

Jasmonates – underestimated signaling compounds that can significantly affect key stages of xylogenesis

Wood is a valuable, renewable material with about 30,000 applications, e.g. as a source of energy or in the construction and paper industry. Over the last decade, wood consumption in Poland has more than doubled and this upward trend is expected to continue. One of the reasons for increasing wood consumption is counteracting the effects of climate change. Wood is a natural alternative to many synthetic materials, and products made of it can store large amounts of carbon dioxide.

Wood (secondary xylem) is produced thanks to the activity of a lateral meristem, the vascular cambium, during the process termed xylogenesis. Formation of this tissue consists of a well-coordinated sequence of events that can be divided into several stages: cambial cell division, cell elongation, cell wall thickening, and lignification followed by programmed cell death (PCD). All of these processes are finely controlled by various regulating factors including phytohormones. However, despite the prominent role of wood in the economy and environment, the xylogenesis remains not fully understood and so far little attention has been devoted to the role of jasmonates (JAs) in the secondary growth. JAs are an important group of plant hormones. Initially, their role was described mainly in relation to accelerating senescence and responding to stress stimuli, however, further research showed that JAs participate in numerous mechanisms responsible for regulating proper growth and development of plants.

The main objective of the presented project will be to determine the influence of JAs on the course of processes related to the development of the secondary structures, especially in the context of the xylogenesis. The aim of the project will be pursued based on the multifaceted knowledge gained during previous studies, and with the use of anatomical, cytological, physiological, and molecular methods. Experiments will be performed on the stem of *Arabidopsis thaliana* and *Populus trichocarpa*. In addition to the wild-type (WT), the analyses will also involve *A. thaliana* mutants with disturbed JA metabolism and signaling. Both species are model organisms, commonly used in biological research, including those related to xylogenesis and the formation of secondary structure.

The project will be a comprehensive venture combining anatomical, cytological, physiological, and molecular approaches that will describe in detail the role of JAs in the secondary growth, especially the xylogenesis. To date, there are only a few published reports on this topic that provide contradictory information and do not address many relevant areas. The results generated as part of the carefully planned experiments will have a high cognitive value and will fill in these knowledge gaps. An important advantage of the submitted innovative research project will be identification of previously unknown mechanisms involved in the formation of the secondary xylem. As wood is a natural alternative to synthetic materials, increasing wood utilization is necessary to create strategies mitigating the climate change. The mechanisms related to secondary tissue development may constitute the basis for further application research allowing for improving the growth and quality of wood.