryops* [Cass.] Cass. and *Ranunculus* [Knox & Palmer, 1995a; Devos *et al.*, 2010; Gehrke & Linder, 2011; Gehrke *et al*., in press]), but generally *in situ* speciation seems to be low especially in genera that colonized the area several times (*Arabis alpina* L., *Moraea* Mill. and *Helichrysum* [Assefa *et al.*, 2007; Galley *et al.*, 2007; Galbany-Casals *et al.*, 2014]). Altogether, the EA tropical Afroalpine contains about 191 genera and 521 species. Of these, 101 genera are represented by only a single species in the tropical Afroalpine, and only about 26 genera have more than five species in the Afroalpine (Gehrke & Linder, 2014). For most of these 26 genera, it is unknown how many times they colonized the area. *Senecio* and *Helichrysum*, the two largest genera in the tropical Afroalpine, have colonized the area frequently (Tab. 3; Galbany-Casals *et al.*, 2014). African *Alchemilla*, the third largest genus in the EA Afroalpine, shows the highest amount of *in situ* speciation after a single colonization of alpine-like regions of EA followed by colonization of SA and Madagascar and at least one recolonization of the EA Afroalpine (14 tropical afroalpine species; 15 montane species; Gehrke *et al.*, in press). In summary, it seems legitimate to conclude that most genera of the tropical Afroalpine did not diversify much after successful colonization.

This contrasts strongly with findings for the tropical alpine-like Páramo regions of the South American Andes (broadly the northern parts of the Andes; ranging from 10°N to 10°S; Sklenář *et al.,* 2011; Sklenář *et al.,* 2014; Gehrke & Linder, 2014). Differences in *in situ* speciation between the Páramo and the tropical Afroalpine can be observed in *Senecio*. There exists one supported subclade (*S. campanulatus*-*S. hypsobates*) of the New World 1-clade as sampled by Pelser *et al.* (2007) and expanded by Dušková *et al.* (2010) that contains 14 species predominantly occurring in alpine-like conditions (plus three montane species) of the northern Andes (Luteyn & Churchill, 1999). Altogether*, in situ* speciation is likely to be higher in the Páramo than in EA because both alpine-like floras are of similar age, but species richness in general and within particular clades is higher in the Páramo (Sklenář *et al.,* 2014). High speciation rates were reported for the Andean species of, e.g. *Gentianella* Moench, *Halenia* Borkh., *Hypericum* L. and *Lupinus* L. (Kadereit & von Hagen, 2003; Drummond *et al.,* 2012; Nürk *et al.,* 2013). However, it has to be considered that different studies of Páramo lineages use a different lower bound of the Páramo, do not differentiate between montane and alpine-like habitats and/or combine tropical alpine-like and temperate alpine-like regions. However, even when considering EA *Senecio* at both montane and alpine-like altitudes, *in situ* speciation is rare. A recent study by Merckx *et al*. (2015) investigated the evolution of endemism of another alpine-like region, the isolated Mt. Kinabalu in East Malaysia. Their data does not contain a single case of *in situ* speciation in the alpine-like region among all angiosperms studied (Merckx *et al.,* 2015). Taken together, these comparative observations in EA, the Andes and Mt. Kinabalu may imply that rates of *in situ* speciation are directly linked to area size, as inferred for true islands (MacArthur & Wilson, 1967), as size of tropical alpine-like areas is highest in the Andes, followed by EA and Mt. Kinabalu (Gehrke & Linder, 2014).

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Supporting Information

Colonization of the tropical Afroalpine by *Senecio*
Martha Kandziora, Joachim W. Kadereit, Berit Gehrke

Appendix S1: Additional information for Material and Methods, including GenBank accession numbers, newly sequenced material, detailed descriptions of laboratory work and information about distribution and altitude of species described as Senecio.

Table S1.1: Sequences obtained from Genbank. Marker indicated at the beginning followed by species name and GenBank accession numbers. Lower case x: GenBank numbers will be obtained during the submission process of the sequences of Chapter 3.

ITS: *Abrotanella emarginata* (Gaudich.) Cass.: EF538143; *Acrisione cymosa* B. Nord.: EF538144; *Acrisione denticulata* B. Nord.: EF538145; *Adenostyles alpina* Bluff & Fingerh.: EF538146; *Adenostyles leucophylla* Rchb.: AY176130; *Antillanthus acunae* (Borhidi) B. Nord.: EF538152; *Antillianthus discolor* (Griseb.) J.S.Girard: EF538153; *Bethencourtia hermosae* G. Kunkel: EF538159; *Bethencourtia palmensis* (Nees) Choisy: EF538160; *Bethencourtia rupicola* (B. Nord.) B. Nord.: EF538161; *Bolandia argillacea* (Cron) Cron: AY953924; *Bolandia pedunculosa* (DC.) Cron: AY953925; *Brachyglottis greyi* (Hook. f.) B. Nord.: EF660537; *Brachyglottis repanda* J.R. Forst. & G. Forst.: EF635458; *Brachyglottis revoluta* (Kirk) B.Nord.: EF660536; *Caputia pyramidata* (DC.) B. Nord. & Pelser: DQ915863; *Caputia medley-woodii* (Hutch.) B. Nord. & Pelser: DQ915861; *Caputia scaposa* (DC.) B. Nord. & Pelser: AF459931; *Chersodoma antennaria* (Wedd.) Cabrera: EF538165; *Chersodoma jodopappa* (Sch. Bip.) Cabrera: EF538167; *Cineraria abyssinica* Sch.Bip. ex A. Rich.: AF459969; *Cineraria grandiflora* Vatke: EF538170; *Crassocephalum vitellinum* (Benth.) S. Moore: x; *Curio acaulis* (L.f.) P. V. Heath: DQ915896; *Curio articulatus* (L. f.) P.V. Heath: AF459951; *Curio citriformis* (G.D.Rowley) P.V. Heath: DQ915891; *Curio crassulifolius* (DC.) P.V. Heath: DQ915892; *Curio herreanus* (Dinter) P.V.Heath: DQ915886; *Curio radicans* (L.) P.V. Heath: DQ915887; *Curio roleanus* (H. Jacobsen) P.V. Heath: AF459933; *Curio sulcicalyx* (Baker) P.V. Heath: DQ915884; *Dauresia alliariifolius* (O. Hoffm.) B. Nord.: AF457413; *Dendrophorbium bomanii* (R.E. Fr.) C. Jeffrey: EF538181; *Dendrophorbium brachycodon* (Baker) C. Jeffrey: EF538182; *Dendrophorbium lucidum* (Sw.) C. Jeffrey: EF538357; *Dendrophorbium multinerve* (Sch.Bip. ex Klatt) C. Jeffrey: EF538184; *Dendrosenecio battiscombei* (R.E. Fr. & T.C.E. Fr.) E. B. Knox: EF538185; *Dendrosenecio kilimanjari* (Mildbr.) E. B. Knox: AF459967; *Dorobaea laciniata* B. Nord. & Pruski: EF538187; *Dorobaea pimpinellifolia* (Kunth) B. Nord.: GU818548; *Doronicum* L.: AJ400039 & AJ400085; *Doronicum pardalianches* L.: AY176137; *Elekmania barahonensis* (Urb.) B. Nord.: EF538190; *Elekmania fuertesii* (Urb.) B. Nord.: EF538192; *Elekmania picardae* (Krug & Urb.) B. Nord.: EF538193; *Emilia coccinea* (Sims) G. Don: EF538194; *Emilia prenanthoidea* DC.: EF538196; *Erechtites valerianifolius* (Link ex Spreng.) DC.: EF538199; *Euryops pectinatus* (L.) Cass.: AF459964; *Euryops spathaceus* DC.: EF538207; *Euryops tysonii* Phillips: EF538209; *Faujasia squamosa* (Bory) C. Jeffrey: EF538210; *Graphistylis dichroa* (Bong.) D.J.N. Hind: EF538212; *Graphistylis organensis* (Casar.) B. Nord.: EF538214; *Gynura calciphila* Kerr: EF538221; *Gynura formosana* Kitam.: AF155966 & AF155999; *Gynura procumbens* (Lour.) Merr.: FJ980339; *Hubertia ambavilla* Bory: EF538235; *Hubertia riparia* (DC.) C. Jeffrey: GU818556; *Hubertia tomentosa* Bory: EF538237; *Iranecio bulghardaghensis* (Soldano) D. Heller: EF538239; *Iranecio cariensis* (Boiss.) C. Jeffrey: GU818561; *Iranecio taraxacifolius* (M. Bieb.) C. Jeffrey: EF538243; *Jacobaea inops* (Boiss. & Balansa) B. Nord.: JX895504; *Jacobaea kirghisica* (DC.) E. Wiebe: JX895484; *Jacobaea maritima* (L.) Pelser & Meijden: AF459941; *Jacobaea racemosa* (M. Bieb.) Pelser: JX895200; *Jacobaea vulgaris* Gaertn.: EF538244; *Kleinia abyssinica* (A. Rich.) A. Berger: EF538247; *Kleinia neriifolia* Haw.: AF459962; *Ligularia stenocephala* (Maxim.) Matsum. & Koidz.: AF459961; *Lomanthus arnaldii* (Cabr.) B. Nord. & Pelser: EF538297; *Monticalia abietina* (Willd. ex Wedd.) C. Jeffrey: EF538255; *Monticalia apiculata* (Sch.Bip. ex Wedd.) C. Jeffrey: EF538256; *Monticalia arbutifolia* (Kunth.) C. Jeffrey: EF538257; *Monticalia corymbosa* (Benth.) C. Jeffrey: EF538258; *Monticalia greenmaniana* (Hieron.) C. Jeffrey: EF538260; *Monticalia peruviana* (Pers.) C. Jeffrey: EF538262; *Othonna amplexifolia* DC.: EF538273; *Othonna capensis* Bailey: AF459960; *Othonna herrei* Pillans: EF538275; *Packera eurycephala* (Torr. & A. Gray) W.A. Weber & Á. Löve: EF538276; *Packera tampicana* (DC.) C. Jeffrey: EF538277; *Pentacalia arborea* (Kunth) H. Rob. & Cuatrec.: EF538283; *Pentacalia desiderabilis* (Vell.) Cuatrec.: EF538284; *Pericallis cruenta* (L'Hér.) Bolle: AF161637 & AF161687; *Pericallis malvifolia* (L'Hér.) B. Nord.: HQ202070; *Pericallis* *multiflora* (L'Hér.) B. Nord.: AY953931; *Pericallis murrayi* (Bornm.) B. Nord.: EF538285; *Petasites japonicus* (Siebold & Zucc.) Maxim.: AY176152; *Petasites tricholobus* Franch.: AY176153; *S. abbreviatus* S. Moore: DQ915895; *S. achilleifolius* DC.: AY953929; *S. adamantinus* Bong.: EF538294; *S. adenotrichius* DC.: EF538295; *S. aegyptius* L.: AJ400777; *S. aegyptius* L.: x; *S. aequinoctialis* R.E.Fr.: KM592486; *S. aethnensis* Jan ex DC.: AJ400779; *S. affinis* DC.: x; *S. albanensis* DC.: x; *S. angulatus* L. f.: AF459953; *S. angustifolius* (Thunb.) Willd.: JN789735; *S. anomalochorus* Hilliard: x; *S. aphanactis* Greene: AF457430; *S. arenarius* M. Bieb.: AF457421; *S. arenarius* M. Bieb (formerly known as *S. cakilefolius* DC.): AF457423; *S. arniciflorus* DC.: x; *S. asirensis* Boulos & J.R.I.Wood: KC751413; *S. aspericaulis* J. Rémy: EF538299; *S. asperulus* DC.: EF538300; *S. austromontanus* Hilliard: x; *S. ayopayensis* Cuatrec.: EF538303; *S. bahioides* Hook. & Arn.: EF538304; *S. bollei* Sunding & G.Kunkel: JN789736; *S. brasiliensis* (Spreng.) Less.: GU818641; *S. brevidentatus* M.D.Hend.: x; *S. bulbinifolius* DC.: EF538308; *S. byrnensis* Hilliard: x; *S. cadiscus* B.Nord. & Pelser: GU818506; *S. californicus* DC.: AF097536; *S. caloneotes* Hilliard: KM592488; *S. carroensis* DC.: JN789741; *S. carroensis* DC. (formerly known as *S. parvifolius* DC.): JN789904; *S. castagneanus* DC.: JX895508; *S. cathcartensis* O.Hoffm.: KM592489; *S. chrysocoma* Meerb.: x; *S. citriceps* Hilliard & B.L.Burtt: x; *S. consanguineus* DC.: AF457420; *S. consanguineus* DC.: KM592490; *S. coriaceus* Aiton: EF538317; *S. costaricensis* R.M.King: AF161639 & AF161689; *S. crassissimus* Humb.: EF538319; *S. cristimontanus* Hilliard: x; *S. crithmoides* Hook. & Arn.: EF538321; *S. cryphiactis* O. Hoffm.: JN789742; *S. cyaneus* O.Hoffm.: KM592492; *S. decurrens* DC.: EF538324; *S. deferens* Griseb.: EF538325; *S. deltoideus* Less.: EF538326; *S. discodregeanus* Hilliard & B.L.Burtt: x; *S. donianus* Hook. & Arn: EF538329; *S. doria* L.: AF459946; *S. doriiformis* DC.: JX895507; *S. doriiformis* DC.: x; *S. doronicum* (L.) L.: EF538330; *S. doronicum* (L.) L.: x; *S. dregeanus* DC.: EF538331; *S. eenii* (S. Moore) Merxm.: AF457425; *S. eenii* (S. Moore) Merxm.: AF457424; *S. elegans* L.: GU818642; *S. eremophilus* Richardson: AF459945; *S. eriopus* Willk.: JX895291; *S. ertterae* T.M. Barkley: AF457433; *S. erysimoides* DC.: JN789743; *S. eubaeus* Boiss. & Heldr.: JX895245; *S. farinifer* Hook. & Arn: EF538333; *S. filaginoides* DC.: EF538334; *S. flaccidus* Less.: EF538336; *S. flaccidus* Less. (formerly known as *S. douglasii* DC.): AF161640 & AF161690; *S. franchetii* C. Winkl.: EF538337; *S. franchetii* C. Winkl.: x; *S. fresenii* Sch.Bip.: KM592494; *S. gallicus* Chaix: AJ400783; *S. gallicus* (formerly known as *S. hesperidium* Jahand., Maire & Weiller) Chaix: AJ400789; *S. giessii* Merxm.: AF457418; *S. glaber* Less.: EF543651 & EF543649; *S. glaberrimus* DC.: EF538338; *S. glanduloso-lanosus* Thell.: x; *S. glanduloso-pilosus* Volkens & Muschl.: x; *S. glastifolius* L. f.: EF538340; *S. glaucescens* DC. (formerly known as *S. achillefolius* var. *glaucescens* [DC.] Harv.): AF155993 & AF156026; *S. glutinosus* Thunb.: AF457427; *S. gnidioides* Phil.: EF538341; *S. gramineus* Harv.: GU818650; *S. gregorii* F.Muell.: GU818651; *S. gunnii* (Hook. f.) Belcher: EF538343; *S. hadiensis* Forssk.: KC311155; *S. harveianus* MacOwan:; *S. harveianus* MacOwan: KM592495; *S. hastatus* L.: EF538345; *S. hemmendorffii* Malme: EF538346; *S. hieracioides* DC.: KM592496; *S. hirsutilobus* Hilliard: x; *S. hispidissimus* I. Thomps.: GU818657; *S. hochstetteri* Sch.Bip. ex A.Rich.: KM592497; *S. hollandii* Compton: GU818661; *S. humillimus* Sch. Bip.: EF538347; *S. hypochoerideus* DC.: KM592498; *S. ilicifolius* L.: GU818662; *S. inaequidens* DC.: AF459943; *S. integerrimus* Nutt.: EF538349; *S. jarae* Phil.: EF538350; *S. junceus* (Less.) Harv.: EF538351; *S. keniophytum* R.E.Fr.: KM592501; *S. kolenatianus* C.A. Mey.: JX895252; *S. laetevirens* Phil.: EF538352; *S. lagascanus* DC.: JX895354; *S. landbeckii* Phil.: EF538353; *S. Lastarrianus* J.Rémy in Gay: GU818663; *S. latifolius* DC.: EF538354; *S. lautus* (Willd.) G. Forst. ex Willd.: EU812814; *S. laxus* DC.: JN789809; *S. lemmonii* A. Gray: AF457432; *S. leptolobus* DC.: EF538355; *S. leptophyllus* DC.: JN789810; *S. leucanthemifolius* Poir. (formerly known as *S. rodriguezii* Willk. ex J.J. Rodr.): AJ400799; *S. lineatus* (L. f.) DC.: AF459939; *S. linifolius* L.: EF538356; *S. littoreus* Thunb.: JN789812; *S. lopezii* Boiss.: JX895264; *S. lydenburgensis* Hutch. & Burtt Davy: x; *S. macedonicus* Griseb.: JX895510; *S. macowanii* Hilliard: x; *S. macroglossus* DC.: DQ915881; *S. macrospermus* DC.: x; *S. mairetianus* DC.: EF538359; *S. maritimus* L. f.: JN789816; *S. maulinus* Reiche: JN789901; *S. mauricei* Hilliard & B.L.Burtt: x; *S. melastomifolius* Baker: DQ915897; *S. meuselii* Rauh: DQ915899; *S. meyeri-johannis* Engl.: KM592503; *S. mooreanus* Hutch. & Burtt Davy: x; *S. muirii* L. Bolus: DQ915883; *S. myriocephalus* Sch.Bip. ex A.Rich.: KM592505; *S. natalicola* Hilliard: x; *S. nemorensis* L.: AF459937; *S. nemorensis* L. (formerly known as *S. sarracenicus* L.): EF538375; *S. niveoaureus* Cuatrec.: EF538178; *S. niveus* (Thunb.) Willd.: JN789903; *S. oederiafolius* DC.: KM592508; *S. olympicus* Boiss.: JX895511; *S. oreophyton* J.Rémy: EF538393; *S. otites* Kunze ex DC.: GU818669; *S. oxyriifolius* DC.: AF459936; *S. paludaffinis* Hilliard: x; *S. panduriformis* Hilliard: EF538364; *S. patens* (Kunth) DC.: EF538151; *S. paulsenii* O. Hoffm. ex Pauls.: JX895235; *S. paulsenii* O. Hoffm. ex Pauls.: x; *S. perralderianus* Coss.: EF538365; *S. pinifolius* Lam.: EF538366; *S. pinnatifolius* A. Rich: GU818679; *S. pinnulatus* Thunb.: JN789907; *S. piptocoma* O. Hoffm. ex Schinz: JN789908; *S. poeppigii* Cuatrec.: EF543650 & EF543652; *S. polyanthemoides* Sch. Bip.: AF085187; *S. polygaloides* Phil.: EF538367; *S. polyodon* DC.: x; *S. praeteritus* Killick: x; *S. provincialis* (L.) Druce: JX895383; *S. pseudoorientalis* Schischk.: x; *S. pseudoorientalis* Schischk.: JX895512.; *S. psilocarpus* Belcher & Albr.: GU818692; *S. pterophorus* DC.: AF085188; *S. pubiger* L.: EF538368; *S. purpureus* L.: EF538370; *S. pyrenaicus* L.: EF538371; *S. pyrenaicus* L.: x; *S. qathlambanus* Hilliard: KM592511; *S. ragazzi* Chiov.: KM592512;

S. rautanenii S. Moore: KM592513; *S. reclinatus* L. f.: KM592514; *S. reptans* Turcz.: x; *S. retrorsus* DC.: EF538372; *S. rhyncholaenus* DC.: x; *S. roseus* Sch. Bip.: EF538373; *S. rosmarinifolius* L.f.: KM592517; *S. rufescens* DC.: EF538374; *S. sabinjoensis* Muschl.: KM592518; *S. sandersonii* Harv.: x; *S. saniensis* Hilliard & B.L.Burtt: x; *S. sarcoides* C. Jeffrey (formerly known as *S. corymbiferus* DC.): DQ915893; *S. saxatilis* Wall. Ex DC.: EF538376; *S. scandens* Buch.-Ham. ex D. Don: AF459932; *S. schimperi* Sch.Bip. ex A.Rich.: KM592519; *S. scopolii* Hoppe & Hornsch. ex Bluff & Fingerh.: JX895513; *S. selloi* (Spreng.) DC.: EF538379; *S. seminiveus* J.M.Wood & M.S.Evans: KM592522; *S. sinuatilobus* DC.: EF538380; *S. sisymbriifolius* DC.: EF538381; *S. snowdenii* Hutch.: KM592523; *S. spartioides* Torr. & A. Gray: EF538383; *S. squarrosus* A. Rich.: GU818703; *S. stigophlebius* Baker: EF538384; *S. stoechadiformis* DC.: EF538385; *S. subnemoralis* Dusén: EF538386; *S. szyszylowiczii* Hieron.: GU818705; *S. tauricolus* V. A. Matthews: GU817570.; *S. telekii* (Schweinf.) O. Hoffm.: EF538387; *S. telekii* (Schweinf.) O. Hoffm.: KM592527; *S. telmateius* Hilliard: x; *S. transsylvanicus* Boiss.: JX895306; *S. trapezuntinus* Boiss.: JX895514; *S. tricuspidatus* Hook. & Arn.: EF538390; *S. trifidus* Hook. & Arn: EF538391; *S. triqueter* Less.: EF538392; *S. tropaeolifolius* MacOwan ex F. Muell.: DQ915880; *S. umbrosus* Waldst. & Kit.: JX895447; *S. unionis* Sch.Bip. ex A.Rich.: KM592529; *S. urundensis* S. Moore: KM592530; *S. vestitus* P.J. Bergius: GU818708; *S. volckmannii* Phil.: EF538395; *S. wairauensis* Belcher: EF538397; *S. windhoekensis* Merxm.: AF457426; *Tetradymia filifolia* Greene: EF538411; *Xenophyllum dactylophyllum* (Sch. Bip.) V.A. Funk: EF538414; *Xenophyllum poposum* (Phil.) V.A. Funk: EF538415

ETS: *Crassocephalum vitellinum* (Benth.) S. Moore: x; *Erechtites valerianifolius* (Link ex Spreng.) DC.: GU818162; *S. aegyptius* L.: JN789686; *S. aegyptius* L.: x; *S. aequinoctialis* R.E.Fr.: x; *S. aethnensis* Jan ex DC.: JN789726; *S. affinis* DC.: x; *S. angustifolius* (Thunb.) Willd.: JN789687; *S. anomalochorus* Hilliard: x; *S. austromontanus* Hilliard: x; *S. bollei* Sunding & G.Kunkel: JN789688; *S. brasiliensis* (Spreng.) Less.: GU818252; *S. byrnensis* Hilliard: x; *S. cadiscus* B.Nord. & Pelser: GU818128; *S. caloneotes* Hilliard: x; *S. carroensis* DC.: JN789690; *S. carroensis* DC. (formerly known as *S. parvifolius* DC.): JN789722; *S. cathcartensis* O.Hoffm.: x; *S. chrysocoma* Meerb.: x; *S. citriceps* Hilliard & B.L.Burtt: x; *S. consanguineus* DC.: x; *S. cristimontanus* Hilliard: x; *S. cryphiactis* O. Hoffm.: JN789691; *S. cyaneus* O.Hoffm.: x; *S. erysimoides* DC.: JN789692; *S. flaccidus* Less.: GU818259; *S. fresenii* Sch.Bip.: x; *S. glanduloso-lanosus* Thell.: x; *S. glanduloso-pilosus* Volkens & Muschl.: x; *S. glastifolius* L. f.: JN789694; *S. gramineus* Harv.: GU818262; *S. gregorii* F.Muell.: GU818263; *S. harveianus* MacOwan: x; *S. hieracioides* DC.: x; *S. hispidissimus* I. Thomps.: GU818266; *S. hochstetteri* Sch.Bip. ex A.Rich.: x; *S. hypochoerideus* DC.: x; *S. ilicifolius* L.: GU818269; *S. inaequidens* DC.: JN789703; *S. integerrimus* Nutt.: GU818270; *S. jarae* Phil.: GU818271; *S. keniophytum* R.E.Fr.: x; *S. Lastarrianus* J.Rémy in Gay: GU818272; *S. lautus* (Willd.) G. Forst. ex Willd.: KC695942; *S. laxus* DC.: JN789706; *S. leptophyllus* DC.: JN789707; *S. littoreus* Thunb.: JN789710; *S. lydenburgensis* Hutch. & Burtt Davy: x; *S. macowanii* Hilliard: x; *S. macrospermus* DC.: x; *S. mairetianus* DC.: GU818275; *S. maritimus* L. f.: JN789713; *S. maulinus* Reiche: JN789718; *S. mauricei* Hilliard & B.L.Burtt: x; *S. meyeri-johannis* Engl.: x; *S. mooreanus* Hutch. & Burtt Davy: x; *S. myriocephalus* Sch.Bip. ex A.Rich.: x; *S. nemorensis* L.: GU818278; *S. niveoaureus* Cuatrec.: GU818280; *S. niveus* (Thunb.) Willd.: JN789721; *S. oederiafolius* DC.: x; *S. oreophyton* J.Rémy: GU818282; *S. paludaffinis* Hilliard: x; *S. patens* (Kunth) DC.: GU818284; *S. pinnatifolius* A. Rich: GU818287; *S. pinnulatus* Thunb.: JN789724; *S. piptocoma* O. Hoffm. ex Schinz: JN789725; *S. polygaloides* Phil.: GU818288; *S. praeteritus* Killick: x; *S. psilocarpus* Belcher & Albr.: GU818290; *S. qathlambanus* Hilliard: x; *S. ragazzi* Chiov.: x; *S. rautanenii* S. Moore: x; *S. reclinatus* L. f.: x; *S. roseus* Sch. Bip.: GU818292; *S. rosmarinifolius* L.f.: x; *S. schimperi* Sch.Bip. ex A.Rich.: x; *S. seminiveus* J.M.Wood & M.S.Evans: x; *S. snowdenii* Hutch.: x; *S. squarrosus* A. Rich.: GU818296; *S. telekii* (Schweinf.) O. Hoffm.: JN789730; *S. unionis* Sch.Bip. ex A.Rich.: x; *S. urundensis* S. Moore: x; *S. vestitus* P.J. Bergius: GU818305

***trn*LF:** *Crassocephalum vitellinum* (Benth.) S. Moore: x; *S. aegyptius* L.: JN789960; *S. aegyptius* L.: x; *S. aequinoctialis* R.E.Fr.: KM592420; *S. aethnensis* Jan ex DC.: EU195499; *S. affinis* DC.: x; *S. albanensis* DC.: x; *S. angustifolius* (Thunb.) Willd.: JN789961; *S. anomalochorus* Hilliard: x; *S. arniciflorus* DC.: x; *S. austromontanus* Hilliard: x; *S. bollei* Sunding & G.Kunkel: JN789962; *S. brasiliensis* (Spreng.) Less.: GU818061; *S. cadiscus* B.Nord. & Pelser: GU817980; *S. caloneotes* Hilliard:; *S. carroensis* DC.: JN789968; *S. carroensis* DC. (formerly known as *S. parvifolius* DC.): JN790001; *S. cathcartensis* O.Hoffm.: KM592422; *S. chrysocoma* Meerb.: x; *S. citriceps* Hilliard & B.L.Burtt: x; *S. consanguineus* DC.: KM592423; *S. cristimontanus* Hilliard: x; *S. cryphiactis* O. Hoffm.: JN789969; *S. cyaneus* O.Hoffm.: KM592425; *S. erysimoides* DC.: JN789970; *S. flaccidus* Less.: GU818066; *S. fresenii* Sch.Bip.: KM592427; *S. glanduloso-lanosus* Thell.: x; *S. glanduloso-pilosus* Volkens & Muschl.: x; *S. glastifolius* L. f.: JN789972; *S. gramineus* Harv.: GU818068; *S. gregorii* F.Muell.: GU818069; *S. harveianus* MacOwan: KM592428; *S. harveianus* MacOwan:; *S. hieracioides* DC.: KM592429; *S. hispidissimus* I. Thomps.: GU818071; *S. hochstetteri* Sch.Bip. ex A.Rich.: KM592430; *S. hypochoerideus* DC.: KM592431; *S. ilicifolius* L.: GU818074; *S. inaequidens* DC.:

JN789979; *S. integerrimus* Nutt.: GU818075; *S. keniophytum* R.E.Fr.: KM592434; *S. lastarrianus* J.Rémy in Gay: GU818076; *S. laxus* DC.: JN789985; *S. littoreus* Thunb.: JN789989; *S. lydenburgensis* Hutch. & Burtt Davy: x; *S. macrospermus* DC.: x; *S. mairetianus* DC.: EF538128; *S. maritimus* L. f.: JN789992; *S. maulinus* Reiche: JN789997; *S. mauricei* Hilliard & B.L.Burtt: x; *S. meyeri-johannis* Engl.: KM592436; *S. mooreanus* Hutch. & Burtt Davy: x; *S. myriocephalus* Sch.Bip. ex A.Rich.: KM592438; *S. natalicola* Hilliard:; *S. nemorensis* L.: EF028730; *S. niveoaureus* Cuatrec.: GU818078; *S. niveus* (Thunb.) Willd.: JN790000; *S. oreophyton* J.Rémy: GU818079; *S. paludaffinis* Hilliard: x; *S. patens* (Kunth) DC.: GU818080; *S. pinnatifolius* A. Rich: GU818081; *S. pinnulatus* Thunb.: JN790004; *S. piptocoma* O. Hoffm. ex Schinz: JN790005; *S. polygaloides* Phil.: GU818082; *S. praeteritus* Killick: x; *S. psilocarpus* Belcher & Albr.: GU818084; *S. qathlambanus* Hilliard: KM592443; *S. ragazzi* Chiov.: KM592444; *S. rautanenii* S. Moore: KM592445; *S. rhyncholaenus* DC.: x; *S. roseiflorus* R.E.Fr.: KM592447; *S. roseus* Sch. Bip.: GU818085; *S. sandersonii* Harv.: x; *S. schimperi* Sch.Bip. ex A.Rich.: KM592448; *S. snowdenii* Hutch.: KM592450; *S. tauricolus* V. A. Matthews: GU818087; *S. telekii* (Schweinf.) O. Hoffm.: JN790009; *S. telekii* (Schweinf.) O. Hoffm.: KM592454; *S. telmateius* Hilliard: x; *S. unionis* Sch.Bip. ex A.Rich.: KM592456; *S. vestitus* P.J. Bergius: GU818089

ycf**6-*****trn*****C:** *Crassocephalum vitellinum* (Benth.) S. Moore: x; *S. aegyptius* L.: x; *S. aequinoctialis* R.E.Fr. KM592407; *S. affinis* DC.: x; *S. anomalochorus* Hilliard: x; *S. arniciflorus* DC.: x; *S. austromontanus* Hilliard: x; *S. caloneotes* Hilliard: KM592403; *S. cathcartensis* O.Hoffm.: KM592404; *S. chrysocoma* Meerb.: x; *S. citriceps* Hilliard & B.L.Burtt: x; *S. consanguineus* DC.: KM592381; *S. cristimontanus* Hilliard: x; *S. cryphiactis* O. Hoffm.: KM592415; *S. cyaneus* O.Hoffm.: KM592385; *S. erysimoides* DC.: KM592416; *S. fresenii* Sch.Bip.: KM592384; *S. glanduloso-lanosus* Thell.: x; *S. glanduloso-pilosus* Volkens & Muschl.: x; *S. harveianus* MacOwan: KM592405; *S. hieracioides* DC.: KM592380; *S. hochstetteri* Sch.Bip. ex A.Rich.: KM592387; *S. hypochoerideus* DC.: KM592406; *S. keniophytum* R.E.Fr.: KM592402; *S. laxus* DC.: KM592417; *S. lydenburgensis* Hutch. & Burtt Davy: x; *S. macrospermus* DC.: x; *S. mauricei* Hilliard & B.L.Burtt: x; *S. meyeri-johannis* Engl.: KM592390; *S. mooreanus* Hutch. & Burtt Davy: x; *S. myriocephalus* Sch.Bip. ex A.Rich.: KM592391; *S. natalicola* Hilliard; *S. niveus* (Thunb.) Willd.: KM592418; *S. paludaffinis* Hilliard: x; *S. qathlambanus* Hilliard: KM592408; *S. rautanenii* S. Moore: KM592379; *S. roseiflorus* R.E.Fr.: x; *S. schimperi* Sch.Bip. ex A.Rich.: KM592394; *S. snowdenii* Hutch.: KM592397; *S. telekii* (Schweinf.) O. Hoffm.: KM592398

Table S1.2: Newly sequenced material used in this study. Lower case x indicates newly obtained sequences (GenBank number will be obtained during submission process); minus (-) indicates that no new sequences were obtained. Herbarium abbreviations: BR: National Botanic Garden of Belgium; C: Natural History Museum of Denmark-Copenhagen; E: Royal Botanic Garden Edinburgh; M: Botanische Staatssammlung München; MJG: Johannes Gutenberg-Universität Mainz; MSB: Ludwig-Maximilians-Universität München; S: Swedish Museum of Natural History-Stockholm; UBT: University of Bayreuth; US: Smithsonian Institution - Washington.

Taxon	**Author**	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
S. abruptus	Thunb	Erik Wall 622	S	53,1	x	-	x	x
S. adenotrichius	DC.	Schuh & Platnick 20	US	2018	x	x		-
S. aequinoctialis	R.E.Fr.	E. Beck 41	UBT	5,1	x	-	x	x
S. aphanactis	Greene	Hoover, Robit 2881	US	2011	x	x	x	x
S. auriculatissimus	Britten	N.G.B. Johnston-Stewart	E	1116	x	-	-	-
S. balensis	S.Ortiz & Vivero	I. Friis, M.G. Gilbert & K. Vollesen 3424	C	58,1	x	x	x	x
S. balensis	S.Ortiz & Vivero	Olov Hedberg 5639	C	58,2	x	-	-	-
S. balensis	S.Ortiz & Vivero	W.J.J.O de Wilde & B.E.E. de Wilde-Duyfjes 9069	C	58,3	x	-	x	-
S. baurii	Oliv.	S.P. Bester 201	E	1102	x	-	-	-
S. brasiliensis	(Spreng.) Less.	Romero *et al*. 4641	US	2015	x	x	x	x
S. caloneotes	Hilliard	Hilliard & Burtt 8761	S	42,2	x	x	x	-
S. cf. Steudelii	Sch.Bip. ex A.Rich.	Ensermu Kelbessa 1447	C	60,1	-	x	-	-
S. chilensis	Less.	Bonifacino *et al*. 364	US	2005	x	x	x	x
S. cisplatinus	Cabrera	Hatschback *et al*. 78202	US	2014	x	x	-	-
S. coronatus	(Thunb.) Harv.	D.A. McCallum & M.J. Balkwill 272	E	1104	x	x	x	x
S. cryptolanatus	Killick.	Hilliard & Burtt 6601	S	1013	x	-	-	-
S. cyaneus	O.Hoffm.	O. Hedberg 2318	S	17,1	x	-	-	-
S. deferens	Griseb.	Sorie, N. 1899	US	2035	x	-	-	-
S. depauperatus	Mattf.	Jean Pawek 13426	BR	1003	x	-	-	-
S. doriiformis	DC.	Thomas Gregor 6651 & Lenz Meierott	M	2030	-	x	-	-
S. doronicum	(L.) L.	F. Schuhwerk 97/363	M	2029	-	x	-	x
S. eremophilus	Richardson	Norrbom, A. & L.H. Rodriguez 07-NM-14	US	2020	x	x	-	x
S. farinaceus	Sch.Bip. ex A.Rich.	Ake Holm 80	S	18,1	x	x	x	x
S. farinifer	Hook. & Arn.	Mahu, Manuel 5153	US	2019	x	x	-	-
S. filaginoides	DC.	Bonfacino *et al*. 461	US	2023	x	x	-	x
S. flaccidus	Less.	Ahart, Lowell 11149	US	2010	x	x	x	x
S. franchetii	C. Winkl.	D. Podlech 21439	M	2031	-	x	-	x
S. fresenii	Sch.Bip.	Arne Anderberg 1705	S	16,2	x	-	-	-
S. hochstetteri	Sch.Bip. ex A.Rich.	M. Thulin & A. Tidigs 195	S	19,1	x	-	x	x
S. humidanus	C.Jeffrey	K. Balkwill & M.J. Balkwill 10728	E	1115	x	-	-	-

Taxon	**Author**	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
S. humillimus	Sch. Bip.	Wood, J.R.I. 8933	US	2007	x	x	x	x
S. humillimus	Sch. Bip.	Bastian E. 1049	US	2034	x	x	x	x
S. inornatus	DC.	A.J. Salubeni & E.J. Tawakali 3920	C	1009	x	x	x	x
S. jacksonii	S. Moore	R. Bussmann 10825	UBT	7,1	x	-	-	-
S. jacksonii	S. Moore	O. Hedberg 1545	S	7,2	x	x	x	x
S. jacksonii	S. Moore	Kare Bremer 28	S	7,3	x	x	x	x
S. keniophytum	R.E.Fr.	E. Beck s.n. (UBT code: 20482)	UBT	4,1	x	x	-	-
S. keniophytum	R.E.Fr.	E. Beck s.n. (UBT code: 20481)	UBT	4,3	x	x	-	-
S. lemmonii	A. Gray	Simmons, NM M-10	US	2012	x	x	x	x
S. leptolobus	DC.	Wasum, R. 702	US	2016	x	x	x	x
S. maranguensis	O. Hoffm.	K. Schmitt 1173	UBT	9,2	x	-	-	-
S. maranguensis	O. Hoffm.	Robert Fries (s 12-19587)	S	9,3	x	-	-	-
S. mariettae	Muschl.	O. Hedberg 409	S	20,1	x	-	-	-
S. mattirolii	Chiov.	O. Hedberg 409	S	21,1	x	x	x	x
S. microglossus	DC.	D.A. McCallum 498	E	1108	x	-	-	-
S. montevidensis	(Spreng.) Baker	Rosengurtt B-5254	US	2017	x	x	-	-
S. moorei	R.E.Fr.	K. Schmitt 34	UBT	3,3	x	-	-	-
S. moorei	R.E.Fr.	T. Eriksson 609	S	3,4	x	-	-	-
S. moorei	R.E.Fr.	M. Thulin & A. Tidigs 167	S	3,5	x	x	x	x
S. nanus	Sch.Bip. ex A.Rich.	R.K. Brummitt 20996	C	59,1	x	x	x	x
S. nanus	Sch.Bip. ex A.Rich.	J.J.F.E. de Wilde & M.G.Gilbert 71	C	59,3	x	-	-	-
S. niveoaureus	Cuatrec.	Cleef, Antoine M. 6665	US	2021	x	x	-	-
S. ochrocarpus	Oliv. & Hiern	Arne Anderberg 1732	S	24,1	x	x	x	x
S. paucicalyculatus	Klatt	L. Mucina 200207/31	S	49,2	x	-	-	-
S. paulsenii	O. Hoffm. ex Pauls.	Don Bedunah 4	MSB	2028	-	x	-	x
S. pergamentaceus	Baker	H. M. Richards 10563	S	35,1	x	-	-	-
S. pinnatipartitus	Sch.Bip. ex Oliv. & Hiern	Olle Svensson 58	S	40,1	x	-	-	-
S. platypleurus	Cuford	I. Friis, S. Bidgood, Malaku Wondefrash & Getu Tefera 9396	C	56,1	x	x	x	x
S. poseideonis	Hilliard & B.L.Burtt	Hilliard & Burtt 7655	E	1109	x	-	-	-
S. pseudoorientalis	Schischk.	D. Podlech & Sh. Zarre 55287	MSB	2027	-	x	-	x
S. pseudoorientalis	Schischk.	Shetekauri, S. 000758	MJG	2003	x	x	x	x
S. purtschelleri	Engl.	E. Beck 146	UBT	2,3	x	x	-	-
S. purtschelleri	Engl.	O. Hedberg 1772	S	2,5	x	x	x	x
S. pyrenaicus	L.	W. Dietrich 6055	M	2033	-	x	-	x
S. qathlambanus	Hilliard	Hilliard 5396	S	50,2	x	-	x	x
S. rhammatophyllus	Mattf.	O. Hedberg 866	S	27,1	x	x	x	x

Taxon	**Author**	**Collector**	**Herb. code**	**ID**	**ITS**	**ETS**	***trn*LF**	***trn*C-*ycf*6**
S. rhammatophyllus	Mattf.	G. Taylor 3500	S	27,2	x	-	-	-
S. rhomboideus	Harv.	Hilliard & Burtt 16796	E	1140	x	-	-	-
S. roseiflorus	R.E.Fr.	O. Hedberg 1884	S	10,3	x	x	x	x
S. rufescens	DC.	Steck & Sutton 13-PE-10	US	2013	x	x	x	x
S. ruwenzoriensis	S. Moore	R. Bussmann 10878	UBT	11,1	x	-	-	-
S. sabinjoensis	Muschl.	Misimba, Muzinga Matamba 1	BR	1004	-	x	-	-
S. schultzii	Hochst. ex A.Rich.	Arne Anderberg 1707	S	29,1	x	-	-	-
S. schultzii	Hochst. ex A.Rich.	Arne Anderberg 1695	S	29,2	x	-	x	x
S. schultzii	Hochst. ex A.Rich.	O. Hedberg / Getachwe Aweke 5488	C	29,3	x	x	-	-
S. schweinfurthii	O.Hoffm.	O. Hedberg 2377	S	1,6	x	-	x	-
S. schweinfurthii	O.Hoffm.	O. Hedberg 1881	S	1,7	x	x	-	x
S. schweinfurthii	O.Hoffm.	E. Beck 400	UBT	1,9	x	-	-	-
S. scitus	Hutch. & Burtt Davy	R.A. Reddy, K.B. Reddy, P. Reddy 685	E	1106	x	-	-	-
S. selloi	(Spreng.) DC.	Soares, F.; HUCS 13772	US	2022	x	x	-	x
S. snowdenii	Hutch.	O. Hedberg 227	S	30,2	x	-	-	-
S. sotikensis	S. Moore	O. Hedberg 871	S	13,2	x	x	x	x
S. spartioides	Torr. & A. Gray	King & Garvey 11108	US	2009	x	x	x	x
S. strictifolius	Hiern.	Robert J. Rodin 4482	S	37,1	x	-	-	-
S. subsessilis	Oliv. & Hiern	K. Schmitt 703	UBT	14,1	x	x	-	-
S. subsessilis	Oliv. & Hiern	K. Schmitt 949	UBT	14,2	x	-	-	-
S. subsessilis	Oliv. & Hiern	J.A. Mlangwa, P.B Phillipson, H. van Vlaenderen & W. Kindeketa 305	S	14,4	x	-	x	x
S. syringifolius	O.Hoffm.	K. Schmitt 814	UBT	15,1	x	-	-	-
S. syringifolius	O.Hoffm.	T. Eriksson, V. Kalema & G. Leliyo 567	S	15,3	x	-	-	-
S. transmarinus	S. Moore	O. Hedberg 357	S	32,3	x	-	-	-
S. transmarinus	S. Moore	O. Hedberg 682	S	32,4	x	x	x	x
S. transmarinus	S. Moore	O. Hedberg 682	S	32,5	x	x	-	-
S. tricuspidatus	Hook. & Arn	Moore 1898	US	2025	x	x	x	x
S. tugelensis	J.M. Wood & M.S. Evans	Hilliard & Burtt 16404	S	52,1	x	-	-	-
S. volckmannii	Phil.	Fortunato 5575	US	2004	x	x	x	x
S. x pirottae	Chiov.	O. Hedberg 726	S	25,1	x	x	x	-

S1.3: DETAILED DESCRIPTION OF EXTRACTION, AMPLIFICATION, SEQUENCING AND ALIGNMENT PREPARATION.

For newly sampled species, we extracted total genomic DNA from herbarium material (Appendix S1.2) using DNeasy Plant Kits (Qiagen Inc., Valencia, CA, USA. Qiagen GmbH, Hilden, Germany) according to the manufacturer's MiniProtocol with minor changes. Samples were incubated for 30 min instead of 10 min after adding the lysis buffer and the DNA elution step was done twice using 50 µl respectively and incubated for 20 min. Sequences were generated using standard methods. We amplified the internal transcribed spacer (ITS), the external transcribed spacer (ETS) as well as the cp regions of *trn*L-*trn*F and *trn*C-*ycf*6. Amplification, sequencing and raw sequence file editing was carried out as described in Chapter 3. For most material we amplified ITS-1 and ITS-2 separately, using primers 'ITS A' (5′-GGA AGG AGA AGT CGT AAC AAG G-3′), 'ITS C' (5′-GCA ATT CAC ACC AAG TAT CGC-3′), 'ITS-B' (5′-CTT TTC CTC CGC TTA TTG ATA TG-3′) and 'ITS-D' (5′-CTC TCG GCA ACG GAT ATC TCG-3′; Blattner, 1999). In some cases, the entire ITS region was amplified using ITS 18S' (5′-CCT TMT CAT YTA GAG GAA GGA G -3′) and 'ITS 28S' (5′-CCG CTT ATT KAT ATG CTT AAA-3′; Muir & Schlötterer, 1999). Amplifications were performed in 20 µl volumes containing 12.86 µl ddH_2O, 2 µl buffer, 1 µl 50 mM $MgCl_2$, 0.4 µl 10 mM dNTPs, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl polymerase (all reaction liquids from NewEngland BioLabs Inc, Ipswich, USA) and 2 µl genomic DNA. Cycling conditions were: 94°C 1 min, 30x (94°C 0.2 min; 52°C 0.3 min; 72°C 1 min), 94°C 0.2 min, 52°C 1.2 min. For some material less genomic DNA was used and in some cases a taq-polymerase by Sigma-Aldrich was used. ETS was amplified using "ETS2" (5′-CAA CTT CCA CCT GGC ATA CCT CCT CA-3′; Bayer *et al.,* 2002) and "18S ETS" (5′-ACT TAC ACA TGC ATG GCT TAA TCT-3′; Baldwin & Markos, 1998). Amplification was performed in 20 µl volumes containing 12.86 µl ddH_2O, 2 µl Buffer, 1 µl 50 mM $MgCl_2$, 0.4 µl 10 mM dNTP's, 0.8 µl of each primer with 10 pmol/µl and 0.14 µl of 5 U/µl taq-Polymerase (Polymerase supplied by Sigma-Aldrich; all other reaction liquids from NewEngland BioLabs Inc, Ipswich, USA) and 2 µl genomic DNA. Sometimes 0.2 µl of 10mg/ml BSA and/or 0.8 µl of DMSO has been added. Cycling conditions were those described in Pelser *et al.* (2012). The *trn*L intron, gene and *trn*L-*trn*F intergenic spacer as well as *trnC-ycf*6 intergenic spacer were amplified as described in Chapter 3. More cp markers are available in GenBank, but they did not contribute to phylogenetic resolution in the genus and were therefore not included in our analyses.

PCR products were purified using ExoSAP-IT PCR Clean-Up (Affymetrix, Santa Clara, USA) following the recommended protocol. Cycle sequencing reactions were carried out with BigDye Terminator 3.1 (Applied Biosystems, Foster City, California, U.S.A.) following the recommended protocol with minor modifications (1 µl of BigDye Terminator instead of 2 µl) using the same primers as used for amplification. Purification was done with Sephadex (GE Healthcare, Waukesha, USA) and sequencing of both strands was done on a 'GA3130XL' Genetic Analyser (Applied Biosystems, Carlsbad, USA; Hitachi Ltd., Tokyo, Japan) at Johannes Gutenberg-Universität Mainz (Germany). SEQUENCHER v.4.1.4 (Gene Codes Corporation, Ann Arbor, MI, U.S.A.) was used for file editing. Here, the sequenced regions were checked by eye and adjusted prior to alignment when necessary.

Each gene region was aligned and adjusted with MACCLADE v. 4.08 (Maddison & Maddison, 2005). Missing data were coded as question marks. Substitution models and best partitioning scheme for each alignment were identified prior to analyses with PARTITIONFINDER v.1.1.1 (Lanfear *et al.,* 2012; Appendix S2.1). Indels larger than 1 base pair were coded for cp regions as these markers contain many insertions and deletions. To code them as binary data (presence/absence), the simple coding method by Simmons & Ochoterena (2000) was used as implemented in

SeqState 1.4.1 (Müller, 2005). Afterwards, indel coding was checked for phylogenetic conflicts between phylogenies with and without indel coding (>0.95 Bayesian posterior probability [PP]; >70 % Maximum Likelihood bootstrap support [BS]). Calculating phylogenies based on the individual clades of interest did not increase resolution within those clades, even though we excluded more species to reduce the amount of missing data which is present due to the low availability of ETS sequences for many southern African species not sampled by us.

Table S1.4: Distribution and altitude of sampled *Senecio* species. Species are sorted by clade affiliation. Minus indicates that no data was available or that the species does not occur in the tropical African mountains. Altitudes were scored for sub-Saharan African species as: 0 – lowland, 1 – montane, 2 – alpine-like, x – not categorized. Abbreviations: NW – New World; Aus – Australasia, EuAs – Eurasia, ESA – eastern southern Africa, TA – tropical Africa, WSA – western southern Africa. Distribution of South African species is further divided by province (CP: Cape Province, EC: Eastern Cape, FS: Free State, G: Gauteng, KZN: KwaZulu-Natal, Lim: Limpopo, M: Mpumalanga, NC: Northern Cape, NW: North West, TVL: Transvaal, WC: Western Cape). Subspecies abbreviated as subsp. References are found in Appendix S1.7.

Species	Region	Distribution	Occurence on TA mountains	Altitude in m	Category	Reference
No clade affiliation						
S. cadiscus	WSA	South Africa (WC)	-	105-260	0	1
Australasia 1-clade						
S. arniciflorus	WSA	South Africa (WC)	-	10-300	0	1
S. hispidissimus	Aus	South Australia, Victoria, Tasmania	-	lowland areas	x	2, 3
S. ilicifolius	ESA, WSA	South Africa (EC, WC)	-	5-700	0	1
S. oederiafolius	WSA	South Africa (EC, WC)	-	15-990	0	1
S. psilocarpus	Aus	Victoria, Tasmania	-	according to distribution: lowland	x	3
S. pubiger	WSA	South Africa (WC)	-	5-1585	10	1, 5
S. rosmarinifolius	ESA, WSA	South Africa (EC, NC, WC)	-	5-1350	10	1
S. squarrosus	Aus	South Australia, Victoria, Tasmania	-	commonly in lower areas	x	3
S. vestitus	WSA	South Africa (NC, WC)	-	700-1690	10	1
Australasia 2-clade						
S. gregorii	Aus	all provinces of Australia, most abundant in central Australia	-	according to distribution: lowland	x	6
S. gunnii	Aus	southwest Australia	-	montane to alpine	x	2, 3
Australasia 3-clade						
S. lautus	Aus	New Zealand	-	coastal to subalpine	x	7
S. pinnatifolius	Aus	Australia	-	depending on subsp. moderate tohigh altitudes	x	8
Consanguineus-clade						
S. arenarius	WSA	Namibia, South Africa (NC, WC)	-	10-1340	10	1
S. asperulus	ESA, WSA	Lesotho, South Africa (EC, FS, G, KZN, M, NC, WC)	-	515-2590	10	1, 9
S. caloneotes	ESA	Lesotho, South Africa (EC, KZN)	-	2700-3300	2	1

Species	**Region**	**Distribution**	**Occurence on TA mountains**	**Altitude in m**	**Category**	**Reference**
S. cathcartensis	ESA	Lesotho, South Africa (EC, FS, KZN)	-	1480-2440, 1800-2700	1	1, 4
S. chrysocoma	ESA, WSA	South Africa (EC, KZN, WC)	-	60-900	0	1
S. consanguineus	ESA, WSA	Botswana, Namibia, South Africa (FS, G, KZN, LIM, NC, NW)	-	915-2000	1	1
S. cyaneus	TA	Tanzania	Kilimanjaro, Mt. Meru, Hanang, Lukwangule Plateau	2300-3350	1	10
S. eenii	WSA	Botswana, Namibia, South Africa (NC)	-	245-1650	10	1
S. giessii	WSA	S Namibia, South Africa (NC)	-	According to distribution	0	11
S. glanduloso-lanosus	ESA	South Africa (EC, KZN)	-	1115-2075	1	1
S. glanduloso-pilosus	ESA	South Africa (FS, G, KZN, LIM, M, NW)	-	915-1295	1	1
S. glastifolius	WSA	South Africa (EC, WC)	-	60-1090	10	5
S. glaucescens	ESA, WSA	Lesotho, South Africa (EC, FS, G, KZN, M, NC, NW, WC)	-	1800-3000, 220-3050	210	4, 5
S. hieracioides	ESA	Lesotho, South Africa (EC, FS, G, KZN, M, NW)	-	1000-3050, 1450-1800	21	5, 12
S. hirsutilobus	ESA	South Africa (EC, KZN)	-	1525-2450	1	1
S. hochstetteri	ESA, TA	from Sierra Leone to Cameroon, Burundi, DR Congo, Ethiopia, Kenya, Malawi, Rwanda, Sudan, South Africa (LIM), Tanzania, Uganda, Zimbabwe	-	900-2800-(3350)	10	10, 13
S. hypochoerideus	ESA	Lesotho, South Africa (EC, FS, KZN)	-	2400-3200, 1800-3200	21	4, 12
S. macowanii	ESA	South Africa (EC, KZN)	-	1675-2745	21	1, 4
S. mattirolii	TA	DR Congo, Uganda	Ruwenzori	3600-4500	2	10
S. mooreanus	ESA, WSA	South Africa (FS, KZN, LIM, M, NW)	-	1435-2200	1	1
S. polyodon	ESA, TA	Lesotho, South Africa (EC, FS, G, KZN, M), Swaziland, Zimbabwe	-	1800-3000, 600-3000	210	4, 12
S. purpureus	ESA, TA	Angola, DR Congo, Malawi, South Africa (EC, KZN, WC), Tanzania, Zambia, Zimbabwe	-	5-1830, (1200-) 1500-2700,	10	1, 10
S. rautanenii	WSA	Botswana, Namibia, South Africa (NC)	-	245-1650	10	1
S. reclinatus	ESA, WSA	-	-	-	x	-
S. reptans	ESA, WSA	South Africa (EC, FS, NC, NW)	-	915-1615	1	1
S. rhyncholaenus	ESA	South Africa (EC, KZN), Swaziland	-	90-1525	10	1

Species	**Region**	**Distribution**	**Occurence on TA mountains**	**Altitude in m**	**Category**	**Reference**
S. roseiflorus	TA	Kenya	Nyandarua/ Aberdares, Mt. Kenya	(2900-)3200-3600	21	10
S. sandersonii	ESA	South Africa (KZN)	-	?-1675	10	1
S. schweinfurthii	TA	DR Congo, Kenya, Tanzania	-	2300-4500	21	10
S. seminiveus	ESA	Lesotho, South Africa (EC, FS, KZN)	-	1600-3355, 2100-3200	21	1, 4
S. sisymbriifolius	WSA	Namibia, South Africa (NC)	-	195-1405	10	5
S. snowdenii	TA	Kenya	Mt. Elgon	2700-4250	21	10
S. transmarinus	TA	DR Congo, Rwanda, Uganda	Ruwenzori, Virunga	3500-4100, 2250-4200 (depending on subsp.)	21	10
S. x pirottae	TA	DR Congo, Uganda	Ruwenzori	3800-4200	2	10
Decurrens-grade						
S. albanensis	ESA	Lesotho, South Africa (FS, G, LIM, M, EC, KZN, WC), Swaziland	-	915-2130	1	1, 12
S. anomalochorus	ESA	South Africa (FS, G, KZN, M)	-	1050-2420	1	1
S. austromontanus	ESA	Lesotho, South Africa (EC, KZN)	-	2350-2670	1	1
S. brevidentatus	ESA	South Africa (EC, FS, KZN)	-	600-2250	10	1
S. byrnensis	ESA	South Africa (EC, KZN)	-	1370-1435	1	1
S. citriceps	ESA	South Africa (EC, KZN)	-	1800-2335	1	1
S. coronatus	ESA, TA, WSA	Angola, Botswana, Lesotho, Malawi, South Africa (EC, FS, G, KZN, LIM, M, NW, S, WC), Swaziland, Tanzania, Zambia, Zimbabwe	-	1800-2400, 1500	10	4, 10
S. cristimontanus	ESA	South Africa (KZN)	-	1950-2435	1	1
S. decurrens	ESA	Lesotho, South Africa (EC, KZN, M)	-	305-2350	10	1
S. discodregeanus	ESA	Lesotho, South Africa (EC, FS, G, KZN, M), Swaziland	-	50-2375	10	1, 4
S. dregeanus	ESA	South Africa (EC, KZN)	-	765-1340	10	1
S. gramineus	ESA, WSA	Lesotho, South Africa (EC, KZN, WC)	-	1400-3275	21	1, 4
S. inornatus	ESA, TA, WSA	Angola, Burundi, DR Congo, Malawi, South Africa (ESA, EC, FS, FSA, G, KZN, L, LIM, M, NW, S, SA), Tanzania, Zambia, Zimbabwe	-	1800-2425, 1600-2700, 1520-3500	10	4, 10, 13
S. lydenburgensis	ESA	South Africa (FS, G, KZN, M, NW)	-	365-1850	10	1
S. macrospermus	ESA	Lesotho, South Africa (EC, KZN)	-	2500-3000	2	12
S. mauricei	ESA	South Africa (KZN)	-	1675-2440	1	1, 12

Species	Region	Distribution	Occurence on TA mountains	Altitude in m	Category	Reference
S. natalicola	ESA	South Africa (EC, KZN)	-	275-365	0	1
S. ochrocarpus	TA	Ethiopia	-	2800-4300	21	13
S. paludaffinis	ESA	South Africa (KZN), Swaziland	-	1370-2440	1	1, 4
S. panduriformis	ESA	South Africa (EC, KZN, LIM, M), Swaziland	-	600-1600	10	12
S. praeteritus	ESA	South Africa (EC, KZN)	-	650-2250	10	1, 4
S. qathlambanus	ESA	Lesotho, South Africa (EC, KZN)	-	2300-3200	21	4
S. saniensis	ESA	Lesotho, South Africa (KZN)	-	2865-3135, 2375-2865	21	1, 4
S. subsessilis	TA	Burundi, DR Congo, Ethiopia, Kenya, Rwanda, Sudan, Tanzania, Uganda	-	1800-3600, 2400-4310	21	10, 13
S. telmateius	ESA	Lesotho, South Africa (KZN)	-	2195-2440	1	1
			Doria-subclade			
S. castagneanus	EuAs	E Turkey, mainly western Anatolia	-	1250-2200	x	14
S. coriaceus	EuAs		-		x	
S. doria	EuAs	Bulgaria, E France, C Tschechoslowakei, SC Russia to S Spain, Sicily	-	Lowland	x	15
S. doriiformis	EuAs	Iraq, Israel, Lebanon, Palastine, Syria, Turkey	-	1800-2700, 1000-2500	x	14, 16
S. doronicum	EuAs	Austria, France, Germany, Italy, Switzerland	-	1690-2930, 1500-2600	x	15, 16
S. eriopus	EuAs	SW Spain, N Marocco	-	300-1450	x	16, 17
S. eubaeus	EuAs	Greece	-	600-1550	x	16
S. franchetii	EuAs	Afghanistan, Kyrgyzstan, Tajikistan, Uzbekistan	-	750-3850	x	16
S. kolenatianus	EuAs	Caucasus, Georgia, Russia, Turkey	-	1200-3050	x	16
S. lagascanus	EuAs	France, Portugal, Spain	-	240-1650	x	16
S. lopezii	EuAs	S Spain, S Portugal	-	110-470	x	16
S. macedonicus	EuAs	Bulgaria, Greece	-	1400-1600, 900-1800	x	16
S. nemorensis	EuAs	much of Europe, much absent from Mediterranean	-	700-3000	x	18
S. olympicus	EuAs	Turkey (endemic of eastern Anatolia, Mysian Olympus)	-	1800-2000, 1600-2550	x	14, 16
S. paulsenii	EuAs	Afghanistan, Pakistan, Tajikistan, Iran, Turkmenistan	-	1700-2400	x	16
S. perralderianus	EuAs	Algeria, Marocco	-	700-2100	x	16
S. provincialis	EuAs	France, Spain	-	175-1800	x	16
S. pseudoorientalis	EuAs	Central Asia, Armenia, Turkey	-	2200-2800, 1400-2850	x	16
S. pyrenaicus	EuAs	S France, Spain, Portugal	-	1000-2750, 1700-2000	x	16, 17

Species	**Region**	**Distribution**	**Occurence on TA mountains**	**Altitude in m**	**Category**	**Reference**
S. ragazzi	TA	Ethiopia	-	2700-3900	21	13
S. scopolii	EuAs	Albania, Bosnia-Herzegovina, Croatia, Greece, Italy, Macedonia?, Montenegro, Serbia?, Slovenia	-	330-2800	x	16, 17
S. subsessilis	TA	Burundi, DR Congo, Ethiopia, Kenya, Rwanda, Sudan, Tanzania, Uganda	-	1800-3600, 2400-4310	21	10, 13
S. tauricolus	EuAs	Turkey, endemic from southern-central Anatolia, Taurus Mts.	-	1450-2500	x	14
S. transylvanicus	EuAs	Bulgaria, Greece, Macedonia, Montenegro, Romania	-	2000-2700	x	16
S. trapezuntinus	EuAs	Armenia	-	200	x	16
S. umbrosus	EuAs	Tschechoslowakei to Bulgaria, Slowakei	-	mountains	x	15
			Fresenii-clade			
S. abruptus	WSA	South Africa (NC, WC)	-	5-1950	10	5
S. aegyptius	TA, EuAs	Egypt, Ethiopia, Sudan	-	1700-2500	1	13
S. aequinoctialis	TA	Kenya	Nyandarua/Aberdares, Mt. Kenya	3000-4250	21	13
S. affinis	ESA	Lesotho, South Africa (EC, FS, G, KZN, LIM, M, NW)	-	155-2250	10	1
S. angustifolius	ESA, WSA	South Africa (EC, NC, WC)	-	10-1020	10	1
S. asirensis	TA, EuAs	Saudi Arabia, Yemen	-	-	x	-
S. carroensis	WSA	South Africa (WC)	-	10-790, 765-1325	10	1
S. cryphiactis	WSA	Botswana, Namibia	-	-	x	-
S. erysimoides	WSA	South Africa (NC, WC)	-	210-915	0	1
S. fresenii	TA	Ethiopia	-	1500-4300	210	13
S. harveianus	ESA, WSA	Lesotho, South Africa (EC, FS, G, KZN, LIM, M, NW)	-	1800-3000, 765-3290,	210	4, 5
S. inaequidens	ESA, WSA	Lesotho, South Africa (EC, FS, G, KZN,LIM, M, NC, NW), Swaziland	-	1000-2850	21	1, 4
S. jacksonii	TA	Kenya, Uganda	Elgon, Nyandarua/Aberdares	3250–4150(–4500)	21	10
S. keniophytum	TA	Kenya	Mt. Kenya	(3700-)4050-4500(-5000)	2	10
S. laxus	WSA	South Africa (NC, WC)	-	75-915	0	5
S. leptophyllus	ESA, WSA	South Africa (EC, NC, WC)	-	550-1830	10	1
S. littoreus	WSA	South Africa (WC)	-	10-100	0	1
S. maritimus	WSA	South Africa (WC)	-	2-15	0	5

Species	Region	Distribution	Occurence on TA mountains	Altitude in m	Category	Reference
S. meyeri-johannis	TA	Tanzania	Kilimanjaro, Ololmoti (Ngorongoro)	2650-4500	21	10
S. moorei	TA	Kenya, Uganda	Mt. Elgon, Kinangop	1750-3500	1	10
S. myriocephalus	TA	Ethiopia	-	2250-3300-(3900)	1	13
S. niveus	WSA	Namibia, South Africa (EC, NC, WC)	-	365-1650	10	5
S. pinnulatus	WSA	South Africa (NC, WC)	-	15-1890	10	1
S. piptocoma	WSA	Namibia, South Africa (NC, WC)	-	5-1400	10	1
S. platypleurus	TA	Ethiopia	-	1900-2200	1	13
S. purtschelleri	TA	Kenya, Tanzania	Mt. Kenya, Kilimanjaro, Mt. Meru	(3350–)3700–4800(–5000)	2	10
S. rhammatophyllus	TA	Kenya, Uganda	Mt. Elgon	3000-4150	21	10
S. schimperi	TA	Ethiopia	-	1600-3300	1	13
S. steudelii	TA	Ethiopia	-	2000-3300	1	13
S. telekii	TA	Tanzania	Kilimanjaro, Mt. Meru	(3350-)3600-5400	2	10
S. unionis	TA	Ethiopia	-	3170-4050	21	13
New World 1-clade						
S. costaricensis	NW	Costa Rica	-	-	x	-
S. integerrimus	NW	California	-	150-3600	x	19
S. jarae	NW	Argentina, Bolivia	-	2300-5000	x	20
S. lastarrianus	NW	Chile	-	900-2000	x	20
S. patens	NW	Colombia, Ecuador	-	2550-3250	x	21
S. roseus	NW	Mexico, Peru	-	3000-4000	x	22
New World 2-clade						
S. adenotrichius	NW	(N) Chile	-	300-1200	x	20
S. aphanactis	NW	California, Mexico	-	10-400	x	23
S. aspericaulis	NW	Argentina,Chile	-	2400-2800	x	20
S. bahioides	NW	Chile	-	0-1000	x	20
S. balensis	TA	Ethiopia	-	3800-4100	2	24
S. brasiliensis	NW	N Argentina, Brazil, Paraguay Uruguay,	-	40–1000	x	25
S. californicus	NW	California	-	0-1200	x	23
S. chilensis	NW	Chile	-	2000-max, 200-1000, 1500-3000	x	20, 26
S. cisplatinus	NW	Argentina	-	0-500	x	20
S. crithmoides	NW	Chile	-	1800-4500	x	26
S. deferens	NW	Argentina, Bolivia, Paraguay	-	400-3000	x	26
S. donianus	NW	Chile	-	2700-4000	x	26
S. eremophilus	NW	Canada, USA	-	200–2300, 2700–3700, 2400-3900 (depending on subsp.)	x	23

Species	**Region**	**Distribution**	**Occurence on TA mountains**	**Altitude in m**	**Category**	**Reference**
S. ertterae	NW	W USA	-	900–1200	x	23
S. farinaceus	TA	Ethiopia	N Ethiopia	3600-4300	2	13
S. farinifer	NW	Chile	-	700-1600	x	20
S. filaginoides	NW	Argentina, Chile, Peru	-	400-2700, 1600-4300 (depending on subsp.)	x	20
S. flaccidus	NW	California	-	800–2400, 100–1500, 600–2000 (depending on subsp.)	x	23
S. glaber	NW	Chile	-	2000-2500	x	20
S. gnidioides	NW	S of South America	-	1000-2500	x	20
S. humillimus	NW	Bolivia	-	3500-4800	x	26
S. laetevirens	NW	Chile, Argentinia	-	2000-4000	x	26
S. landbeckii	NW	Chile	-	1500-2500	x	20
S. lemmonii	NW	S USA	-	500-1000	x	23
S. leptolobus	NW	Brazil, Uruguay	-	0-1400	x	20
S. mairetianus	NW		-	3500-4150	x	27
S. maulinus	NW	Chile	-	200-2800	x	20
S. montevidensis	NW	Uruguay, Brasil, Argentina	-	0-1000	x	20
S. nanus	TA	Ethiopia	Simien	3250-4100	21	13
S. niveoaureus	NW	Columbia	-		x	
S. oreophyton	NW	Chile, Argentina	-	3100-4000, 3150-3600	x	20, 26
S. poeppigii	NW	Chile	-	1300-2000, 1800-max (depending on subsp.)	x	26
S. polygaloides	NW	Chile	-	2000-3050	x	26
S. rufescens	NW	from Colombia to Argentina	-	3500-5200	x	26
S. schultzii	TA	Ethiopia	depending on var. either widely or only Bale Mts.	3900-4375	2	13
S. selloi	NW	Uruguay	-	0-500	x	20
S. sinuatilobus	NW	Chile		0-1500		20
S. sotikensis	TA	Kenya, Uganda	Mt. Elgon	3000-4500	21	10
S. spartioides	NW	S USA	-	1000–3500	x	23
S. stoechadiformis	NW	Mexico	-	2400-3000	x	22
S. tricuspidatus	NW	S Chile	-	0-800/1200 (depending on subsp.)	x	20
S. trifidus	NW	Chile	-	2700-4000	x	26
S. volckmannii	NW	Chile	-	3300-4400	x	26
			Sabinjoensis-clade			
S. sabinjoensis	TA	DR Congo, Rwanda, Uganda	Virunga Mts. (Mgahinga, Muhavura)	2900-3950	21	10

Species	Region	Distribution	Occurence on TA mountains	Altitude in m	Category	Reference
S. urundensis	TA	Burundi, DR Congo, Malawi, Rwanda, Tanzania, Zambia	-	1500-2700	10	10
			Vulgris-clade			
S. gallicus	EuAs	S Europe to C France, SW Europe, Sicily, Algeria, Alboran Island	-	0-1000	x	28
S. aethnensis	EuAs	Sicily, Mt. Etna	-	>1000	x	17, 29
S. bollei	EuAs	Canaries	-	Zone maritime	x	30
S. leucanthemifolius	EuAs	Mediterranean	-	0-100, -2250 (depending on subsp.)	x	28
			Windhoekensis-clade			
S. elegans	WSA	South Africa (EC, WC)	-	5-200	0	5
S. glutinosus	WSA	Namibia, South Africa (EC, NC, WC)	-	5-1920	10	5
S. hastatus	ESA, WSA	Lesotho, South Africa (EC, FS, KZN, NC, WC)	-	2000-2650	1	4
S. windhoekensis	WSA	Namibia, South Africa (NC)	-	900-1675	1	1

Table S1.5: Distribution and altitude of sub-Saharan African species not belonging to *Senecio* but being listed as *Senecio* in the African Plant Database. Minus indicates that no data was available. Altitudes were scored as: 0 – lowland, 1 – montane, 2 – alpine-like. Abbreviations: western southern Africa – WSA; eastern southern Africa – ESA; tropical Africa – TA; Distribution of South African species is further divided by province (CP: Cape Province, EC: Eastern Cape, FS: Free State, G: Gauteng, KZN: KwaZulu-Natal, Lim: Limpopo, M: Mpumalanga, NC: Northern Cape, NW: North West, TVL: Transvaal, WC: Western Cape), MA – Madagascar, NW – New World, EuAs – Eurasia. References are found in Appendix S1.7.

Species	**Region**	**Distribution**	**Altitude in m**	**Category**	**Reference**
S. abbreviatus	WSA	South Africa (NC, WC)	30-?	0	5
S. achilleifolius	ESA, WSA	Lesotho, South Africa (EC, FS, G, KZN, M, NC, NW, WC)	1800-3000	21	4
S. angulatus	WSA	South Africa (EC, WC)	5-700	0	1
S. auriculatissimus	TA	Zimbabwe, Malawi, Mozambique	-	-	-
S. baurii	ESA	South Africa (EC, KZN)	1065-2135	1	1
S. bulbinifolius	WSA	Namibia, South Africa (NC, WC)	[?]-730	0	1
S. cryptolanatus	ESA	Lesotho, South Africa (EC, KZN)	2200-3355	21	5
S. deltoideus	TA, ESA, WSA	Tanzania, Kenya, Malawi, Mozambique, South Africa (EC, KZN, WC, M, LIM, FS), Swasiland, Zimbabwe	1800-1950, 700-2200	10	4, 10
S. depauperatus	TA	Tanzania	1550-2900	10	10
S. glaberrimus	ESA	Lesotho, South Africa (EC, FS, G, KZN, M), Swaziland	5-2700	10	1
S. hadiensis	TA	Burundi, DR Congo, Ethiopia, Kenya, Madagascar, Rwanda, Saudi Arabia, Somalia, Tanzania, Uganda, Yemen	500-2600; 1200-2400	1	10, 13
S. hollandii	WSA	South Africa (EC, WC)	365-860	0	1
S. humidanus	WSA	Lesotho, South Africa (EC, KZN) Swaziland	765-2425	10	1
S. junceus	WSA	South Africa (EC, NC, WC)	15-1370	10	1
S. latifolius	TA, ESA	South Africa (EC, FS, KZN, LIM, M, NW), Swaziland, Zimbabwe, Zambia	245-1700	10	1
S. lineatus	WSA	South Africa (EC, WC)	20-1370	10	1
S. linifolius	ESA, WSA	Lesotho, South Africa (EC)	20-1700	10	1
S. macroglossus	TA, ESA, WSA	Ethiopia, South Africa (EC, KZN, M), Zimbabwe,	15-915, 2000-2500	1	5, 13
S. maranguensis	TA	Uganda, Tanzania, Kenya, Congo, Rwanda, Burundi, Malawi	1800-3250	1	10
S. mariettae	TA	Burundi, DR Congo, Rwanda, Uganda	2550-3400	1	10
S. microglossus	ESA	South Africa (EC, KZN, Lim, M), Swaziland	305-1830	10	1
S. muirii	WSA	South Africa (NC, WC)	-	-	-
S. oxyriifolius	TA, ESA	Angola, DR Congo, Malawi, Mozambique, South Africa (EC, G, KZN, LIM, M, NW), Swaziland, Tanzania, Zambia, Zimbabwe,	1800-2100, 15-2400, 950-2800	10	4, 5, 10
S. paucicalyculatus	ESA	Lesotho, South Africa (FS, KZN, M	1065-2560	1	1
S. pergamentaceus	TA	Tanzania, Zambia, Malawi	950-2250	10	10
S. pinifolius	WSA	South Africa (EC, WC)	45-2490	10	1
S. pinnatipartitus	TA	Ethiopia	1800-2500	1	13
S. polyanthemoides	ESA	South Africa (LIM, KZN, EC)	40-1800	0	5
S. poseideonis	ESA	South Africa (EC, KZN)	915-1295	1	1

Species	Region	Distribution	Altitude in m	Category	Reference
S. pterophorus	ESA, WSA	Lesotho, South Africa (EC, KZN, WC)	15-1980	10	1
S. retrorsus	ESA	Lesotho, South Africa (EC, KZN)	20-2135	10	1
S. rhomboideus	ESA	Lesotho, South Africa (EC, FS, KZN, LIM, M, WC)	1800-3000, 30-3020	210	4, 5
S. ruwenzoriensis	TA, ESA, WSA	Kenya, Tanzania, Uganda, Nigeria to Sudan, South to South Africa (EC, FS, WC, NW, M)	1150-3000	10	10
S. sarcoides	WSA	Namibia, NC, WC	5-1005	10	1
S. scitus	ESA	Lesotho, South Africa (EC, FS, G, KZN, Lim, M), Swaziland	1115-3050, 1800-2160	21	1, 4
S. strictifolius	ESA, TA, WSA	Tanzania, Congo, Angola, Malawi, Zambia, Zimbabwe, Botswana, Namibia	1700-2150	1	10
S. syringifolius	TA	Kenya, Malawi, Rwanda, Tanzania, Uganda,	1500-3300	1	10
S. triqueter	WSA	WC	120-640	0	1
S. tropaeolifolius	WSA	South Africa (EC)	640-825	0	1
S. tugelensis	ESA	Lesotho. South Africa (EC, KZN)	2700-3355, 2400-3000	21	1, 4

Table S1.6: Distribution and altitude of non-sampled species occurring in tropical African and listed in the African Plant Database as *Senecio*. Minus indicates that no data was available. Altitudes were scored as: 0 – lowland, 1 – montane, 2 – alpine-like. Distribution of South African species is further divided by province (CP: Cape Province, EC: Eastern Cape, FS: Free State, G: Gauteng, KZN: KwaZulu-Natal, Lim: Limpopo, M: Mpumalanga, NC: Northern Cape, NW: North West, TVL: Transvaal, WC: Western Cape). References are found in Appendix S1.7.

Species	Author	Region	Altitude in m	Category	Reference
S. acroleucus	Merxm.	Zimbabwe	-	-	Trans. Rhodesia Sci. Assoc. 43: 68 (1951)
S. aetfatensis	B. Nord.	Mozambique, Zimbabwe (Chimanimani Mts.)	1400-1900	0	31, 33
S. amplificatus	C.Jeffrey	Kenya (Aberdare Mts)	3500	1	10
S. antunesii	O. Hoffm.	Angola	-	-	Bot. Jahrb. Syst. 32(1): 151. 1902
S. bampsianus	Lisowski	Burundi, DR Congo, Rwanda	1900-2300	1	32
S. barbertonicus	Klatt	South Africa (GA, KN, LP, MP, NW), Swaziland, Zimbabwe	35-1675	0	33
S. brachyantherus	(Hiern) S. Moore	Angola	-	-	Cat. Afr. Pl. 1: 606 (1898)
S. brachypodus	DC.	South Africa (EC, KN), Swaziland	5-1400	0	12, 34
S. brittenianus	Hiern	Angola	-	-	Cat. Afr. Pl. 1: 601 (1898
S. burtonii.	Hook	Cameroon	2000-3650	1	35
S. caudatus	DC	DR Congo, South Africa (EC, KN, LP, MP), Swaziland	460-2470	10	5, 32
S. confertus	Sch.Bip. ex A.Rich.	Ethiopia, Rwanda	2200-3355	1	13

Species	**Author**	**Region**	**Altitude in m**	**Cate-gory**	**Reference**
S. conrathii	N.E. Br.	South Africa (EC, FS, KN, LP, MP), Swaziland, Zimbabwe	10-2200	10	4, 12, 33
S. crassorhizus	De Wild.	Burundi, DR Congo, Rwanda	1400-1500	0	32
S. crispatopilosus	C.Jeffrey	Kenya, Uganda	2700-3050	1	10
S. dentatoalatus	Mildbr. ex C.Jeffrey	Tanzania, known from the Uluguru Mts	1800-2150	1	10
S. dilungensis	Lisowski	Burundi, DR Congo, Rwanda	1550-1850	0	32
S. diphyllus	De Wild. & Muschl.	DR Congo, Malawi, Zambia	1100-1420	0	32
S. discokaraguensis	C.Jeffrey	Tanzania	1620	0	10
S. doryphoroides	C. Jeffrey	Tanzania	1650	0	10
S. doryphorus	Mattf.	DR Congo, Tanzania	1700-2000	10	10, 32
S. dumeticolus	S. Moore	Angola	-	-	J. Bot. 56: 228. 1918
S. ellenbeckii	O. Hoffm.	Ethiopia?	-	-	Bot. Jahrb. Syst. 38: 208 (1906
S. erlangeri	O. Hoffm.	Ethiopia?	-	-	Bot. Jahrb. Syst. 38: 208 (1906)
S. erubescens	Aiton	Angola, Botswana, DR Congo, Malawi, Swaziland, South Africa, Tanzania, Zambia, Zimbabwe,	(990-) 1600-2400	10	10, 32
S. exarachnoideus	C.Jeffrey	Tanzania	1100-1900	0	10
S. gazensis	S. Moore	Zimbabwe, Mozambique	1520-2250	10	33
S. gossweileri	Torre	tropical Africa	-	-	Garcia de Orta, Ser. Bot. 2(1): 57 (1974)
S. gramineticola	C.Jeffrey	Malawi, Tanzania	1500-2250	10	10
S. greenwayi	C.Jeffrey	DR Congo, Malawi, Tanzania, Zambia	1300-2450	10	32
S. hedbergii	C.Jeffrey	Kenya, Tanzania	3300-3650	2	10
S. helminthioides	(Sch. Bip.) Hilliard	Mozambique, South Africa (EC, KZN, LIM, M), Swaziland, Zimbabwe	5-1525	0	1
S. homoplasticus	S. Moore	Zimbabwe	-	-	J. Linn. Soc., Bot. xl. 120 (1911)
S. immixtus	C.Jeffrey	DR Congo, Tanzania	2400-2600, 1590	10	10, 32
S. jeffreyanus	Lisowski	Burundi, DR Congo, Rwanda	-	-	32
S. kacondensis	S. Moore	Angola	-	-	J. Bot. 56: 229 (1918)
S. karaguensis	O.Hoffm.	Burundi, Rwanda, Tanzania, Uganda, Zambia	1200-2100	10	10, 32
S. katangensis	O.Hoffm.	Burundi, DR Congo, Rwanda	1400-2250	10	32
S. kayomborum	Beentje	Tanzania, Zambia	1800-2100	1	10
S. kuluensis	S. Moore	Angola	-	-	J. Bot. 56: 231 (1918)
S. kundelungensis	Lisowski	Burundi, DR Congo, Rwanda	1600	0	32
S. laticorymbosus	Gilli	Malawi, Tanzania	2150-2550	1	10

Species	**Author**	**Region**	**Altitude in m**	**Cate-gory**	**Reference**
S. lawalreeanus	Lisowski	Burundi, DR Congo, Rwanda	2350-2459	1	32
S. lejolyanus	Lisowski	Burundi, DR Congo, Rwanda	1550-1600	0	32
S. lelyi	Huteh	Cameroon, Guinea, Nigeria, Sudan, Tanzania	950-2100	10	10, 35
S. letouzeyanus	Lisowski	Burundi, DR Congo, Rwanda	2700-3308	1	32
S. lewalleii	Lisowski	Burundi, DR Congo, Rwanda	2000-2100	1	32
S. luembensis	De Wild. & Muschl.	Burundi, DR Congo, Rwanda	1100-1700	0	32
S. lyratus	Forssk.	Ethiopia, Kenya, Sudan, Somalia,	(1000-) 1300-2800	10	13
S. mabberleyi	C. Jeffrey	Tanzania	1800-2300	1	10
S. macroglossus	Hilliard	Zimbabwe, Cape	2000-2500	1	13
S. malaissei	Lisowski	DR Congo, Rwanda and Burundi Zaire	-	-	Fragm. Florist. Geobot. 41(1): 484 (1996)
S. margaritae	C. Jeffrey	Kenya	1800-1950	0	10
S. mesogrammoides	O.Hoffm.	Ethiopia, Kenya, Tanzania	1200-2500, 2500-3250	10	10, 13
S. microalatus	C. Jeffrey	Tanzania	2310	1	10
S. mooreioides	C. Jeffrey	Tanzania	(1750-)2400-3450	10	10
S. mooreioides × hochstetteri	[Hell.]	Tanzania	3050	1	10
S. morotonensis	C.Jeffrey	Uganda (Mt. Moroto)	±2900	1	10
S. navugabensis	C.Jeffrey	Uganda	±1200	0	10
S. ngoyanus	Hilliard	Mozambique, South Africa (KZN)	5-460	0	5, 12
S. ornatus	S. Moore	Angola, Burundi, DR Congo, Rwanda	1590-1700	0	32
S. pachyrhizus	O.Hoffm.	Angola, Burundi. Cameroun, DR Congo, Malawi, Tanzania, Uganda, Zambia	1070-1900	0	32
S. peltophorus	Brenan	Malawi (Mt. Mulanje)	-	-	36
S. pentecostus	Hiern	Angola	-	-	Cat. Afr. Pl. 1: 598 (1898)
S. perrottetii	DC	Senegal, Mali	along sandy riverbanks	0	35
S. plantagineoides	C.Jeffrey	Kenya	2000-3150	1	10
S. polyadenus	Hedberg	DR Congo, Uganda (endemic to Mts Muhavura and Karisimbi)	3500-4000	2	10, 32
S. pseudosubsessilis	C.Jeffrey	Kenya	1900-3050	1	10
S. randii	S. Moore	DR Congo, Zambia, Zimbabwe	-	-	32
S. rugegensis	Muschl.	Zimbabwe	1850-2450	1	32
S. salviifolius	Sch. Bip.	Ethiopia	-	-	Beitr. Fl. Aethiop.: 160 (1867)
S. semiamplexifolius	De Wild.	DR Congo, Tanzania	1600-2600	10	10, 32

Species	**Author**	**Region**	**Altitude in m**	**Category**	**Reference**
S. shabensis	Lisowski	Burundi, DR Congo, Rwanda	-	-	32
S. sororius	C.Jeffrey	Tanzania	1000	0	10
S. spartareus	S. Moore	Burundi, DR Congo, Kenya, Uganda	1450-1900	0	10, 32
S. speciosus	Willd.	Lesotho, South Africa (EC, FS, KZN, LIM, M, WC), Swaziland	10-3200	210	12, 34
S. steudelioides	Sch. Bip.	Ethiopia	3200	1	39
S. subfractiflexus	C.Jeffrey	Tanzania, Uluguru Mts	1600-2100	10	10
S. swynnertonii	S. Moore	Zimbabwe	-	-	J. Bot. 54: 283 (1916)
S. tabulicola	Baker	Malawi, Mozambique, Tanzania	1200-2350	10	10
S. tamoides	DC.	From Zimbabwe to Cape, Ethiopia	10-1905, 1700-2400,	10	5, 13
S. teixeirae	Torre	Angola	-	-	Bol. Soc. Brot., Ser. 2 44: 289 (1970)
S. tenuicaulis	Muschl.	Angola	-	-	
S. torticaulis	Merxm.	Zimbabwe	-	-	Trans. Rhodesia Sci. Assoc. 43: 69 (1951)
S. transmarinus × *hochstetteri*	[Hell.]	Uganda	2250-2400	1	10
S. triactinus	S. Moore	Zimbabwe	-	-	J. Linn. Soc., Bot. xl. 119 (1911)
S. vicinus	S. Moore	Angola	-	-	J. Bot. 56: 230. 1918
S. viminalis	Bremek.	South Africa (KZN, LIM, M), Swaziland	55-1010	0	5, 12
S. vitellinoides	Merxm.	TA	-	-	trans. Rhodesia Sci. Assoc. 43: 70 (1951)
S. volcanicola	C. Jeffrey	Tanzania (Ngorongoro, Mt. Meru and Kilimanjaro)	2100-2750	1	10
S. whyteanus	Britten	Malawi (Mt. Mulanje)	1800-2200	1	36
S. xenostylus	O. Hoffm.	Angola	-	-	Bot. Jahrb. Syst. 32: 150 (1902)

TABLE S1.7: REFERENCES GIVEN IN APPENDIX S1.4-S1.6.

Abbreviation	Resource
1	African Plant Database, 2012
2	Wapstra *et al.*, 2008
3	Thompson, 2004a
4	Hilliard, 1987
5	POSA Flora (2007)
6	Thompson, 2004b
7	Webb *et al.*, 1988
8	Thompson, 2005
9	Pooley, 2003
10	Jeffrey & Beentje, 2005
11	Manning & Bruyns, 2013
12	Hilliard, 1977
13	Tadesse, 2004
14	Matthews, 1975
15	Hegi *et al.*, 1987
16	Calvo *et al.*, 2015
17	Chater & Walters, 2010
18	Jeffrey & Chen Yi-Ling, 1984
19	Calflora, 2014
20	Instituto de Botánica Darwinion, 2014
21	Silva-Moure *et al.*, 2014
22	García-Pérez, 1985
23	Barkley, 2006
24	Ortiz & Vivero, 2005
25	Hind, 2011
26	Cabrera *et al.*, 1999
27	Rzedowski & de Rzedowski, 1985
28	Alexander, 1979
29	Brennan *et al.*, 2009
30	Pitart & Proust, 1909
31	Hyde *et al.*, 2015c
32	Botanic Garden Meise, 2015
33	Hyde *et al.*, 2015a
34	Harvey, 1865
35	Hutschinson & Dalziel, 2014
36	Hyde *et al.*, 2015b

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Appendix S2: Additional results regarding phylogenetic reconstructions, incongruences between markers and ancestral area and altitude reconstruction of the consanguineus-clade.

TABLE S2.1: ALIGNMENT LENGTH, SUBSTITUTION MODELS AND INFORMATIVE CHARACTERS OF DNA REGIONS.

Dataset	**Region**	**Substitution model**	**Partition scheme in combined analyses**	**# of sequenced species**	**Alignment length in bp (excl. bases)**	**# of variable positions/ informative characters**
Senecio.	ITS	SYM+I+G	Unpartitioned, GTR+I +G	247	687	362/255
(including	ETS	GTR+I+G		138	420	207/143
outgroup)	*trn*LF	HKY	Unpartitioned; HKY+I+G	117	887	88/42
	*trn*C-*ycf*6	F81+G		85	884 (26)	150/58
Senecioneae	ITS	SYM+I+G		152	773	514/439

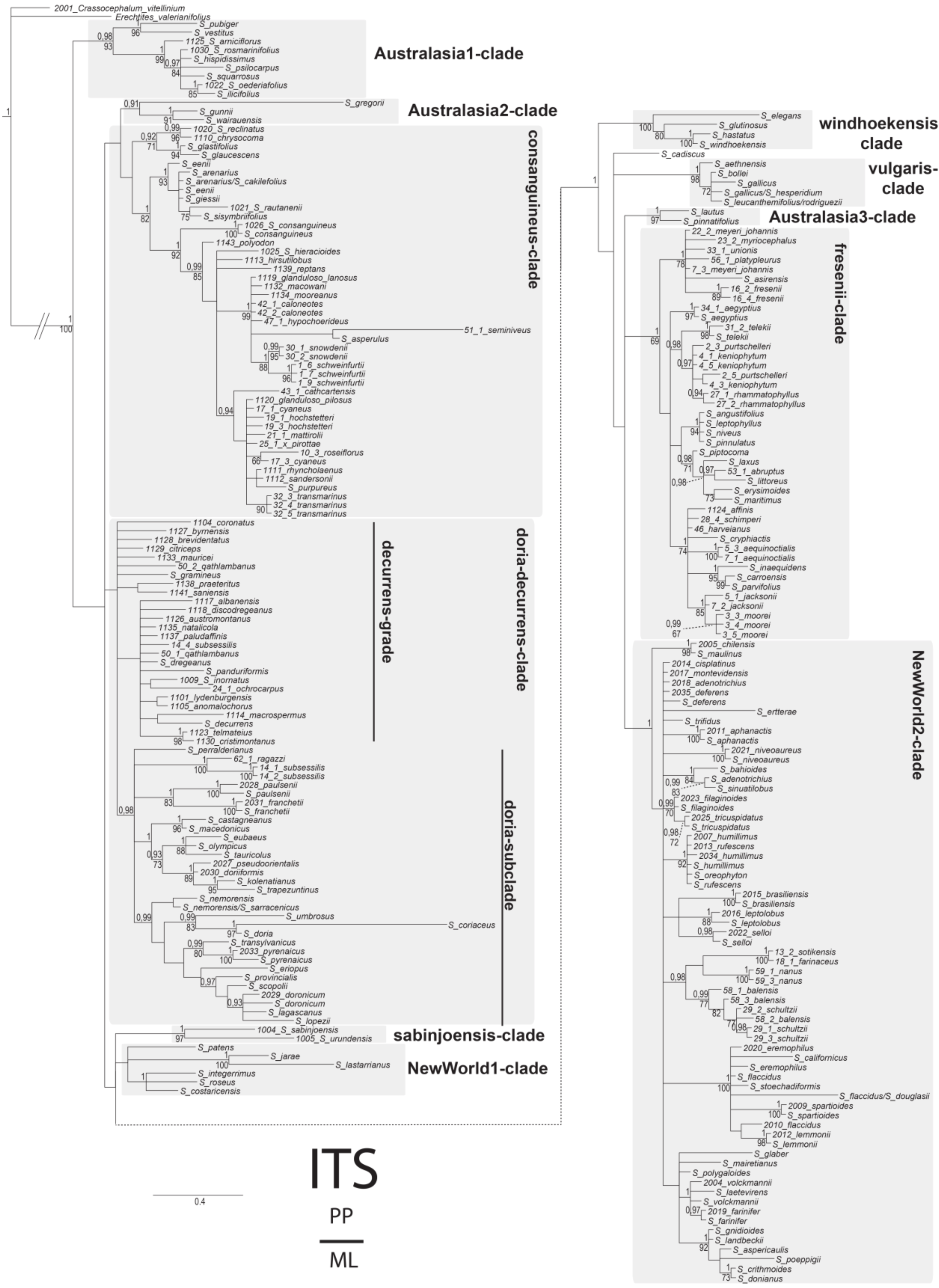

FIGURE S2.2 PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON THE NR ITS MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES. BAYESIAN 50% MAJORITY RULE CONSENSUS TREE OF NR ITS WITH BAYESIAN >0.90 (PP) SUPPORT VALUES AND MAXIMUM LIKELIHOOD >65 (ML) BOOTSTRAP VALUES MAPPED ON THE BI MAJORITY RULE CONSENSUS TREE.

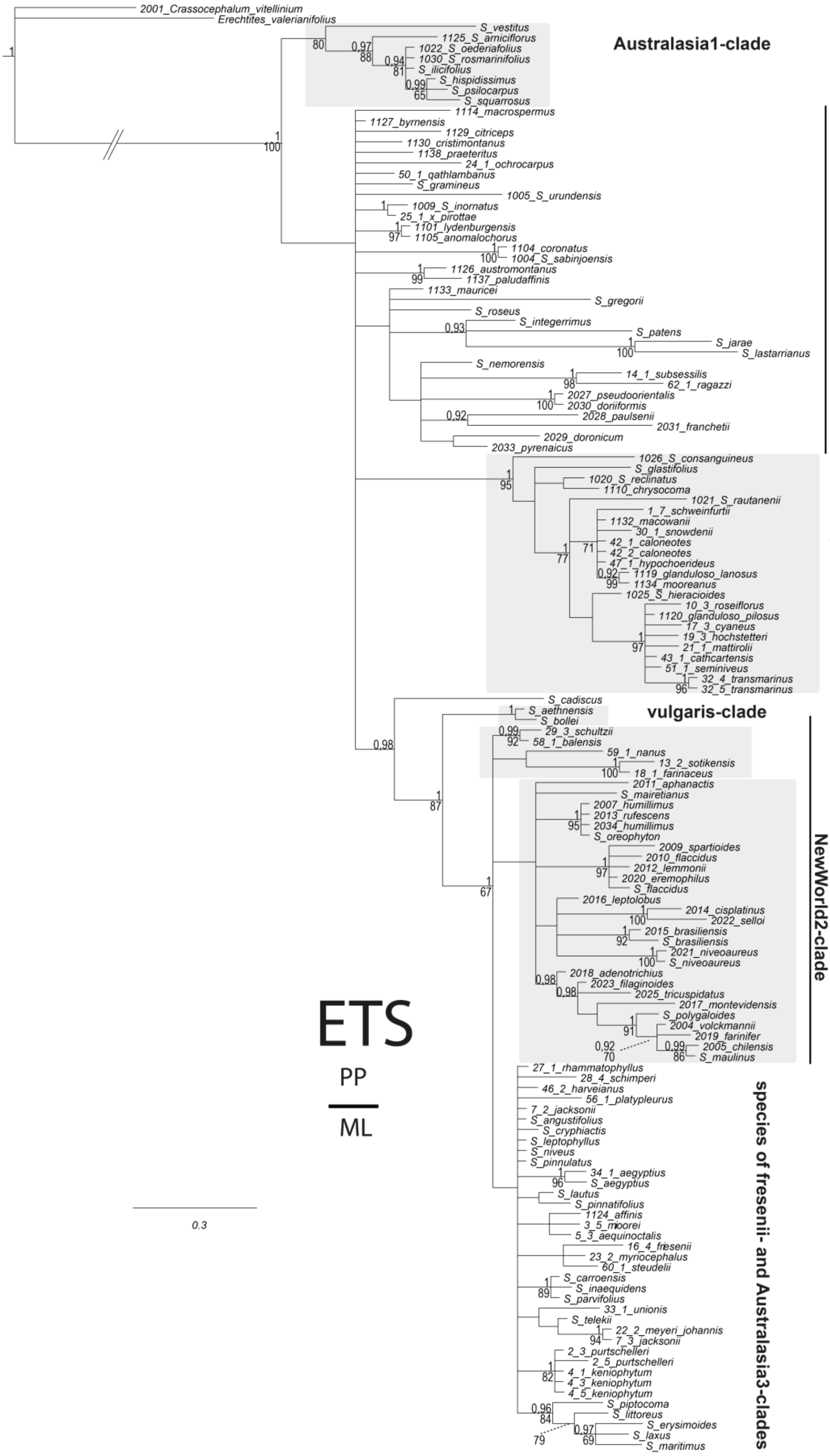

Figure S2.3: Phylogenetic reconstruction of *Senecio* based on the nr ETS majority rule consensus tree, calculated with Bayesian Inference (BI) method. Support values for BI >0.95 posterior probability (PP) and for Maximum Likelihood (ML) bootstrap support values >70 are shown at the nodes. Bayesian 50% majority rule consensus tree of nr ETS with Bayesian >0.90 (PP) support values

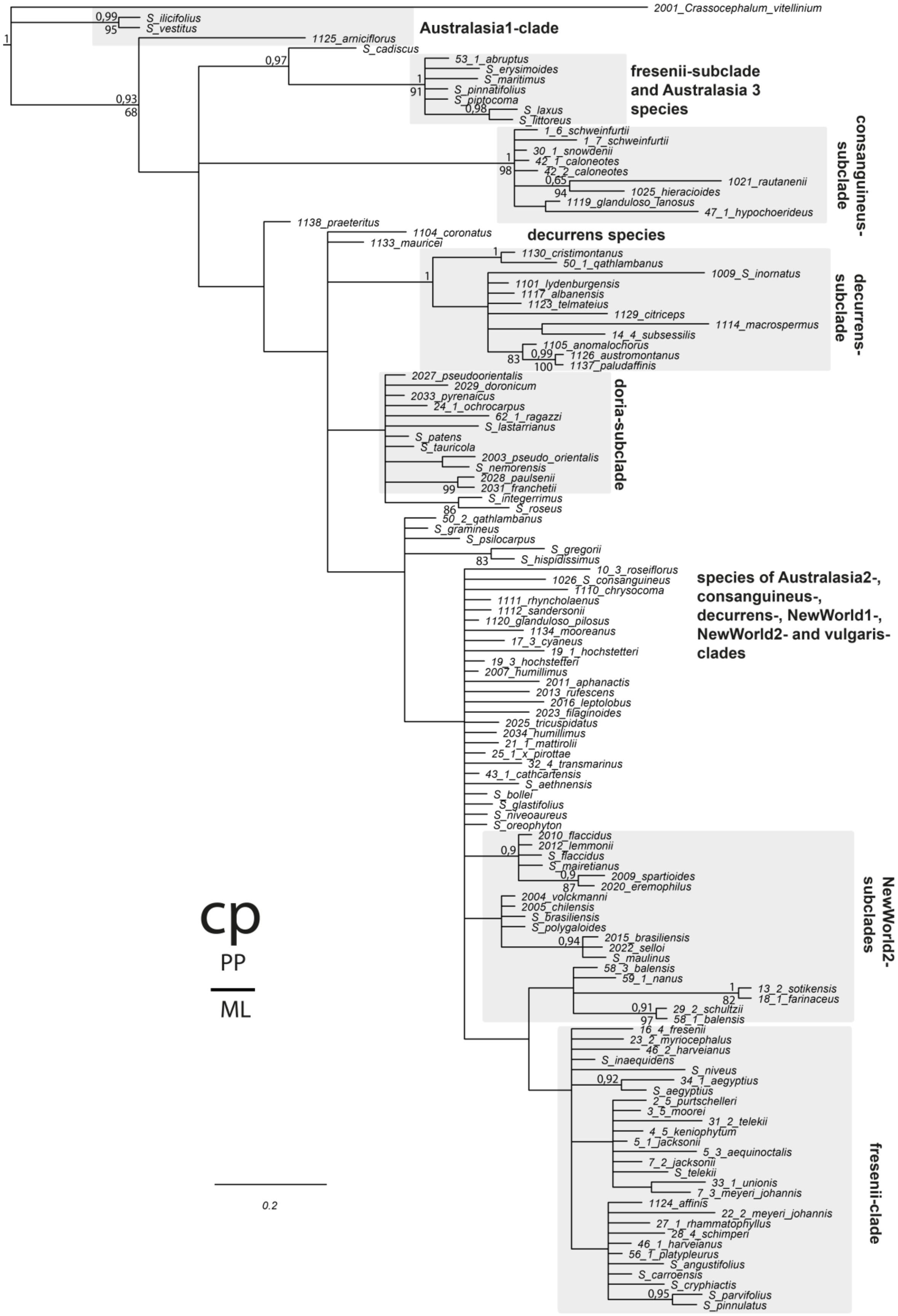

FIGURE S2.4: PHYLOGENETIC RECONSTRUCTION OF *SENECIO* BASED ON THE COMBINED CHLOROPLAST MAJORITY RULE CONSENSUS TREE, CALCULATED WITH BAYESIAN INFERENCE (BI) METHOD. SUPPORT VALUES FOR BI >0.95 POSTERIOR PROBABILITY (PP) AND FOR MAXIMUM LIKELIHOOD (ML) BOOTSTRAP SUPPORT VALUES >70 ARE SHOWN AT THE NODES.

S2.5: INCONGRUENCES BETWEEN MARKERS

The ITS and ETS phylogenies revealed some incongruences with low support. Those where mostly observed in SA, Eurasian and New World species (Appendix S2.3 & S2.4). Treating those sequences as independent accessions did not increase support or resolution and combining the two did not change overall support. No incongruences were observed in the EA afroalpine species with two exception: *Senecio x pirottae*, which was already described as hybrid species (Jeffrey & Beentje, 2005) and *S. sabinjoensis*. ITS and ETS sequences were not concatenated but treated as independent accessions for the latter two species in the final combined nr analyses.

The combined cp phylogeny showed incongruences with the nr phylogeny (Figure 3 & Appendix S2.6). In two clades with tropical afroalpine species incongruences were detected in different subclades: one subclade of the fresenii-clade, the maritimus-subclade, together with *S. pinnatifolius* A. Rich. (Australasia 3 species), as well as one subclade of the consanguineus-clade, the snowdenii-subclade. Also, two consanguineus-clade species (*S. hieracioides* and *S. rautanenii*) are placed more basally in the cp phylogeny. Although the phylogeny is not well supported, the two subclades (maritimus- and snowdenii-) are clearly in conflict with the better supported nr phylogeny (Fig. 3 & Appendix S2.6). Incongruences between nr and cp data have been reported before (Pelser *et al.*, 2007; Pelser *et al.*, 2010; Pelser *et al.*, 2012; Calvo *et al.*, 2013, Chapter 3) and interpreted as the result of both incomplete lineage sorting and hybridisation (Pelser *et al.*, 2010; Pelser *et al.*, 2012).

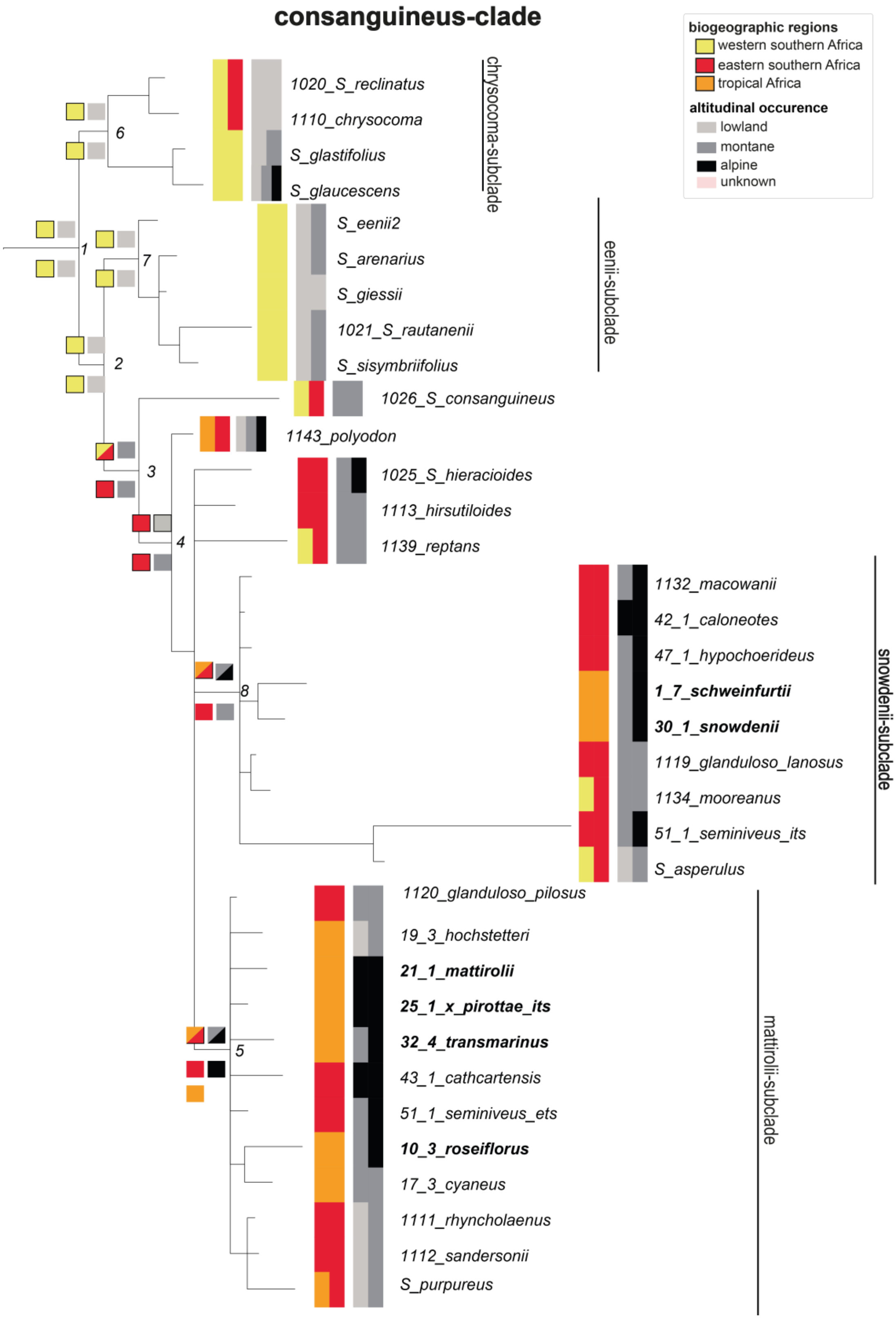

Figure S2.6: Extracted consanguineus-clade of Figure 3. Reconstruction with Lagrange mapped onto supported nodes. Numbers at nodes correspond to numbers in Tab. S2.7. Distribution and altitude of species is shown at the tips of the tree and reconstruction is shown along the branches. Here, the biogeographic reconstruction is shown on the left and the altitude on the right (boxes above the node represent the ancestral character state of the branch above, and boxes below the node represent the ancestral character state of the branch below). Two boxes per reconstruction at one branch of a node are only shown when the relative probability of the most likely reconstruction was less than 5% more than of the second most likely one.

Table S2.7: Results of the Lagrange reconstructions of the consanguineus-clade. Reconstructed regions and altitude with their likelihood and relative probability for major nodes (corresponding node numbers are shown in Figure S2.6). Upper and lower branch correspond to the branches as displayed in Figure S2.6. Abbreviations: ESA – eastern southern Africa, WSA – western southern Africa, trop – tropical Africa excluding EA. Mathematical abbreviations: Log-Likelihood – lnL; relative probability – rel. Prop.

	Region				**Altitude**			
Node	**Upper branch**	**Lower branch**	**lnL**	**Rel. Prob**	**Upper branch**	**Lower branch**	**lnL**	**Rel. Prob**
1	WSA	WSA	-76.82	0.50	low	low	-96.95	0.52
	WSA	WSA+ESA	-78.25	0.12	low	low+montane	-98.57	0.10
	WSA	WSA+trop	-78.26	0.12	low	montane	-99.02	0.07
	WSA+ESA	WSA	-78.57	0.09				
	others			0.12	others			0.26
2	WSA	WSA	-76.84	0.49	low	low	-97.33	0.36
	WSA	WSA+ESA	-78.06	0.15	montane	montane	-98.17	0.15
	WSA	ESA	-78.08	0.14	low+montane	montane	-98.24	0.14
	WSA	WSA+trop	-78.76	0.07	low	montane	-98.68	0.09
	WSA	ESA+trop	-78.82	0.07	low	low+montane	-99.14	0.06
	others			0.05	others			0.15
3	WSA+ESA	ESA	-76.87	0.48	montane	montane	-97.38	0.34
	ESA	ESA	-78.18	0.13	montane	low+montane	-97.88	0.21
	WSA	ESA+trop	-78.44	0.10	montane	low+montane+alpine-like	-98.26	0.14
	ESA	ESA+trop	-78.49	0.09	montane	montane+ alpine-like	-99.15	0.06
	WSA	ESA	-78.59	0.09	others			0.21
	WSA	trop	-79	0.06				
	others			0.03				
4	ESA	ESA	-76.79	0.51	low+montane+ alpine-like	montane	-97.45	0.32
	ESA+trop	ESA	-77.29	0.31	montane	montane	-97.98	0.19
	ESA+trop	trop	-79.12	0.05	low+montane	montane	-98.1	0.17
	others			0.09	montane+ alpine-like	montane	-98.84	0.08
					low+alpine-like	montane	-99.15	0.06
					low+montane+ alpine-like	alpine-like	-99.17	0.06
					others			0.09
5	ESA+trop	trop	-76.83	0.50	montane+ alpine-like	montane	-96.89	0.56
	ESA+trop	ESA	-76.83	0.50	montane	montane	-97.9	0.20
					montane+ alpine-like	low	-98.01	0.18
					others			0.04

	Region				**Altitude**			
Node	**Upper branch**	**Lower branch**	**lnL**	**Rel. Prob**	**Upper branch**	**Lower branch**	**lnL**	**Rel. Prob**
6	WSA	WSA	-76.54	0.67	low	low	-96.69	0.68
	WSA+ESA	WSA	-77.9	0.17	low	low+montane	-98.56	0.10
	ESA	ESA	-79.02	0.06	low	low+alpine-like	-99.25	0.05
	others			0.07	low	low+montane+ alpine-like	-99.28	0.05
					others			0.08
7	WSA	WSA	-76.13	1	low	low	-97.11	0.45
					low+montane	low	-97.27	0.38
					others			0.13
8	ESA+EA	ESA	-94.86	0.95	montane+ alpine-like	montane	-96.93	0.53
	ESA+trop	WSA	-78.94	0.04	montane+ alpine-like	alpine-like	-97.58	0.28
					montane+ alpine-like	low	-98.08	0.17

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5. Synthese

Die Evolution und historische Biogeographie von *Senecio* wurde mit Hilfe von molekularen Phylogenien, die auf nukleär ribosomalen und chloroplastidären Daten beruhen, nachvollzogen. Insgesamt wurden 294 *Senecio*-Arten untersucht, die in unterschiedlichen Zusammensetzungen in den Phylogenien enthalten sind. Um die Verwandtschaft der neu aufgenommenen Arten zu *Senecio* zu prüfen, wurde ein Teildatensatz der tribusweiten Phylogenie von Pelser *et al*. (2007) verwendet.

In der Arbeit konnte gezeigt werden, dass die phylogenetischen Untersuchungen zum einen frühere Erkenntnisse bestätigen (Pelser *et al.*, 2007; Pelser *et al.*, 2010a; Pelser *et al.*, 2012, Calvo *et al.*, 2013) und zum anderen neue Rückschlüsse zu lassen. Wie schon in vorangegangenen Arbeiten gezeigt wurde, können die nukleären und plastidären Daten nicht kombiniert werden, da es gut unterstützte phylogenetische Konflikte zwischen beiden Datensätzen gibt. Daher erfolgten Rückschlüsse über die Evolution und historische Biogeographie der Gattung nur auf Grundlage der nukleären Daten. Denn in der nukleären Phylogenie gibt es einige gut unterstützte Kladen, wohingegen die Phylogenie der plastidären Daten kaum unterstützte Auflösung zeigt. In den einzelnen nukleären Kladen von *Senecio* befinden sich meist Arten eines Florenreichs. Die neu untersuchten Arten gehören fast alle in Kladen, die schon von Pelser *et al.* (2007) gefunden wurden, mit Ausnahme der neuen Sabinjoensis-Klade, die aus zwei Arten besteht.

Die Datierung der Gattung erfolgte mit verschiedenen Kalibrierungsmethoden. Mit Hilfe eines Fossils der Familie (später mit einem weiteren) wurde eine Familienphylogenie kalibriert, um daraus einen sekundären Kalibrierungspunkt bestimmen zu können mit dem anschließend der Stammbaum der Gattung datiert werden konnte. Außerdem wurde die Gattungsphylogenie mit Hilfe von Substitutionsraten der Familie kalibriert. Die Ergebnisse zeigen, dass die Gattung im Miozän entstand. Die Diversifizierungsrate von *Senecio* ist höher als von der Tribus und vergleichbar mit anderen schnellen Radiationen. Vergleiche mit anderen Gattungen zeigen, dass *Senecio* eine Besonderheit darstellt. *Senecio* ist die einzige große Gattung, die fast weltweit verbreitet und jung ist (vgl. Kapitel 2). Die meisten bisher untersuchten Radiationen sind entweder artenärmer, nicht nahezu weltweit verbreitet oder deutlich älter, mit Ausnahme von *Poa* L. und nahverwandte Gattungen (Kapitel 2). Oft können hohe Diversifizierungsraten mit Schlüsselentwicklungen in Verbindung gebracht werden. Bei *Senecio* lässt sich zwar kein morphologisches Merkmal finden, das die hohe Diversifizierungsrate erklären würde, es ist jedoch möglich, dass die Kombination von einer guten Ausbreitungsfähigkeit, einem hohen Samenansatz und einer Präferenz für offene und gestörte Standorte die Diversifizierung positiv beeinflusst hat (Kapitel 2). Denn zum Zeitpunkt der Diversifizierung von *Senecio* kam es zu großen klimatischen und geologischen Veränderungen, viele der heute existierenden Gebirge entstanden in demselben Zeitraum und boten dadurch offene oder gestörte Habitate. Eine Anpassung an solche Habitate bedeutet, dass sich die Arten dort gut etablieren konnten und konkurrenzfähig waren, was wiederum die weitere Ausbreitung und Artbildung begünstigen könnte (Yuan *et al.*, 2005; Moore & Donoghue, 2007; Vilà *et al.*, 2007).

Des Weiteren konnte in dieser Arbeit gezeigt werden, dass die Gattung *Senecio* in den trocken oder Winterregengebieten des südlichen Afrikas entstand. Von dort ausgehend wurden andere afrikanische Regionen sowie andere Kontinente besiedelt. Die Ausbreitung in die Paläarktis durch *Senecio* geschah zweimal unabhängig voneinander, am wahrscheinlichsten ausgehend von zwei unterschiedlichen Regionen des südlichen Afrikas (Kapitel 3). Die Doria-Klade, besteht aus mehrjährigen Arten und lässt sich vermehrt in den Bergen der Paläarktis finden. Der letzte gemeinsame Vorfahr dieser Klade, wie auch der Gattung, war mehrjährig und der Ursprung der Doria-Klade liegt wohl in den Drakensbergen, im Osten des südlichen Afrikas. Es ist anzunehmen, dass sich der letzte gemeinsame Vorfahr in den Drakensbergen an die ökologischen Bedingungen von Bergen angepasst hatte, bevor die Paläarktis erfolgreich besiedelt wurde. Die andere paläarktische Klade, die Vulgaris-Klade, findet sich zumeist entlang des Mittelmeeres und besteht hauptsächlich aus einjährigen Arten. Ihr letzter gemeinsamer afrikanischer Vorfahr stammt am wahrscheinlichsten aus den trockenen oder Winterregengebieten im Westen des südlichen Afrikas und wies vermutlich schon eine einjährige Lebensweise auf. Die Evolution von Einjährigkeit scheint eine Anpassung an die vorgefundenen ökologischen Bedingungen zu sein, da durch den schnelleren Lebenszyklus Trocken- und Hitzestress vermieden werden kann (Verboom *et al.*, 2003; Evans *et al.*, 2005; Datson *et al.*, 2008). Mehrjährigkeit hingegen scheint in montanen und alpin-ähnlichen Regionen von Vorteil zu sein (Drummond, 2008).

Außerdem konnte gezeigt werden, dass auch die alpin-ähnlichen Regionen der ostafrikanischen Berge, die ein kontinentales Inselhabitat darstellen, mehrmals unabhängig voneinander während des späten Pliozäns und/oder frühen Pleistozäns besiedelt wurden (Kapitel 4). Es kam zu fünf bis 14 unabhängigen Ausbreitungsereignissen in die sogenannte tropisch afroalpine Region. Zumeist lässt sich der Ursprung der tropisch afroalpinen Arten und Linien in montanen Regionen der Drakensberge vermuten, aber es existieren auch evolutionäre Verbindungen zur Paläarktis und zur Neuen Welt. In der vorwiegend paläarktisch verbreiteten Doria-Klade befinden sich Arten, die heute in den Bergen Ostafrikas vorkommen. Ob die ostafrikanischen Berge als Trittsteine für die Besiedelung der Paläarktis dienten oder ob die ostafrikanischen Berge von der Paläarktis aus besiedelt wurden ist unklar, da die Auflösung des Stammbaums nicht ausreicht um hier eine definitive Aussage machen zu können (Kapitel 3 und 4). Auch bei der Verbindung zur Neuen Welt bleibt unklar, ob die Neue Welt von Ostafrika aus besiedelt wurde oder umgekehrt (Kapitel 4). Insgesamt kommen nur sehr wenige Arten von *Senecio* im afrikanisch-tropischen Tiefland vor. Die große Artenanzahl von *Senecio* im ostafrikanischen Hochgebirge ist das Ergebnis von vielen unabhängigen Ausbreitungsereignissen, die Bedeutung von *in situ* Artbildung ist eher gering (Kapitel 4). Dies konnte auch schon für andere tropisch afroalpine Linien gezeigt werden (Assefa *et al.*, 2007; Gehrke & Linder, 2009; Ahmed, 2013; Galbany-Casals *et al.*, 2014). Vergleiche von *in situ* Artbildung und der Anzahl unabhängiger Kolonisierungsereignisse von Pflanzengattungen in tropisch alpin-ähnlichen Bereichen Ostafrikas, Südamerikas und Malaysias zeigen, dass auch in Malaysia Einwanderung wichtiger ist, in Südamerika aber *in situ* Artbildung eine größere Bedeutung zu kommt (Kapitel 4). Dies scheint, wie für echte Inseln gezeigt wurde, ein Effekt der Arealgröße zu sein, die tropisch alpin-ähnliche Bereiche Südamerikas sind deutlich größer als in Ostafrika oder Malaysia.

Insgesamt lässt sich erkennen, dass die Ausbreitung von *Senecio* von Nischenevolution und -stabilität abhängt. Auf der einen Seite kam es zu einer Diversifizierung und Ausbreitung in trockene und/oder Winterregengebiete nachdem sich Einjährigkeit entwickelte und nach einer Anpassung an die ökologischen Bedingungen von montanen und alpin-ähnlichen Regionen konnten weitere Bergregionen besiedelt werden. Auf der anderen Seite haben sich nur wenige Arten erfolgreich im afrikanisch-tropischen Tiefland etablieren und an die dortigen Bedingungen anpassen können. Der Artenreichtum von *Senecio* in höheren Lagen und die mehrfache Ausbreitung entlang der Berge, scheint ein Phänomen zu sein, das sich nicht nur in Afrika und Europa finden lässt. Schon Small (1919) erklärte, dass die Ausbreitung von *Senecio* mit Bergen in Verbindung gebracht werden kann. Diese Aussage hat wohl heute noch Gültigkeit, auch wenn zu seiner Zeit mehr Arten zu der Gattung gezählt wurden, ihr Ursprung in Bolivien angenommen und von einer basalen Stellung im Familienstammbaum ausgegangen wurde.

6.Quellenangaben der Einleitung und Synthese

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7.Danksagung

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10. Anhang

Informationen zu den Fotos der Abbildung 1

a) *Delairea odorata* Lem.
Aufnahme von: Kerry Woods
URL: https://www.flickr.com/photos/93854456@N03/9806267204/in/photostream/
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Vorgenommene Änderungen: keine

b) *Caputia medley-woodii* (Hutch.) B. Nord. & Pelser
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c) *Curio roleanus* (H. Jacobsen) P.V. Heath
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d) *Kleinia neriifolia* Haw.
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e) *Dendrosenecio* cf. *adnivalis* Stapf
Aufnahme von: Martha Kandziora

f) *Jacobaea vulgaris* Gaertn.
Aufnahme von: Christian Fischer
URL: https://commons.wikimedia.org/wiki/File:SenecioJacobaeaJacobaea.jpg
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Informationen zu den Fotos der Abbildung 2

a) *Senecio superandinus* Cuatrec
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b) *Senecio canescens* (Bonpl.) Cuatrec.
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Vorgenommene Änderungen: keine

c) *Senecio mattirolii* Chiov.
Aufnahme von: Martha Kandziora

d) *Senecio* cf. *transmarinus* S. Moore
Aufnahme von: Martha Kandziora

e) *Senecio masafuerae* (Skottsberg) Pelser
Aufnahme von: Jardín Botánico Nacional, Viña del Mar, Chile
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f) *Senecio elegans* L.
Aufnahme von: Martha Kandziora

g) *Senecio suaveolens* (L.)
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Informationen zur Abbildung 3

Abbildung aus: Thomé, Otto Wilhelm (1885) Flora von Deutschland, Österreich und der Schweiz, Gera, Deutschland. Eingescannt von Kurt Stueber.
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11. Lebenslauf

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