

3. FABATROPIMED

Ecological services of legumes for nitrogen and phosphorus bio-geochemical cycles and C sequestration in cereal cropping systems in Africa and the Mediterranean basin

OBJECTIFS

Fabatropimed aims to increase the benefit of legumes for cereal cropping systems and the environment, by reducing the use of mineral fertilisers and increasing carbon sequestration, by promoting interactions between soil microorganisms for the acquisition and use of nitrogen and phosphorus by plants.

ACTIONS

Fabatropimed is conducting participatory research in six agro-ecosystems on the basis of an agronomic and environmental diagnosis (WP1) associated with a sustainability and innovation study (WP5) in interdisciplinarity with the monitoring of soil and atmospheric C, N and P cycles (WP2), the characterisation of microbial, symbiotic and rhizospheric (i.e. in the root influence zone) functional diversity (WP3) and the search for phosphorus acquisition and use efficiency genes for symbiotic nitrogen fixation (WP4). (i.e. in the root zone of influence) (WP3) and the search for phosphorus acquisition and utilisation efficiency genes for symbiotic nitrogen fixation (WP4).

RESULTATS

The 24 publications of Fabatropimed (FTM) during the three first years of the project, without taking into account those under revision, lead to the following preliminary conclusions of the project : i) the nodular diagnosis, as innovative methodology to assess the spatial variability of grain-legume nodulation in agro-ecosystem, leads for common-bean under Mediterranean climate, lead to distinguish soils A&B so rich in N that nodulation is inhibited although their P content may vary ; soils C so poor in P that nodulation is too low and cannot contribute to the legume N nutrition ; soils D poor in N where nodulation contributes significantly to the legume N nutrition and varies with soil P content ; ii) the genotypes with high efficiency in use of P for symbiotic nitrogen fixation (EUP/SNF) generally have better growth in soils D than the genotypes with low EUP/SNF, confirming that this functional trait can be selected in hydroaerobic cultures and may contribute to improve the legume-rhizobia symbiosis in low-P soils ; iii) genotypes with low EUP/SNF show a high growth in some soils D, suggesting that these soils harbour microbes that may help to the legume adaptation to low P ; iv) some rhizobia from soil D of the agro-ecosystem in South of France revealed first evidence of phytase activity within the family of Rhizobiaceae, whereas rhizobacteria with phytase were inhibited in the rhizosphere of common bean by high P fertilization of the soil of the INRA agronomic station in Melgueil ; v) the innovative methodology of in situ RT-PCR made it possible to localize the transcripts of plant phytase and such other phosphatases as TPPase, RUBPase, PEPase in various nodule parenchyma-tissues, and the genes HAP et BBP of rhizobial phytases in the nodule infected-zone, and also for the first time, the gene BBP of *Bacillus subtilis* on the surface of the root and inside the cortical parenchyma where it may be endophytic. The relations of the genes and their organisms with the use of P for SNF, and their consequences for yields of legumes and cereals in associations or rotations are questioned in detail in the discussion of the publications. They are the aims of finalization of the results in the other agro-ecosystems of the project, and the relations with soil parameters under on-going analyses. The modeling of the bio-chemical-physical interactions face soil–nodulated-root have been published with the MOMOS model for C and N cycles. They are extended to P cycle of which the availability with the MIN3P model is commented in a first publication with legume.

PERSPECTIVES

i) submission of on-going publications with the doctoral theses that will be defended before the end of 2015 ; ii) analyses of N and P contents of soils of the agro-ecosystems in order to assess the genericity of above conclusions and modeling of the cycles ; iii) assess the diversity of phytase sequences of microbes isolated from