

The phytohormone abscisic acid (ABA) plays a fundamental role in plant development, retrograde signalling and plant adaptation to stress. For decades, understanding of ABA perception and signal transduction have been a major goal of plant research studies. Numerous ABA signalling effectors have been identified including protein kinases, protein phosphatases, transcription factors, and ion channels. In recent years the pantheon of ABA signalling regulators has increased and among them some unexpected representatives appeared as the WHIRLY proteins. Despite multiple players involved in ABA signalling further complexity of the pathway is achieved by multilevel regulation via various mechanism operating at transcriptional and post-translational levels. Among them, ubiquitination is the most important modification affecting ABA signalling transducers.

Therefore the aim of the project is to decipher cellular mechanism regulating WHIRLIES functions. This will include studies aimed at: 1) analysis of ubiquitin-dependent regulation of WHIRLIES function and targeting; and 2) definition of the role of WHIRLIES in ABA signalling.

Presented project concerns important and universal biological phenomena: what cellular mechanism regulate WHIRLIES functions? The results from this study will provide novel findings which will be beneficial for understanding the role of ubiquitination in regulation and localization of WHIRLIES. We will gain a new insight into ubiquitination dynamics during cell growth, differentiation, and response to stress. Most importantly protein degradation by the 26S proteasome pathway is an integral part of plant hormone signalling, protein trafficking and retrograde signalling. Therefore our studies allow identification of a novel signalling routes mediated via WHIRLY proteins.