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How to classify a species-rich genus Title

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INTRODUCTION & AIM

Species-rich genera with various circumscriptions are always a source of controversy. This controversy is illustrated in questions such as which taxonomic level did the taxa belong to? Which characters help botanists to classify taxa in natural groups? The taxa show diversity in life form, leaf shape, and texture, flower shape, and in the pieces of flowers. Genetic diversity and accommodation make some genera rich, like the genus Silene. Silene, currently numbering 870 species, is a large genus. It grows in temperate to arctic zones in the northern hemisphere. The following three central diversities are discerned for it: SW Asia, the Mediterranean area, and Central Asia. Several species have been shown to be polyploid. In order to use the species-rich genus as a model in genetic, ecological, and evolutionary study, it is necessary to classify the genus.

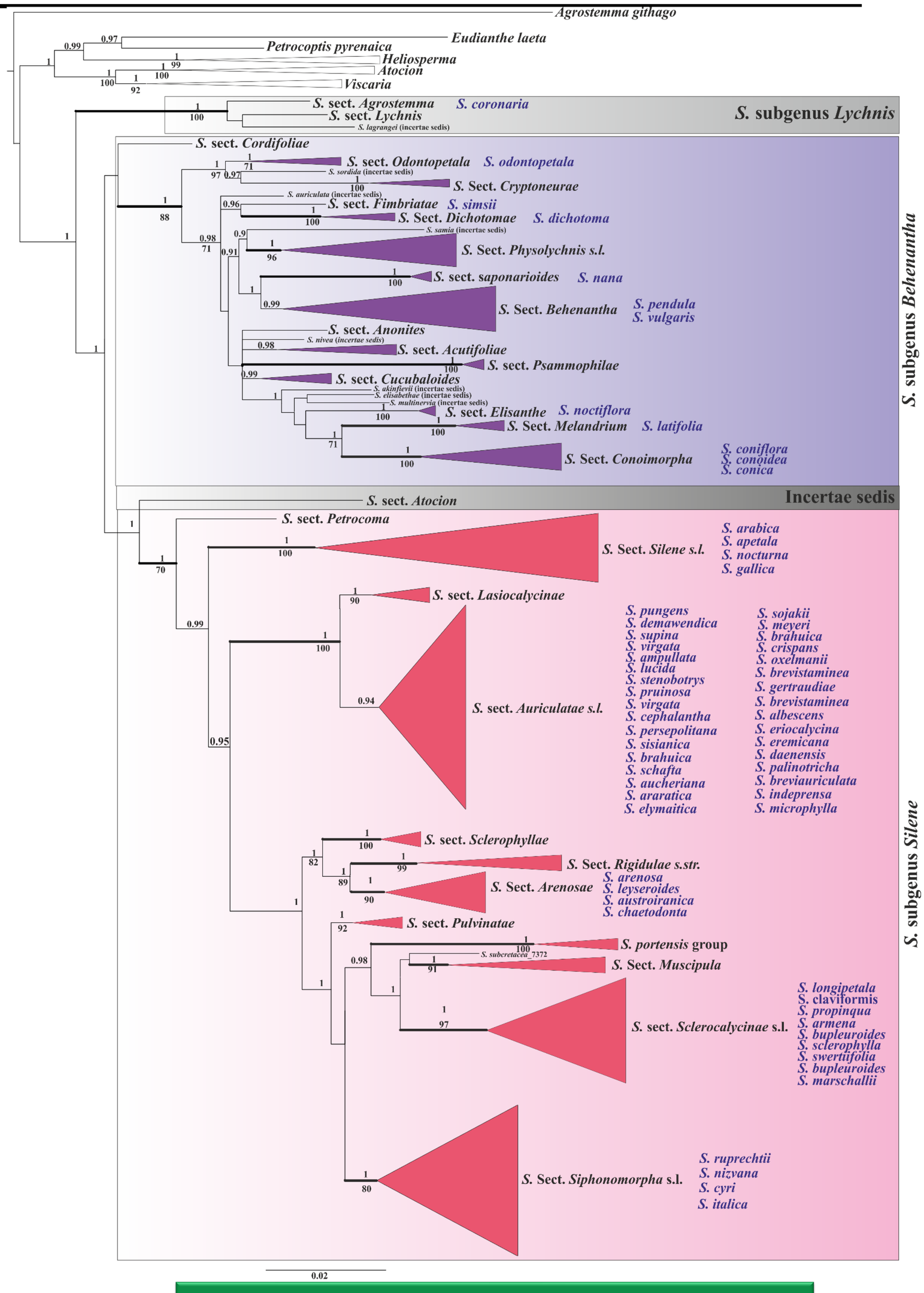
METHOD

Phylogeny reconstruction could be one way to find natural groups. To this end, a comprehensive sampling of Silene and allied genera in the tribe Sileneae was provided. Two common and very useful markers, nrDNA ITS and cpDNA rps16, were used. All 44 sections recognized by Chowdhuri (1957) covered the entire geographical range of the genus. The analyses were performed with STACEY v.1.2.5 as implemented in BEAST v.2.5.1.

RESULTS & DISCUSSION

Nuclear and chloroplast tree topologies were congruent. The polyploidy in some taxa can distort the phylogeny and classification of the species-rich genus. Differences in acclimating to different habitats can also make the phylogeny and classification unclear. These led us to face limitations in defining the diagnostic morphological characters of subgrouping.

Here, the *Silene* sects *Auriculatae*, *Physolychnis*, *Sclerocalycinae*, *Silene*, and *Siphonomorpha* are each defined in a broad sense.



CONCLUSION

To circumvent these limitations and define subgrouping, a broad sense was used. Three subgenera, Lychnis, Behenantha, and Silene, and 35 sections were recognized for the genus. However, one section has uncertain placement.

FUTURE WORK / REFERENCES

The next step, phylogeny, using more loci, will be reconstructed to discover the natural subgrouping of these sections.