

Exhaustive molecular genetic analysis of trees and ectomycorrhizal fungi and establishment of their molecular ecology database

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【 Outline of survey 】

Vegetation distribution and its genetic properties in forest depend on reproductive mechanism of each species. Therefore, when we consider and take measures to vegetation change by global warming, maintenance of forest biodiversity and sustainable forest management, it is indispensable to know reproductive mechanisms of each constituent species of forest. Forest trees and fungi maintain reproduction of their populations according to their specific dispersal patterns of pollen, seeds and spores. In a longer term, their specific genetic geographical distribution is established by accumulating the short-term reproduction. In this project, we exhaustively select species of trees and ectomycorrhizal fungi as many as possible, and analyze their reproductive processes by use of molecular ecological methods. Moreover, we analyze genetic geographical structure of the tree species. All of the results will be finally synthesized into a "molecular ecological database". Concrete procedure of the project is as follows: first of all, we exhaustively select tree species according to their geographical distribution and the pollination manners such as anemophilous and entomophilous ones. We also select species of ectomycorrhizal fungi according to their phylogenetic positions and habitat environment. We analyze these species mainly by polymorphic microsatellite markers, and infer their dispersal mechanisms of pollen, seeds and spores. Structure (species composition) of underground mycorrhizal communities is also analyzed by use of DNA polymorphism analysis. On the other hand, genetic differentiation of the tree species in Japan is analyzed by polymorphism analysis of chloroplast DNA. Summing up all obtained genetic data, we construct a molecular ecological database on reproductive processes and genetic geographical structure of many trees and ectomycorrhizal fungi.

【 Expected results 】

The present project accumulates enormous amounts of detailed genetic information on reproductive processes of trees and ectomycorrhizal fungi mainly by microsatellite polymorphism analysis, and reveals the general rules and effective factors of their reproduction. Although several studies on these lines have been already reported, enough information has not been obtained to draw general rules of dispersal of pollen, seeds and spores. The present project would enable it. Moreover, we have pioneered researches on reproduction of ectomycorrhizal fungi using microsatellite markers in the world. Thus, we keep the pioneer position by this project. Since we also analyze in this project genetic geography of many Japanese domestic trees, overall features of the genetic differentiation of domestic trees can be grasped. The molecular ecological database that is finally established is indispensable for considering and taking measures to vegetation change by global warming, maintenance of forest biodiversity and sustainable forest management.

【 References by the principal researcher 】

1. Zhou Z, Hogetsu T (2002) Subterranean community structure of ectomycorrhizal fungi under *Suillus grevillei* sporocarps in a *Larix kaempferi* forest. *New Phytol.* 154:529-539
2. Lian C, Oishi R, Miyashita N, Nara K, Nakaya H, Zhou Z, Wu B, Hogetsu T (2003) Genetic structure and reproduction dynamics of *Salix reinii* during primary succession on Mt. Fuji, as revealed by nuclear and chloroplast microsatellite analysis. *Molecular Ecology* 12:609-618

【 Term of project 】 F Y 2004 - 2008

【 Budget allocation 】 80,500,000 yen

【 Homepage address 】 http://www.adm.u-tokyo.ac.jp/IRS/IntroPage_E/intro63261179_e.htm