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Abstract-Volume

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Galium pusillum agg. (Rubiaceae), an intricate polyploid complex harbouring 2x, 4x, 6x and 8x cytotypes, represents a unique example of rapid postglacial speciation in Europe. In northern half of Europe it splits into approximately ten morphologically, cytologically and ecologically distinct microspecies, including at least four diploid and low polyploid (4x) endemics of formerly glaciated areas of southern Scandinavia, Great Britain, and Iceland. Using cytological (flow cytometry) and molecular (AFLP, sequencing of low copy nuclear genes) methods together with ecological observations we aim at identifying major mechanisms involved in evolution of these postglacial endemics. Specifically, the main goal of our study is to distinguish between the *Galium* diversity originating via (i) independent postglacial immigration from different refugia and (ii) rapid postglacial in situ evolution (such as allopatric speciation, recurrent polyploidization and/or hybridization). Previous studies advocated a hypothesis of several independent immigration ‘waves’ of different *Galium pusillum* agg. lineages into the deglaciated area. In contrast, our flow cytometric data and preliminary molecular data distinguish two monoploid genome size groups of species, both at di- and tetraploid level, in formerly glaciated and unglaciated regions, suggesting possible independent evolutionary histories of these major lineages.

**The first eleven years of post-pyrogenic succession
in the Arctic pine forest [Poster]**

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This work describes the post-pyrogenic succession pattern of the pine forest on the Oleniy Island, White Sea, during the first eleven years of its recovery. We analyzed two separate cases of post-pyrogenic succession differing in the degree of initial soil damage. Investigated factors included the total projective cover and abundance of individual plant species. Multivariate data analysis revealed that the rate of recovery was relatively stable at the better preserved site and changed from almost zero to higher values at the more damaged site. The difference in species composition at the two sites increased over time, which indicates diverging succession patterns. While *Vaccinium* genus contributed mostly to the similarities in the site development, *Ledum palustre* and *Equisetum sylvaticum* (from the better preserved site) and *Pinus sylvestris* and *Calluna vulgaris* (from the less preserved site) were responsible for the differences in succession flow.