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### Genetic diversity and phylogenetic relationships of alder, *Alnus hirsuta*, revealed by AFLP

Choi Joo Soo<sup>1</sup>, Man Kyu Huh<sup>\*2</sup>, and Hong Wook Huh<sup>2</sup>

<sup>1</sup>Department of Biology, Dong Eui University and  
<sup>2</sup>Department of Biology Education, Pusan National University

Alder, *Alnus hirsuta* (Thunb.), has not extensive with molecular markers. The objective of this study was to investigate the genetic relationships among 15 natural populations by amplified fragment length polymorphism (AFLP). *EcoRI*-AAC+*MseI*-CTG combinations were found to reveal highest polymorphism (64.7%). A total of 158 DNA fragments were identified. On average 47.1% of AFLP markers generated using four primer pairs were polymorphic. The diversity showed nonsignificant differences between the 15 populations. The combinations of wind-pollinated, outcrossing breeding system, large population sizes, and the ability to regenerate by stump sprouting may explain the high level of genetic diversity within population. The majority of genetic variance of alder (94.7%) resided within populations. The average number of individuals exchanged between populations per generation was very high ( $Nem = 4.5$ ). Gene dispersal of alder seems to be by seed dispersal due to water and human activity as well as pollen and seed dispersal. Five individuals per each population were claded in the same cluster.

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