## Abstract of Poster Presentation

**Characterization of the plant molecular mechanisms governing the Nod-independent symbiosis between *Aeschynomene* and photosynthetic *Bradyrhizobium***

K. Bonaldi (1), H. Gherbi (1), C. Franche (1), J. Fardoux (1), B. Gourion (1), L. Hannibal (2), L. Moulin (1), N. Nouwen (1), Y. Prin (3), A. Renier (1), E. Giraud (1), F. CARTIEAUX (1)
(1) IRD, Montpellier, FRANCE; (2) IRD, Noumea, Nouvelle-Calédonie; (3) CIRAD, Montpellier, France
Presenter's E-mail: fabienne.cartieaux@ird.fr

The most studied plant / bacteria symbiosis is the legume-rhizobia interaction which results in the formation of nodules, a specialized organ in which bacteria fix nitrogen for the plant benefit. The establishment of this symbiosis involves a complex molecular dialogue between the 2 partners for their mutual recognition. Nod factors (derived from lipochitooligosaccharide) synthesized by rhizobia and encoded by nod genes, are recognized by specific plant kinases. This first step of recognition triggers a succession of events leading to the formation of nodule. This molecular recognition process has been described in all rhizobia / legume couples characterized so far, but the universality of this paradigm has been recently overturned by our study of the *Bradyrhizobium* photosynthetic-*Aeschynomene* symbiosis. Indeed, an analysis of the genomic sequences of two photosynthetic *Bradyrhizobium* strains failed to detect the presence of canonical nod genes from these bacteria; this demonstrates that Nod factors are not required to induce nodular organogenesis in *Aeschynomene* (Giraud et al. Science, 2007). This result raises the question of the degree of conservation of the symbiotic signalling pathway in this original Nod-independent interaction. Our purpose is thus to study the plant molecular mechanisms governing this new interaction and in particular to determine whether the signalling pathway triggering nodulation in *Aeschynomene* is common to the one described in the model legumes *Medicago truncatula* and *Lotus japonicus*. We are currently developing molecular tools in *Aeschynomene* with the aim of study the function of candidate plant genes implied in the early phases of the interaction with photosynthetic *Bradyrhizobia*. First results and considered approaches will be presented.