

**2<sup>nd</sup> World Congress on****Beneficial Microbes: Food,  
Pharma, Aqua & Beverages Industry****September 22-24, 2016 Phoenix, USA****Molecular evolution of paralogous symbiotic receptor kinase genes in pea (*Pisum sativum* L)****Vladimir A Zhukov<sup>1</sup>, Anton S Sulima<sup>1</sup>, Alexander<sup>1</sup> Zhernakov<sup>1</sup>, Liudmila A Lutova<sup>2</sup> and Igor A Tikhonovich<sup>1,2</sup>**<sup>1</sup>All-Russia Research Institute for Agricultural Microbiology, Russia<sup>2</sup>Saint-Petersburg State University, Russia

In the course of interactions between legume plants and nodule bacteria, the signal molecules excreted by bacteria (Nod factors) are specifically perceived by plant receptor kinases. In pea, 3 paralogous genes (*Sym37*, *K1* and *LykX*) encoding receptor kinases probably binding Nod factors are located in cluster on LG I of pea and mutations in any of these genes hamper bacteria penetration into the plant root. In this work, the fragments of 1<sup>st</sup> exons of the genes *Sym37*, *K1* and *LykX* encoding the receptor parts of the corresponding proteins were sequenced and analyzed in 99 pea genotypes that represent virtually all the diversity within the genus *Pisum*. The *Sym37* gene sequence, according to the McDonald-Kreitman test, underwent the pressure of positive (directional) selection. The *K1* gene sequence possesses multiple polymorphic sites, suggesting that the positive selection acts in favor of several allelic states of the gene. The sequence of the third receptor gene (*LykX*) possesses the site, which seems to be critical for the functioning of the encoded protein; this site was found to be under the significant negative selection pressure. The assumption that these paralogous genes were differentiated for realization of the diverse functions is reinforced by the results obtained. In general, the data obtained provide insights on the evolution and functioning of symbiotic systems formed by leguminous plants.

**Biography**

Vladimir A Zhukov was graduated from Saint-Petersburg State University, Faculty of Biology, Department of Genetics and Biotechnology (St. Petersburg, Russia) and then completed his PhD at from Saint-Petersburg State University (St. Petersburg, Russia). He has worked at Aarhus University (Aarhus, Denmark) and in CNRS (Gif-sur-Yvette, France) within the frame of joint international projects devoted to studying the genetic bases of beneficial plant-microbe interactions. Presently he works as the Head of the Laboratory in All-Russia Research Institute for Agricultural Microbiology (St. Petersburg, Russia). He has published more than 20 papers in reputed Russian and international scientific journals.

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