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东北野生大豆核心种质单核苷酸多样性分析

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摘要: 对196个东北野生大豆核心种质的NRT2、AspAT2和CPK13三个基因片段进行单核苷酸扫描，共检测到94个SNPs位点及10个插入/缺失位点（Indel），碱基转换和颠换平均比例约2∶1。稀有SNPs位点（＜10%）39个，比率约为41.5%。196份核心种质平均多态性位点比例约为74%，Shannon′s指数是0.366，多样性指数为0.241；不同纬度群体的平均多样性指数随纬度下降逐渐升高，在44° N时达到峰值，然后随纬度降低缓慢下降，多样性指数变化呈近似正态曲线模式。初步推测N 42° ～N45° 区域为东北野生大豆的多样性中心。

Abstract: One hundred and ninety-six wild soybean germplasm were selected from core collection of Northeastern China and the NRT2, AspAT2 and CPK13 gene sequences were used for SNP analysis. We detected 94 SNPs and 10 Indel with average proportion of nucleotide transitions and transversions of about 2∶1. There was 39 rare SNPs（＜10%）, with ratio of approximately 41.5%. The average proportion of polymorphic sites for 196 core collection was 74%, Shannon′s index of 0.366 and diversity index was 0.241. With the decline of latitude, average diversity index of populations of different latitudes was increased, reaching peak at 44° N. Changes in diversity index exhibited normal mode curve. It showed that the central diversity of wild soybean in Northeastern China was found at 42° N-45° N.

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