

**Molecular Diagnosis for Sustainable Forest
----- from an individual to a population -----**

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A natural forest, which is a population made up of individuals, carries genetic diversity even if they consist of the same species. Such diverse population provides the traits resistant against environmental stress. On the contrary, plantation prefers generally to being consisted of a dominant tree or a selected clone because diverse quality is undesirable character. Even in a natural forest stand, the population may suffer from a selective pressure by pathogen, causing biased traits in the population. The latter example is a breeding by selection of survived trees in the natural forest stands suffered from pine wilt diseases.

Japanese pine forest has been severely suffered from pine wilt diseases and the dead trees are the biggest loss in biomass of Japan. Furthermore, the diseases have ignited in East Asia and Europe, causing political affairs. Pesticide spray for controlling pine wilt diseases has gradually been diminished because of environmental concerns. New strategies are now required for controlling pine wilt disease. In administration related works, survived pine trees have been selected from the natural pine forest stands, being suffered from the pine wilt disease. There have been many debates on the diversity of a population from viewpoints of wood utilization and ecology. Newly selected traits such as the resistant pine trees will be examined in various aspects.

We found that a gene in a secondary metabolism shows such diversity in a pine population. Furthermore, the diverse gene translates, or enzymes, can distinctly control the nematicide biosynthesis, suggesting important roles on the resistant against pine wilt diseases [1]. In other words, these diverse genes are distinctly produced a series of phytoalexins, some of which probably control the wood nematodes. Thus a 3-year project for pine trees has started from this year, where studying biochemical and molecular diagnosis for the resistance against pine wilt diseases. We have already successfully extracted mRNAs from tree trunks [2] and cloned several cDNAs with full coding sequences. Few dozens of samples can be simultaneously analyzed for the gene expression [3]. In addition to those methods, biochemical and molecular diagnosis will be studied for an individual and a population of pine trees in the new project.

Lastly, let me touch on the expected output of this project. Tree EST libraries, especially in pine and aspen, are rich in the source of cDNA fragments. Virtual full coding sequences, which may or may not represent substantial genes, are now easily obtained from the fragments. We have successfully obtained a substantial cDNAs from a trunk by using such virtual sequences [2]. This technique is useful for providing molecular markers for the diagnosis of a tree and probably of a population. We may need diagnostic markers, for example, for active oxygen control, vapor production, carbon fixation and resistant against pathogen and so on. This strategy is also applicable to tropical forests and expected to be a strong diagnostic tool for environmental cleanup and conservation of forest, wood quality and productivity. This diagnosis will also give useful information to evaluate forest in social standpoint of view.

REFERENCES

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