

nomenclatural stability for the Neotropical species commonly known as *Dennstaedtia bipinnata* (now *Mucura bipinnata*) (Art. 14), and to prevent loss of the newly described *Mucura*, we propose the conservation of *Dicksonia bipinnata* with a conserved type: the Ventenat specimen at B-W (with a duplicate/fragment at US). If approved, the Ventenat specimen at MA would no longer be the type.

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## (2943) Proposal to conserve *Selaginella*, nom. cons., (*Selaginellaceae*) with a conserved type

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(2943) *Selaginella* P. Beauv. in Mag. Encycl. 9(5): 478. 1804, nom. cons.

Typus: *S. flabellata* (L.) Spring (*Lycopodium flabellatum* L.), typ. cons. prop.

*Selaginella* (*Selaginellaceae*) is the largest genus in lycophytes and known for its special phylogenetic position in vascular plants, its heterospores, its resurrection ability, and its pharmacological value (Banks & al. in Annual Rev. Pl. Biol. 60: 223–238. 2009). Phylogenetically, *Selaginella* is sister to *Isoëtiales* and both taxa share heterospores and a ligule at the base of each leaf and sporophylls (Pryer & al. in Nature 409: 618–622. 2001). *Selaginella* is notorious for its many species with a seemingly undifferentiated gross morphology and a paucity of modern monographic treatments that consider the totality of species in a phylogenetic context. These factors have led to great difficulty in identifying species.

Following PPG I (in J. Syst. Evol. 54: 563–603. 2016), *Selaginella* alone constitutes the family *Selaginellaceae* and the order *Selaginellales*. However, it is unique for an order/family in pteridophytes with 700–800 species (Jermy in Kubitzki, Fam. Gen. Vasc. Pl. 1: 39–45. 1990; Tryon & Lugardon, Spores Pteridophyta: 606–621. 1991; Zhou & Zhang in Taxon 64: 1117–1140. 2015) to contain only one genus. There were three most important arguments for maintaining

a broadly defined single genus. Firstly, the major phylogenetic relationships within *Selaginella* had been unclear. Although quite a few phylogenetic studies were carried out (Korall & al. in Int. J. Pl. Sci. 160: 585–594. 1999; Korall & Kenrick in Amer. J. Bot. 89: 506–517. 2002, in Molec. Phylogen. Evol. 31: 852–864. 2004; Arrigo & al. in Amer. J. Bot. 100: 1672–1682. 2013), they were based on relatively small taxon samplings. This has been much improved by two recent molecular works (Westrand & Korall in Amer. J. Bot. 103: 2136–2159. 2016a; Zhou & al. in Cladistics 32: 360–389. 2016) in which over 200 species of *Selaginella* were sampled, but the overall relationships were either not well resolved (Westrand & Korall, l.c. 2016a) or well resolved but the enigmatic Sinensis group was excluded (Zhou & al., l.c.). Secondly, the morphological discontinuity among the lineages within *Selaginella* had not been well understood in spite of the fact that two infrageneric classifications have been proposed recently based on molecular and morphological evidence (Zhou & Zhang, l.c. 2015; Westrand & Korall in Amer. J. Bot. 103: 2160–2169. 2016b). Thirdly, the current type of the generic name, *S. selaginoides* (L.) P. Beauv. ex Schrank & Mart., is resolved as a member of the first diverging clade with only two species (Westrand & Korall, l.c. 2016a; Zhou & al., l.c.) and, morphologically, this clade has no rhizophores at all, completely different from all other species in the family. Recognizing multiple genera in the

family would inevitably result in nomenclatural instability for most species in the family unless a new conserved type of *Selaginella* is designated.

Most recently, we have conducted a new phylogenetic study based on expanded character sampling of 684 accessions representing ca. 300 species of *Selaginella* and analyzed the evolution of 10 most important morphological characters in the context of the new phylogeny to understand the diagnosing characters of various major clades (Zhou & Zhang, submitted). Our new study resolves well the relationships among all the major clades and these clades are found to be diagnosable morphologically. We therefore propose to recognize seven subfamilies and 17 genera in *Selaginellaceae*, which appears to be a dramatic deviation from the current single-genus classification but is consistent with our earlier classification albeit with different ranks in which six subgenera were recognized and three of the subgenera were further divided into five, six, and seven sections, in addition to the untreated Sinensis group (Zhou & Zhang, l.c. 2015). Our new classification also agrees with some earlier treatments in which 2–5 or more genera were recognized (Palisot de Beauvois in Mag. Encycl. 9: 472–483. 1804; Kuntze, Revis. Gen. Pl. 2: 824–827. 1891; Börner, Fl. Deut. Volk: 285. 1912; Rothmaler in Feddes Repert. Spec. Nov. Regni Veg. 54: 55–82. 1944; Sakurai in Bot. Mag. (Tokyo) 57: 255–256. 1943; Kung in Fl. Sichuan. 6: 56–80. 1988; Soják in Preslia 64: 151–158. 1993; Satou in Hikobia 12: 269. 1997; Tzvelev in Novosti Sist. Vyssh. Rast. 36: 22–27. 2004; Weakley, Fl. S. Mid-Atlantic States: 64–66. 2012; Weakley, Fl. Southeast. U.S.: 72–74. 2020). Our new classification is further in line with the recent trend of classifications of pteridophytes, for example, ca. 380 species in 17 genera in *Lycopodiales* (Chen & al. in Taxon 71: 25–51. 2022; Zhang & Zhou in Indian Fern J. 38: 125–136. 2022), the sister order of *Selaginellales* + *Isoëtiales*; ca. 265 species in 25 genera in *Blechnaceae* (PPG I, l.c.; de Gasper & al. in Phytotaxa 275: 191–227. 2016; González & al. in Darwiniana, ser. 2, 8: 525–529. 2020); ca. 1200 species in 37 genera in *Thelypteridaceae* (Fawcett & Smith in Sida Bot. Misc. 59: 23. 2021); and ca. 900 species in 33 genera in *Polypodiaceae* subfam. *Grammitidoideae* (Sundue & al. in Molec. Phylogen. Evol. 81: 195–206. 2014). The new classification of *Selaginellaceae* will hopefully facilitate communication, promote further analyses, and help conservation.

In this new phylogenetic study, the current type of the generic name, *Selaginella selaginoides*, is again confirmed as a member of

the first diverging clade. In fact, the monophyly of this clade and its relationship as sister to the rest of the genus have always been consistent in all previous phylogenetic studies (Westrand & Korall, l.c. 2016a; Zhou & al., l.c.). This means that, based on the phylogenetic relationships and morphology, any division of *Selaginella* into several genera would lead to the genus *Selaginella* including only two species. Following our new classification, over 300 species including most species in the New World would need to be transferred to a different genus.

Therefore, we propose to conserve the name *Selaginella* with a new type, *S. flabellata* (L.) Spring. Multiple accessions of *S. flabellata* have been included in earlier studies and have been consistently resolved in the most species-rich clade, the *Stachygynandrum* clade (*S.* subg. *Stachygynandrum* sensu Zhou & Zhang, l.c. 2015; becoming *Selaginella* s.str. if this conservation proposal is accepted) in all studies (Westrand & Korall, l.c. 2016a; Zhou & al., l.c.). In this way, the original type, *S. selaginoides*, will be retained in the genus *Selaginoides* Ség. (Pl. Veron. 3: 51. 1754, currently rejected in favour of *Selaginella* P. Beauv. 1805, nom. cons.), although the species epithet will need to be changed because use of ‘*selaginoides*’ would create a tautonym (Art. 23.4 of the *ICN*; Turland & al. in Regnum Veg. 159. 2018). The morphology of the new type is found to match the general description of *Selaginella* and all major features of the genus as understood by modern authors by having different-sized and dorsiventral leaves in four rows, with a ligule at the base of each leaf and sporophyll, by being heterosporous, and by having rhizophores (Thomas in Rev. Palaeobot. Palynol. 95: 129–153. 1997). By this proposal, names of most species in the New World and a portion of species in the Old World would be preserved and this would minimize nomenclatural instability in the family caused by the new classification. One other minor effect of the proposal is that the entries for two of the names currently rejected in favour of *Selaginella*, nom. cons., will change. *Selaginoides* will cease to be homotypic with *Selaginella*, but *Stachygynandrum* will become homotypic with it.

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