生态学报 2006 26 (2006(10)): 3175～3183 ISSN: 1004-616x CN: 44-1063/R

研究论文

不同放牧压力下大针茅种群的遗传多样性

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收稿日期 2005-12-24 修回日期 2006-7-28 网络版发布日期: 2006-10-25

摘要 针茅是亚洲中部草原亚区特有的蒙古草原种，以大针茅建群的草原在内蒙古的分布面积为2 798 081hm ^{2}。从遗传多样性上探讨了大针茅种群在放牧压力下的适应机制，结果表明：虽然放牧导致部分基因位点丢失，但整个种群仍表现出丰富的多态性，ISSR检测的多态性条带比率为89%。Nei’s指数计算的大针茅种群间的遗传分化为0.1984，说明有19.8%的遗传变异存在于种群之间， 80.2%的遗传变异存在于种群内。 由Shannon’s和Nei’s多样性指数检测的大针茅种群内遗传多样性随着放牧压力的增加有逐渐减弱的趋势。根据遗传距离构建的UPGMA聚类图中， 中度和重度放牧样地首先聚为一类， 不放牧和轻度放牧样地聚为一类， 随后聚在一起。

关键词 放牧；大针茅；遗传多样性；ISSR
分类号 Q143,Q943

Genetic diversity of *Stipa grandis* under different grazing pressures

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Abstract The area of the Stipa grandis steppe in Inner Mongolia is 2798081 hm ^{2}. Based on the genetic variation, the adaptability of Stipa grandis under grazing pressure was significant. Changes to genetic diversity of the Stipa grandis population under different grazing pressures were studied by Inter-Simple Sequence Repeat (ISSR). The plant materials were collected from a series of grazing gradients of the Stipa grandis steppe in Dalinuoer national nature reserve in Inner Mongolia. The location of the reserve is 116°38′～116°41′E and 43°25′～43°27′N , and it has abundant vegetation types; Leymus chinensis is the constructive species. Dominant species include Stipa grandis, Cleistogenes squarrosa， Artemisia frigida, with the companion species being Potentilla acaulis. Four grazing gradients were identified, from herdsmen residence to enclosure site according to the grazing pressure. They were no grazing (CK enclosure site), light grazing (LG), moderate grazing (MG) and heavy grazing (HG). Young leaves of each Stipa grandis were collected during the growing season.

The results showed that Stipa grandis has abundant genetic diversity although some polymorphic loci were missing. At the same time new polymorphic loci emerged when grazing pressure increased. 10 primers were used, with 74 bands produced in total and 65 of the bands being polymorphic. The total percentage of polymorphism was 89%. With the increase of grazing pressures, the percentage of polymorphic loci of the Stipa grandis population decreased. The percentage of polymorphic loci was 62.2% in the no grazing (CK) population, 64.9% in the light grazing (LG) population, 58.1% in the moderate grazing (MG) population and 56.8% in the heavy grazing (HG) population. The genetic diversity of the population from highest to lowest by the Shannon’s information index is as follows: light grazing (0.3486), no grazing (0.3339), moderate grazing (0.3249) and heavy grazing (0.2735), with the same distributional pattern as the Nei’s genetic diversity index. The test showed that as grazing pressures increased, the change of genetic diversity decreased. The genetic differentiation coefficient among the population (Gst) was 0.1984, which showed small partial genetic diversity (19.8%) present among populations. Gene flow (Nm*) between primers varied from 0.9806 to 3.4463 and the mean Gene flow (Nm*) was 2.0202. The UPGMA cluster figure that was constructed based on the genetic distance matrix showed four populations that became genetically closer at each step. The first group was the moderate grazing (MG) population and the heavy grazing (HG) population, group two consisted of the no grazing (CK) populating and the light grazing (LG) population, then the two groups closed together.

Key words grazing _ Stipa grandis _ genetic diversity _ ISSR
DOI

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