

## Heterotrimeric G-Proteins of Conifers – Where did they come from and how do they contribute to plant defense response?

Plants are challenged with an enormous number of signals every second of their lives, many of which dictate the organism's development, while others give information of the environment and possible threats. A major component needed to integrate these different inputs is the heterotrimeric G-protein complex. This complex consists of three different subunits, namely the  $G\alpha$ ,  $G\beta$ - and  $G\gamma$ -subunits and is present within most eukaryotes. Upon activation the complex dissociates into the  $G\alpha$ -subunit and the  $G\beta\gamma$ -dimer. The signaling can then either be mediated by one of the two components or by both in antagonistic or synergistic manner. Of all eukaryotes plants were thought to have the smallest G-protein repertoire, as most of their species only possess one  $G\alpha$ - and  $G\beta$ -subunit. However, plants expanded in their number of  $G\gamma$ -subunits and variation in this number and high sequence diversification has evolved throughout the different plant lineages.

Evolutionary studies suggest that one  $G\alpha$ - and one  $G\beta$ -subunit were present in the common ancestor of all land plants, and some species specific single gene duplications are likely to have occurred recently. The  $G\gamma$ -subunits can be divided in three types (A, B and C), where A and C are present in all seed plants and B probably first occurred within the angiosperm lineage. The functions of this protein-complex are diverse. An important function in pathogen resistance has been shown and analyses of transcription patterns of the heterotrimeric G-protein complex encoding genes demonstrate alterations upon pathogen inoculations. Anyhow, most studies have been done in angiosperms. Reports concerning themselves with the functions of heterotrimeric G-proteins in more land basal plants, i.e. mosses and gymnosperms are scarce.

We are interested in the repertoire and function of this protein-complex in conifers. Therefore, we analyzed what and how many subunits are present in these trees and further investigated the types of  $G\gamma$ -subunits and their evolutionary relationship with other angiosperm and moss representatives in more detail. We characterized the transcriptional patterns in different tissues of the two conifers Norway spruce and Scots pine. One of our main interests is the interactions of conifers with the necrotrophic pathogen *Heterobasidion annosum sensu lato*, a very important pathogen on conifers in economical terms and consequently the best studied host-pathogen system in gymnosperms. Defense responses against *H. annosum s. l.* are shown to be general and to involve jasmonic acid signaling pathways. We studied the transcriptional response of Norway spruce and Scots pine upon *H. annosum s. l.* and other defense response-associated signals in cotyledons and roots.

We show that conifers possess all G-protein subunits, needed to form the heterotrimer; they possess A- and C- type  $G\gamma$ -subunits as well as a conifer specific type, indicating a lineage specific diversification important for conifer adaption. Contrastingly to other studies tissue specific expression of the heterotrimeric G-protein subunits behaves different in Norway spruce and Scots pine, indicating species specific functions of the heterotrimer. Our results, suggest an ability of conifers to respond to *H. annosum s. l.* by altering the heterotrimeric G-protein transcription in different inoculated tissues, but this response seems not to be mediated *via* higher hormone levels of jasmonic and abscisic acid. We suggest that, similar to other studied defense responses, it is a general pattern as wounding shows a similar pattern at the site of treatment, while in distal locations the fungus elicits stronger responses.

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