

**The Evolutionary Moulding in plant-microbial symbiosis: coevolution of signal transduction system components.**

Igolkina A.A.,

(1) *Laboratory of Microbiological Monitoring and Bioremediation of Soils, All-Russia Research Institute for Agricultural Microbiology, Saint-Petersburg, Russia.*

(2) *Laboratory of Mathematical biology and Bioinformatics, SPbPU, Saint-Petersburg, Russia*

*igolkinaanna11@gmail.com*

Bazykin G.A.,

(1) *Sector for Molecular Evolution, Institute for Information Transmission Problems of the RAS (Kharkevich Institute), Moscow, Russia.*

(2) *M. V. Lomonosov Moscow State University, Moscow, Russia.*

(3) *Skolkovo Institute of Science and Technology, Skolkovo, Russia.*

Andronov E.E.

(1) *Laboratory of Microbiological Monitoring and Bioremediation of Soils, All-Russia Research Institute for Agricultural Microbiology, Saint-Petersburg, Russia.*

(2) *Laboratory of Biology and Biochemistry of Soils, V.V. Dokuchaev Soil Science Institute, Moscow, Russia.*

(3) *Department of Microbiology and Genetics of Saint-Petersburg State University, Saint-Petersburg, Russia.*

Coordinated evolution of partners in nitrogen-fixing rhizobium-legume symbiosis was traced in nucleotide polymorphism of symbiotic genes encoding two components of the plant-bacteria signalling system: receptor *NFR5* gene from the plant side and *nodA* gene involved in the NOD factor synthesis from the rhizobium side.

We collected three wild growing legume species (30 samples per species) together with rhizosphere soil from one large fallow: the common vetch *Vicia sativa*, the meadow vetchling *Lathyrus pratensis* and the alsike clover *Trifolium hybridum* specifically forming symbiotic nodules with two *Rhizobium leguminosarum* biovars (*viciae* and *trifolii*). For each species we prepared three pools for DNA extraction: the plant pool (30 plant per sp.), the nodule pool (100 nodules per sp.) and the rhizosphere soil pool (30 samples per sp.). *NFR5* gene libraries from plant pool and *nodA* gene libraries from nodule and soil pools were sequenced by Sanger technology and High-throughput pyrosequencing, respectively. Analysis of obtained sequences demonstrated significantly increased diversity in nodule *nodA* gene popsets (set of sequences from populations) compared to corresponding soil popsets. Moreover, the relation between diversity of *NFR5* gene

in plant populations and *nodA* gene in nodule rhizobium populations was monotonic and almost linear. By comparing phylogenetic structures of each plant popset and the corresponding nodule popset, we evinced the “moulding” effect of the host-plant population structure on the *nodA* gene nodule popset. The mechanism of this Evolutionary Moulding was indicated by statistically significant positive selection in nodule popsets that was probably responsible for increased diversity in them. In contrast to the Red Queen and the Red King hypothesis describing the evolution of host-parasitic and symbiotic systems mostly by ratios of evolutionary rates, the Evolutionary Moulding hypothesis appeals to incoordination of genetic diversities of symbiotic partners. Mutualistic symbiotic system strives to relax this incoordination by fine-tuning of signalling systems, where genetic diversity of one partner is moulding into the genetic diversity of another. To be specific, under Evolutionary Moulding, the slowly evolving partner (host) performs the role of “rigid matrix”, and the faster evolving partner (microsymbiont) provides a “flexible genetic material” shaped by the “rigid matrix” which enhances host-plant specificity.