

Introduction

The climatic oscillations during the last 2 million years caused many changes in the distribution of most organisms all over the world, which lead to changes in their genetic structures and shaping their phylogeographic patterns. In Europe, the repeated glacial and interglacial cycles forced temperate species to retreat into refugia during periods of advancing ice and allowed them to expand from their refugia during interglacial warming. The origin of many species is reconstructed on the basis of paleontological, pollen and genetic data. The bark beetle *I. typographus* is a serious forest pest but also considered as interesting subject in population ecology and phylogeographic studies. It has been suggested that there is a close association between refugial areas and postglacial migration routes that *I. typographus* and its host tree have followed in the last 15,000 years. However, occurrence of the chronic outbreaks of this beetle was the main factor, which has triggered extensive research on its population ecology since it has a significant impact on ecological and economic environment of the Norway spruce forests. Some questions in ecology are difficult to answer using traditional approaches. As a result, molecular techniques have been applied to study *I. typographus*. Allozyme electrophoresis has revolutionized many research fields at the beginning of the 1960's. In the middle of 1990's, the polymerase chain reaction (PCR) improved DNA sequencing and lead to the flourish of molecular markers for systematic and population genetic studies for analyzing the relations and origin of European *Ips* species. Molecular studies on *I. typographus* are limited. However, several studies have improved our understanding of ecology, epidemiology and evolution of the bark beetle. Currently, a future perspective is relying on next generation sequencing as a strong candidate for resolving of phylogeographic patterns. The present study reports a small scale genetic study of *I. typographus* in the Carpathians, because they belong to one of the major refuges of the last ice ages for many organisms. This study is an original work and provides new knowledge about the genetic structure of bark beetle populations at a small spatial scale as well as the role of the Carpathians in re-colonization of Europe by *I. typographus* after the last glaciation. Moreover, this study is dealing with several biological factors which may influence genetic diversity of *I. typographus* populations. Natural enemies of the bark beetles have been assigned only a minor role in controlling their populations. However, they play an important role in endemic situations and towards the end of an outbreak. In general, it is

difficult to develop ways for *I. typographus* population control and protect environment from their invasion. The investigation, identification and selection of bioagents (e.g., *Beauveria*) serve as a basis for the development of biological protection of conifer forest from *I. typographus* in the future.