Aphids are highly specialized group of insects feeding in sap within the sieve elements, epidermis and mesophyll cells of the hosts. Infestation with aphids leads to occurrence of circumstantial physiological, metabolic and molecular disturbances in the colonized plants. Salivary enzymes, phytotoxic substances and effectors injected by the aphids trigger local and/or systemic defense reactions within the plant tissues. The major purpose of the biotests will be focused on identification of transcriptomic (mRNA and microRNA) markers of maize (*Zea mays* L.) resistance towards infestation with females of three cereal aphids' species (i.e., rose-grain aphid, *Metopolophium dirhodum* Walk., bird cherry-oat aphid, *Rhopalosiphum padi* L. and grain aphid, *Sitobion avenae* F.). Furthermore, it will be assessed damages of plasma membranes and chosen macromolecules in maize plants, stimulated by oxidative stress in response to the aphids' attack. Additionally, it will be compared activities of the stylets and specific modes of aphids' feeding in tissues of resistant and susceptible maize varieties.

Biotests will include the use of the most advanced methods used in molecular biology: 1) high-density expression microarrays, and 2) next generation sequencing (NGS), leading to identification of global changes in expression of mRNA and microRNA transcriptomes in maize plants infested with the cereal aphids. Measurements of conductivity will allow to evaluate integrity of the cell membranes in *Z. mays* seedlings. In addition, it will be determined the selected biochemical markers of oxidative damages of macromolecules (e.g. DNA, proteins and lipids). Application of the EPG technique will help to perform electronic recordings of the stylets' activities and identify feeding models of the cereal aphids during infestation of the hosts.

Application of advanced research methods outlined in frame of the project will contribute to deciphering the molecular basis of complex plant-aphid interactions. The planned research tasks innovatively integrate modern techniques and expertise in the field of molecular biology, ecophysiology and plant protection. The use of molecular biology tools will allow to identify transcriptomic markers of maize resistance to examined species of the cereal aphids (based on comparison of global-scale changes in mRNA and microRNA transcriptomes of *Z. mays* genotypes resistant and susceptible to the hemipterans) as well as to characterize the differences in expression of genes encoding proteins and regulatory miRNAs in maize plants infested with *M. dirhodum*, *R. padi* and *S. avenae*. In the case of a positive verification of the research hypotheses, it will be developed new molecular tools, that will be utilized in selection of maize varieties characterized with enhanced resistance to the aphids' infestation. Important element of the research project is to identify differences in stylets' activities and feeding models of tested cereal aphids in tissues of maize plants characterized with distinct resistance degrees.