

**The aim of the planned study is to assess the genetic variation of the horse-chestnut tree in the natural populations of horse-chestnut (*Aesculus hippocastanum* L.),** as well as at better understanding of introduction of this species into artificial stands. Horse-chestnut is one of the most important European relict. This species was introduced to central and northern Europe from Istanbul. To Poland, it was brought by John III Sobieski in the 17th century and quickly it became a very important element of urban landscape. Nowadays, the species is **highly valued in horticulture and pharmaceutical industry.** Due to its low habitat requirements, it has been widely planted. The natural occurrence of the species was unknown until the end of the 19th century. Botanical expedition to Greece in 1879 proved that the natural distribution of the horse-chestnut in the mountainous areas of the Balkans, mostly Greece. Horse-chestnut tree is an endemic species occurring in Pindos Mts. in highly fragmented and low-density populations with declining dynamic tendencies. **The natural genetic resources of the species have not been evaluated yet.** Meanwhile, investigations on the genetic structure and its spatial distribution are **crucial for efficient conservation activity** aiming at the protection of this threatened species. Additionally, the horse-chestnut belongs to the remnants of the Tertiary flora once vastly distributed in Europe and therefore it can serve as a perfect object for studies on relict and endemic species in Europe. As a part of preliminary works, material from nine natural populations was collected in Greece in June 2015. Additionally, material from individuals occurring in several artificial sites in Europe will be collected and analyzed. This will allow a better understanding of the process of introduction of this species. Chloroplast DNA and microsatellites (SSR) were chosen as molecular tools for this study. Results of the population genetic studies will give us a needed knowledge on the species' genetic structure in its native range. They will enable us to understand better genetic factors shaping species gene pool during its introduction. The history of the introduction of horse-chestnut is unique: the approximate time and possible routes in Europe are known. Therefore, this species can be used as a model and our analysis may be useful in the case of other relict and endemic species.