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摘要: 在分析ms1轮回群体遗传多样性和群体内材料分组关系的基础上, 探讨了定向选择对群体遗传基础的影响。从ms1轮回群体中随机抽取216份材料为原始群体, 利用38个均匀分布于大豆全基因组的SSR标记, 检测原始群体等位变异数目和遗传多样性指数。并分别根据成熟期、株高和百粒重对群体定向选择形成6个不同类型的定向选择群体, 比较选择前后群体遗传多样性变化。结果表明: 在原始群体中, 共检测出216个等位变异, 平均每个位点等位变异数5.68, 平均多样性指数PIC为0.71。对原始群体进行熟期、株高和百粒重定向选择后, 各定向选择群体平均每个位点等位变异数介于4.89~5.13, 平均多样性指数PIC介于0.67~0.71。定向选择群体中有16个位点的等位变异频率发生了变化。对大豆ms1轮回群体定向改良, 目标性状及相关农艺性状的表现值及群体分布频率随之发生改变, 对群体遗传结构和遗传多样性指数的影响显著小于对目标性状及相关农艺性状的影响。

Abstract: The use of male sterile 1 (ms1) in a recurrent selection scheme can facilitate the soybean [Glycine max (L) Merr.] breeding process and improve breeding efficiency. In this study, the effect of artificial selection on agronomic traits, genetic diversity, and genetic structure was analyzed using an ms1 recurrent population. Two hundred and sixteen individuals from a recurrent soybean population were used as a base population, and six improved populations derived from the base population were defined, based on maturity (early vs late-maturing), plant height (tall vs short), and seed size (large vs small). Genetic diversity was assessed by allele number and polymorphism information content (PIC) using 38 simple sequence repeat (SSR) loci. The base population was compared with the improved populations to identify changes in agronomic traits and genetic diversity. Significant differences were found in growth duration, plant height, and 100-seed weight in different improved populations. A total of 216 alleles were detected in the base population, with an average of 5.68 and a mean PIC of 0.71 per SSR locus, while the total allele numbers ranged from 186 to 195 in the improved populations, with the average ranging from 4.89 to 5.13 and the mean PIC ranging from 0.67 to 0.71 per SSR locus. The allele frequencies of 16 loci varied among different populations. Improving the ms1 soybean recurrent groups, performance value of target traits and agronomic traits and population distribution of

frequency changed as well, the impact of population genetic structure and genetic diversity index was significantly less than the target properties and agronomic traits.

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