



Genetic and epigenetic diversity and structure of *Phragmites australis* from local habitats of the Songnen Prairie using amplified fragment length polymorphism markers

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ABSTRACT. The genetic and epigenetic diversity and structure of naturally occurring *Phragmites australis* populations occupying two different habitats on a small spatial scale in the Songnen Prairie in northeastern China were investigated by assessing amplified fragment length polymorphisms (AFLPs) and methylation-sensitive amplified polymorphisms (MSAPs) through fluorescent capillary detection. The two groups of *P. australis* were located in a seasonal waterlogged low-lying and alkalized meadow with a pH of 8-8.5 and in an alkaline patch

without accumulated rainwater and with a pH greater than 10. These groups showed high levels of genetic diversity at the habitat level based on the percentage of polymorphic bands (90.32, 82.56%), Nei's gene diversity index (0.262, 0.248), and the Shannon diversity index (0.407, 0.383). Although little is known about the between-habitat genetic differentiation of *P. australis* on a small spatial scale, our results implied significant genetic differentiation between habitats. Extensive epigenetic diversity within habitats, along with clear differentiation, was found. Specifically, the former habitat (Habitat 1, designated H1) harbored higher levels of genetic and epigenetic diversity than the latter (Habitat 2, designated H2), and population-level diversity was also high. This study represents one of few attempts to predict habitat-based genetic differentiation of reeds on a small scale. These assessments of genetic and epigenetic variation are integral aspects of molecular ecological studies on *P. australis*. Possible causes for within- and between-habitat genetic and epigenetic variations are discussed.

Key words: AFLP; MSAP; *Phragmites australis*; Genetic diversity; Genetic differentiation; Habitat