

研究论文

玉米新合成群体8种等位酶17个位点的遗传多样性及与数量性状相关性研究

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收稿日期 1999-2-2 修回日期 1999-5-19 网络版发布日期 接受日期

摘要 采用淀粉凝胶平板电泳方法, 研究了华中农业大学4个玉米新合成群体(WBM, LBM, WLS, LLS), 2个美国群体(BSSSR和BS16)和6个自交系的ADH, CAT, EST, GLU, GOT, MDH, PGD, PHI 8种等位酶的17个位点的47个等位基因的遗传多样性及其与数量性状的相关。采用NC II遗传交配设计, 6个群体与6个自交系组成36个组合, 田间试验在武昌、安阳两地进行两年。标记分析表明, 17个等位酶位点中有14个具有多态性, 群体的位点多态性水平介于64.7%~76.5%之间, 每位点的平均等位基因数介于1.941至2.294之间, 群体的总基因多样性介于22.4%~29.0%之间, 每位点的基因多样性分布为0~66%之间, 用36个组合14个多态性位点的MRD值与相应的两年、两地4次试验的数量性状均值进行相关分析, 结果在182个相关系数中有28个达到显著或极显著水平。

关键词 [玉米合成群体](#) [等位酶](#) [遗传多样性](#) [多样性](#) [数量性状](#)

分类号

Polymorphism of 8 Allozymes at 17 Loci from Maize Synthesized Populations and Correlated with Quantitative Traits

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Abstract The horizontal starch gel electrophoresis were performed to assess genetic diversity in 6 maize populations (4 Chinese synthesized and 2 U. S. populations) and 6 inbreds at 17 loci of 8 allozymes which are alcohol dehydrogenase (ADH), catalase(CAT), estase(EST), glutamicoxaloacetic transaminase(GOT) β -D-Glucosidase(GLU), malte dehydrogenase (MDH), 6-Phosphogluconate dehydrogenase (6-PGD), and phosphohexose isomerase (PHI). Allozyme variation was observed among all of populations studied. The results showed that, for 6 populations, the average of allozyme alleles number per locus was investigated to be from 1.941 to 2.294, the proportion of polymorphic loci ranged from 64.7% to 76.5%, the single locus heterozygosity among all allozyme loci was from 0 to 66%, the means of population the heterozygosity of all allozyme loci was from 22.4% to 29.0%. Analysis of gene diversity demonstrated that there was plentiful allelic variation within population for recurrent selection. Genetic distances between populations and inbreds were estimated with modified Rogers' distance (MRD) on the basis of allozyme marker locus. All 182 possible coefficients of correlation between average of 13 quantitative traits with 14 MRD were analyzed. 28 coefficients of them are significant.

Key words [Maize synthesized population](#); [Allozyme](#); [Quantitative traits](#); [Heterozygosity](#)

DOI:

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