Signalling and communication in the symbiosis *Casuarina-Frankia*

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Abstract

Two nitrogen-fixing root nodule symbioses between soil bacteria and plants have been described: one between rhizobium and legumes, and the other between *Frankia* and actinorhizal plants. Legume and actinorhizal nodules differ in their ontogeny and structure. However, phylogenetic studies based on *rbcL* gene sequence analysis have shown that all plants able to enter a root nodule symbiosis belong to the same clade, suggesting thus that they share a predisposition for symbiosis. The molecular bases of this predisposition are so far unknown.

Although several genetic components of the host-symbiont interaction have been identified in legumes, the genetic basis of actinorhizal symbiosis remains largely unknown. In actinorhizal root nodule symbiosis, major developments in *Frankia* and plant signalling have been (i) the determination of the genome sequences and the absence of *nod* genes in three *Frankia* strains (ii) the presence of a symbiosis receptor kinase (*SymRK)* in *Casuarina glauca and Datisca glomerata* that determines the development of actinorhizal nodules as well as endomycorhizae and the presence in *C. glauca* and *A. glutinosa* of homologs of the whole common symbiotic signaling cascade (iii) the recent observation that *Frankia* induces Ca spiking in root hair cells of actinorhizal plants.

All these studies, have led to the emergence of a vision of a diversity of bacterial symbiotic signalling determinants and the presence of an evolutionarily partly conserved pathway on the plant side.

transformed *C. glauca* plant with *A. tumefaciens*, whereas the expression of chimeric genes in composite plants can be studied in less than four months .

To ensure a commercial use of transgenic Casuarinaceae trees, the evaluation of potential risks resulting from their release into the environment need to be studied.