Maples as a model system for comparative seed biology

H. Fuchs[*]*, E. Ratajczak*

*Institute of Dendrology, Polish Academy of Sciences, Parkowa 5, 62-035 Kórnik, Poland, *hkijak@an.poznan.pl*

Keywords: maple seed physiology (*Acer* spp.), redox regulation, seed dormancy, tree model systems, seed proteomics

Trees represent a particularly challenging system for biological research due to their long life cycles, large size, structural complexity, and the limited availability of standardized model organisms. These features often constrain experimental approaches; however, understanding tree biology is essential because woody species play fundamental roles in ecosystem functioning, biodiversity conservation, and responses to climate change. Consequently, identifying suitable model systems for studying tree physiology remains an important objective in plant science. The long research tradition of the Institute of Dendrology PAS in Kórnik has generated extensive knowledge on the seed physiology of *Acer platanoides* and *Acer pseudoplatanus*. These closely related species provide a valuable comparative system for studying tree seed biology. Their well-characterized physiology, regular seed production, and contrasting seed traits make them suitable candidates for developing a model framework for investigating physiological processes in tree seeds. In this contribution, we summarize several years of research on maple seed physiology, including studies on redox regulation, proteomic profiles, and the physiological mechanisms controlling seed dormancy. Particular attention is given to the role of key redox-related proteins, such as thioredoxin h and cysteine peroxiredoxin, which participate in maintaining cellular redox balance and regulating metabolic processes during seed storage and germination. Because no single universal model organism can represent the diversity of the plant kingdom, complementary species-specific models are necessary. The use of maple seeds as a research system contributes to a broader understanding of seed physiology in woody plants and highlights the importance of integrating multiple model systems to capture the complexity and diversity of plant biological processes.

Part of this research was funded by the National Science Centre, Poland (NCN), grant no. 2018/31/B/NZ9/01548.