

研究论文

构建作物种质资源核心库的一种有效抽样方法

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摘要 本文提出了基于基因型值构建作物种质资源核心库的抽样方法。采用包括基因型与环境互作的遗传模型及混合线性模型统计分析原理, 无偏预测基因型值。用基因型值计算基因型间的马氏距离, 并采用不加权类平均法进行聚类。根据树型图, 确定合理的分类水平, 将群体分成若干不同的类群。计算各基因型的平均离差度, 在各类群内按确定的比率, 选取平均离差度大的材料构建资源核心库。以棉花168个基因型5个纤维性状为例构建核心库, 所获得的48个核心资源能保存原棉花资源的遗传多样性。

关键词 [统计抽样方法](#) [基因型值](#) [核心资源](#) [种质资源](#)

分类号

An Efficient Method of Sampling Core Collection from Crop Germplasm

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Abstract A method for sampling core collection from crop germplasm was proposed. A genetic model with GE interaction and mixed model approaches were used for analyzing the genetic data. Mahalanobis distance among varieties calculated from predicted genotype values were employed for clustering crop germplasm using unweighted pair group method with arithmetic average of hierarchical cluster. After specifying the appropriate threshold value of classification based on the dendrogram, all genotypes could be clustered into some different sets. The mean of deflection for each genotype was calculated. The core collection was constructed by the core entries sampled from each set, with the larger mean of deflection. A worked example on 168 varieties of cotton with five fiber traits was presented. The results showed that the 48 genotypes as a core collections could represent the genetic diversity of original resources.

Key words [Statistical sampling method](#) [Genotypic value](#) [Core collection](#) [Germplasm](#)

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