

Abstract

Polyploidization in angiosperms, a well-documented phenomenon, often correlates with a diversity of reproductive strategies, including sexual polymorphism, impacting their evolution and expression. This relationship is particularly intriguing in high polyploids, where the interaction can be complex yet largely enigmatic. We investigated the connection between high polyploidy and sexual polymorphism in *Stellaria palustris* (Caryophyllaceae), a species complex with exceptionally high levels of polyploidy exceeding decaploids and reportedly exhibiting variable sexual expression. To broaden our analysis, we included its relatives, diploid-tetraploid *S. graminea* and diploid *S. longifolia*. Our study focused on Central and Northern Europe, utilizing various methodological approaches, including genome size estimation, chromosome counting, genetic analyses based on Sanger sequencing, and evaluating floral organ variability and sexual expression. Major hypotheses examined associations between ploidy level and latitude, as well as ploidy level and sexual polymorphisms. Chromosome counts of *S. palustris* ranged from $2x = 154 - 208$, corresponding to $2n=12x, 14x, \text{ and } 16x$, while for *S. graminea* and *S. longifolia*, we confirmed their originally known ploidies. Although chromosome counts did not unambiguously reflect genome size, we found a weaker but significantly negative correlation of genome size with latitude, with Central European populations having slightly larger genome sizes, suggesting that marginal European populations may experience stressful conditions fostering genome size expansion and/or ploidy level increase. A similar trend was observed in flower organ size between these regions. Genetic analysis showed that all taxa forming their clusters, but with intermediate accessions, presented a blurred overall structure. *S. palustris* was closely related to *S. graminea*, while being more distant from *S. longifolia*. Notably, a unique clade related to *S. palustris* and *S. graminea* was identified, including tetraploid cytotypes ($2n = 4x = 52$) with different genome sizes from *S. graminea* and differing at least partially in morphology. We tentatively named this clade the 'Scandinavian entity,' exclusively collected in Northern Europe. Populations of *S. palustris* exhibited high sexual polymorphism, including female, hermaphroditic, and intermediate individuals with partially developed stamens, occurring at both population and individual levels. Despite varying ploidy levels, flower size dimorphism remained consistent, suggesting sexual selection as a driving force. No specific pattern in genome size correlated with latitude was identified. We propose that the intricate pattern of sexual expression in this high polyploid species is influenced by its high polyploidy, introducing complexity and dynamics into sex expression further influenced by intrinsic and extrinsic factors.