Aim of this project is verification of taxonomical status of weevils from subgenus *Liophloeodes* Weise, 1894. Species that belongs to this subgenus are very similar to each other and they can be distinguished only basing on shape of aedeagus (part of male genitalia). Moreover, even this trait is not so clear and easy to distinguishe it is very variable within particular species. Thus, assigning males to species is hard, assigning females is impossible. This raises the question whether those species are "real" species? But how to check it? And, actually, why we should do this?

Let me begin with second question. Building reliable taxonomy is hard, careful, time-consuming, painstaking work, connected with costs. As the effect of our work, we obtain complex system of grouped and described organisms. So maybe it is not worth to do this? This is wrong answer. Despite all controversies connected with definition of species, it is still most important unit in biology. Only with knowledge about species division we are able to understand most of phenomena that occur in environment, evolutionary processes and even some physiological traits and pathways that are specific to species or to bigger taxonomical groups. Our knowledge about species diversity is still insufficient. Moreover, we are witnesses and, unfortunately, the causes of species extinction. Many species, which were not even described, disappear. But more important thing is the problem that without knowledge about biodiversity (which is, in a matter of fact, diversity of species), we cannot save it. Thus, establishing reliable taxonomy is very important thing.

Now time for the question: how to do this? After years of scientific mistakes and controversies connected with taxonomy, we should learn that basing taxonomy only on one trait is not the best idea. Most proper method is integrative approach, which connects as wide as possible variety of sources of reliable information. This method, now being in progress, is still not very popular. My study is designed basing on integrative methodology. I will study Liophloedes weevils with molecular, morphometric and ecological methods. First step will be collection of those weevils from their whole known range. Then, following traits will be studied:

1) Diversity and phylogeny of DNA. I will test diversity and phylogeny of three molecular markers: *COI* (mitochondrial DNA), *EF-1* and *ITS-2* (nuclear DNA). I will test differences between sequences among studied populations. I will also resolve their phylogeny.

2) Morphological diversity. I will conduct morphometric measurements on several parts of body (head, leg, elytra, genitalia). Obtained results also will help me to observe differences between populations.

3) Host plants diversity. Basing on plants of collection of specimens and on DNA sequences of plants isolated from digestive systems of studied insects I will define differences between host plants of different populations.

4) *Wolbachia* strains diversity. I will test diversity of strains (marker *wsp*) of endosymbiotic bacterium *Wolbachia* that lives in gonads of *Liophloeodes* weevils. This diversity will be use as additional data, that will help me to interpret the results of previous methods.

Basing on obtained results will I will propose verification of taxonomy of *Liophloeodes*. My research will also contribute to develop integrative approach to weevil taxonomy.