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**TAXONOMIC AND PHYLOGENETIC
RELATIONS OF *ALLIUM CHAMAESPATHUM*
BOISS., A REMARKABLE SPECIES OF
BALKAN FLORA**

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Based on recent systematic and phylogenetic researches, the genus *Allium* L. currently includes 920 species arranged in 15 subgenera and 15 sections. Among these groups, subgen. *Allium* is the largest one with over 300 species, 130 of which belong to the sect. *Allium*, well supported as monophyletic. Within this section, *Allium chamaespathum* Boiss. stands out as the only autumn-flowering species, considered a Tertiary wild relative of a potential gene donor to many *Allium* crops, including *A. cepa*, *A. fistulosum*, *A. porrum*, *A. sativum* and *A. schoenoprasum*. It represents a typical Balkan element, occurring in several localities of Albania, mainland Greece, Peloponnese, Evvia, Crete, Ionian and Aegean islands, extending to South Italy, and growing in rocky places, usually garrigues and grasslands, rarely open woodlands and dunes. This species is very rare, with restricted populations. Literature data, herbaria examination, and new field surveys throughout its distribution area revealed a significant morphological variation among populations which suggested more detailed bio-systematic investigations. To clarify the taxonomic position of this peculiar *Allium*, and assess the variability range of its populations, living plants from several sites were analysed. Qualitative and quantitative morphological features were measured under stereomicroscope (6–66×) from both fresh and herbarium materials; karyotypes were obtained and characterized from somatic mitotic plates of root meristematic cells, through traditional karyotyping methods; leaf anatomy was studied on leaf cross sections from leaf blades of maximum size and optimal vegetative development; seed coat microsculpturing was assessed by SEM technique; for phylogenetic investigations, DNA extractions by CTAB2× and PCR amplifications of *nr*- and *cp*-DNA sequences using specific protocols were performed. Obtained sequences for ITS, *trnL-trnF* and *trnH-psbA* genes were assembled to generate MP, ML, and BI phylogenetic trees, and TCS haplotype networks. Though all populations share the same chromosome count $2n=16$ and the typical karyotype structure of sect. *Allium*, with chromosomes having long linear satellites, relevant macro- and micro-morphological features, different ecological requirements, and significant genetic diversity, suggest that *A. chamaespathum* should be treated as a complex species, with

several populations, from Crete, Albania, S Italy for instance, needing a deep revision of their taxonomic status.

KEYWORDS: *Allium chamaespathum*, Balkan flora, biosystematics, phylogenetics, section *Allium*