



Genetic diversity and population structure of *Stipa bungeana*, an endemic species in Loess Plateau of China, revealed using combined ISSR and SRAP markers

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ABSTRACT. Sequence-related amplified polymorphism (SRAP) and inter-simple sequence repeat (ISSR) markers were used to assess the genetic diversity within and among 15 natural populations of *Stipa bungeana* from the Loess Plateau of China. Using 15 SRAP primers, 504 (99.80%) polymorphic loci were detected, and 372 polymorphic loci (96.12%) were identified using 15 ISSR primers. At the species level, the *S. bungeana* populations showed relatively low levels of genetic diversity ($H_E = 0.2017$ for SRAP; $H_E = 0.2066$ for ISSR). The results of analysis of molecular variance indicated that genetic variation within populations (42.02% for SRAP and 38.40% for ISSR) is lower than that among populations (57.98% for SRAP and 61.60% for ISSR). The genetic distance was significantly correlated with geographical distance by the Mantel test ($r = 0.3978$, $P = 0.002$). Our results demonstrated that both SRAP and ISSR markers are effective and reliable for assessing

the genetic diversity of *S. bungeana*. In addition, these data inform conservation and breeding strategies for *S. bungeana*.

Key words: *Stipa bungeana*; SRAP; ISSR; Genetic diversity