Insects are the most numerous group of animals living on Earth. They inhabit various ecosystems, from the sands of hot deserts to cold mountain streams. Insects bodies are colonized by microorganisms living not only on their exoskeletons but also in the gut, hemocoel and even within insect cells. A significant part of these microorganisms are bacteria, which can be beneficial for their host, e.g. by synthesizing essential amino acids or by protecting against pathogens. Studies on bacterial communities associated with insects enjoy researchers' unflagging interest. Particular attention is paid to endosymbiotic bacteria, which have developed mechanisms for the manipulation of insect reproduction processes, thus ensuring their transmission to the next hosts' generations. An example of such bacteria is *Wolbachia*. Its transmission, similarly to the mitochondrial genome, occurs in the maternal line. Furthermore, *Wolbachia* is also associated with changes in host genetic variation, especially at the mitochondrial level, as well as interactions with other microorganisms associated with the infected host. However, most studies on these dependencies among insects are focused on infected terrestrial hosts. In the case of aquatic insects, few available reports have been focused only on endosymbionts detection.

Noting the knowledge gap, I decided to conduct study, which will be focused on the assessment of the degree of endosymbionts infections among population of freshwater insects (in wide spatial scale), determination of the propable impact of these bacteria on the hosts genetic variation, analyses of host-symbiont coevolution, and assessing the impact of endosymbionts (and *Wolbachia* in particular) on other groups of bacteria associated with hosts. Freshwater true bug *Aphelocheirus aestivalis* (Insecta, Heteroptera) has been chosen as the model species. Selected species inhabit clean rivers and streams with sandy and sandy-gravel bottom. *A. aesitvalis* is the only representative of the monotypic family Aphelocheiridae and commonly occurs in Europe. Nevertheless, due to its sensitivity to the pollution and regulation of watercourses, a progressive quantitative regression of *A. aestivalis* and populations decline in part of its distribution range have been observed. Thus, *A. aestivalis* has been recognized as species endangered with extinction in the part of its distribution range (e.g. in the Czech Republic and Slovakia). Moreover, *A. aestivalis* has limited dispersion abilities, what may be related to limited gene flow between populations resulting in turn in an increased genetic diversity of populations inhabiting distant areas. Nevertheless, the preliminary analyses of *A. aestivalis* revealed its low genetic variation, both at the mitochondrial and nuclear levels. Moreover, the common presence of *Wolbachia* infecting all tested individuals has been identified.

The designed study will involve analyses of selected mitochondrial (COI, 16S) and nuclear (ITS2, EF1α, and 20 polymorphic microsatellites) markers that will allow estimating the genetic variation of 30 *A. aestivalis* populations inhabiting rivers within European main river basins. In addition, the variation of bacterial DNA fragments will be analyzed, what will allow testing potential host-endosymbiont coevolution. Moreover, based on the high throughput next-generation sequencing, the microbiota profiles associated with both *Wolbachia* infected and uninfected individuals will be determined and thus, the evaluation of *Wolbachia* influence on host' microbiota complexes will be possible. Therefore, the designed study will be the first such comprehensive research on the representative of aquatic insects.