The studing of the intraspecific polymorphism and protein-protein interactions of the LykX and Sym-10 Pisum sativum LysM receptor-like kinases using structural bioinformatics approaches

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The symbiosis between legume plants and rhizobial bacteria is triggered by nodulation factors (Nod factors) recognition by plants receptor complex. It was shown that Nod factors, as well as chitin, are recognized by receptor-like kinases with LysM domains in the extracellular region[4]. These proteins interact with microbe-associated molecular patterns (MAMPs) and are presented in plants by LYK and LYR gene subfamilies[1]. *Lotus japonicus* Nod factor recognition complex is formed by Nod factor receptor 1 (NFR1) and Nod factor receptor 5 (NFR5) protein dimer complex, that corresponds to LysM receptor kinase 3 (LYK3) - Nod factor perception (NFP) complex in *Medicago truncatula*[2]. Obtained protein dimer complexes bind Nod factor directly in unknown binding site with high affinity. LykX and Sym-10 proteins are involved in Nod factor recognition in *Pisum sativum* and are close homologs of NFR1 and NFR5 receptors from *Lotus japonicus*[3].

Despite the fact, that proteins involved in Nod factor reception are previously described, there are no crystal structure or a model of the receptor complex. The primary goal of our research is to explain the role of polymorphism in #44, 45, 75, and 76 amino acids of LykX protein from Afghanistan, Tajic and European *Pisum sativum* subpopulations in Nod factors recognition and in protein-protein interactions between LykX and Sym-10 proteins. We applied the homology modeling approach to creating LykX and Sym-10 protein models, as the template crystal structure of LysM receptor-like chitin-binding protein from *L. japonicus* was used (PDB code: 5LS2). LykX - Sym-10 protein dimer model was obtained by protein-protein docking assay. Variable amino acids are located in the protein-protein contact area. Proteins from all 3 *Pisum sativum* subpopulations form quite similar heterodimer complexes with the huge hydrophobic hole between LysM-1/LysM-2 domains of LykX and LysM-2/LysM-3 domains of Sym-10. According to the performed Nod factor docking, it interacts with the fatty acyl group and anchors ligand in the protein complex.

Источники и литература

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