

Department of Biology and Ecology,
Faculty of Sciences and Mathematics, University of Niš
Institute for Nature Conservation of Serbia
Science Technology Park Niš

**15th Symposium on the Flora of
Southeastern Serbia
and Neighboring Regions**
Niš, 23th to 25th May, 2025

Abstracts

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Micromorphology of *Corylus avellana* L. pollen grains analyzed by scanning electron microscopy

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Hazelnut (*Corylus avellana* L., (Corylaceae)) is a monoecious species in which male flowers - catkins and female flowers - glomerule are spatially separate. According to the flowering time, hazelnuts belong to the group of protandrous plants, meaning that male flowers ripen first. Since pollination is anemophilous, male flowers produce large amounts of pollen for successful fertilization. Examination of the pollen grain morphological features such as size, shape, polarity, symmetry, exine ornamentation, type, number and size of apertures, length of polar (P) and equatorial axis (E), were made using scanning electron microscopy (SEM) in order to contribute to palynological studies of cultivated fruit trees in Serbia. The pollen grains are isopolar, radially symmetrical and medium-sized. Grains are triporate with 3 pori arranged meridionally. The length of the polar axis (P) is $22.34 \pm 4.8 \mu\text{m}$, and of the equatorial diameter (E) $25.62 \pm 4.3 \mu\text{m}$. The P/E ratio is 0.86 ± 0.05 indicating suboblate shape. The outline in polar view is triangular convex, since the apertures are situated at the angles. Pore diameter amounts to 3.27 ± 0.68 . The exine ornamentation is scabrate. Sculptural elements are less than $1 \mu\text{m}$ in diameter, while their number per unit area of $5 \times 5 \mu\text{m}$ is 57.14 ± 7.8 .

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Relative genome size variation in the *Stachys recta* group in southeastern Europe

Ranimirović, M.¹, Đurović, S.², Tomović, G.³, Kuzmanović, N.³, Buzurović, U.⁴, Milivojević, L.³, Niketić, M.^{5,6}

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With many subordinate or presumably closely related local endemic or subendemic taxa, *Stachys recta* forms a polymorphic group. To explore the variation in relative genome size and to identify patterns that may unravel the evolutionary history of the taxonomically complex *S. recta* group, relative genome size (RGS) was assessed for a total of 155 accessions from 55 populations of 18 taxa in southeastern Europe (*S. albanica*, *S. angustifolia*, *S. anisochila*, *S. atherocalyx*, *S. beckeana*, *S. goulimyi*, *S. graeca*, *S. leucoglossa*, *S. parolinii*, *S. patula*, *S. recta* subsp. *baldaccii*, *S. r.* subsp. *doerfleri*, *S. r.* subsp. *olympica*, *S. r.* subsp. *recta*, *S. r.* subsp. *rhodopaea*, *S. r.* subsp. *subcrenata*, *S. tetragona* and *S. zepcensis*). Flow cytometry was used to estimate the relative genome size, expressed here as a ratio of fluorescences between the individual and the standard (*Bellis perennis*), and varying from 0.43 to 0.71. Although several studies of other taxonomically complex taxa have shown correlations between intraspecific GS variation and morphology or environmental factors, and geographic segregation, we found no patterns in the RGS variation of the analysed samples with respect to taxonomy, geography or ecology.

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Cytogenetic diversity in *Crocus chrysanthus* Herb. in Türkiye: Insights from karyotype and genome size variation

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