

论文

浙江省茶树地方品种与选育品种遗传多样性和群体结构的EST-SSR分析

乔婷婷**, 马春雷**, 周炎花, 姚明哲, 刘饶, 陈亮*

中国农业科学院茶叶研究所茶树资源与改良研究中心/国家茶树改良中心, 浙江杭州310008

摘要:

以茶树品种龙井43幼根为材料, 构建cDNA文库并测序, 获得4833条EST序列, 拼接后得到3482条无冗余EST, 总长2290 kb. 对其进行SSR搜索, 共检测到577个SSR位点, 分布于500条茶树幼根EST中, 其中含有EST-SSR的序列占14.36%, 平均每3.97 kb出现一个SSR. 利用Primer premier 5.0, 对含有SSR的EST设计引物416对, 通过退火温度和多态性筛选, 确定可用的引物及其最佳退火温度, 并从筛到的引物中选取63对及1对已发表引物作为核心引物, 对浙江省茶树地方品种和选育品种进行遗传多样性和遗传结构分析. 结果显示64对引物均在供试材料中表现出多态性, 共检测到232个等位点, 平均每对引物3.6个; 每对引物可鉴定的基因型为2~13个, 平均4.3个. 供试材料多态性信息量(PIC)介于0.02~0.84, 平均0.44; 扩增位点的观测杂合度平均为0.44, 期望杂合度平均为0.48. 地方品种的遗传多样性水平略高于选育品种(系). 不同地方资源群体多态性信息量为0.24~0.36, 举岩群体的多样性最高, 惠明群体的多样性最低. 浙江各地区以杭州资源的多态性最高, PIC达0.41; 丽水的多态性最低, PIC为0.24. Structure 2.2群体结构分析和UPGMA聚类分析表明, 地方品种、选育品种(系)具有相对独立的群体结构, 选育品种(系)根据亲缘关系的不同形成不同的类群.

关键词: 茶树 遗传多样性 遗传结构 EST-SSR

EST-SSR Genetic Diversity and Population Structure of Tea Landraces and Developed Cultivars (Lines) in Zhejiang Province, China

Research Center for Tea Germplasm and Improvement, Tea Research Institute of the Chinese Academy of Agricultural sciences/National Center for Tea Improvement, Hangzhou 310008, China

Research Center for Tea Germplasm and Improvement, Tea Research Institute of the Chinese Academy of Agricultural sciences/National Center for Tea Improvement, Hangzhou 310008, China

Abstract:

Tea [*Camellia sinensis* (L.) O. Kuntze] has long history in production and consumption in Zhejiang Province, China. Improvement of tea, therefore, is of great importance and a good understanding of the genetic diversity and population structure of tea germplasm is a prerequisite to the improvement. In spite of great advances on the use of molecular markers in tea, achievement is still gotten very slowly compared with in other cereal crops and woody species. Expressed sequence tag derived simple sequence repeat (EST-SSR) is a less costly alternative way of developing new markers for genetic diversity analysis, functional markers development and marker assisted breeding of tea plant. A total of 4 833 ESTs generated from a cDNA library of tea young root were subjected to SSR mining using DNASTAR 5.0 software, 577 EST-SSRs were identified and 416 primer pairs were designed by Primer premier 5.0. After the determination of annealing temperatures and polymorphism of all the primers, 64 core primers were selected and used for genetic diversity and population structure analyses of tea landraces and improved cultivars in Zhejiang province. All selected primers were polymorphic and 232 alleles were amplified, with 3.6 alleles per primer pair on an average. Each primer pair identified 2 to 13 genotypes, with an average of 4.3. The mean of polymorphism information content (PIC) was 0.44, ranging from 0.02 to 0.84. Observed heterozygosity (H_o) was 0.44, while expected heterozygosity (H_e) was 0.48. The level of genetic diversity among landraces was slightly higher than that among improved cultivars and breeding lines. There were 226 alleles amplified in 22 landraces with 14 of them that were special. In the thirty-seven improved cultivars, however, two hundred and eighteen alleles were amplified but only six were special. The PIC of the landrace groups varied from 0.24 to 0.36, in which Juyan Qunti was the highest and Huiming Qunti was the lowest. Deqing Qunti was closest to Juyan Qunti in genetic relationship, but farthest from Huiming Qunti. The genetic diversity of tea cultivars from Hangzhou was the highest with PIC of 0.41, while those from Lishui recorded the lowest PIC of 0.24. Population structure revealed by software Structure 2.2 and UPGMA cluster analysis showed that landraces and improved cultivars were relatively independent. The improved cultivars were further clustered into smaller groups according to their pedigree. Hybrid offspring from Fuding Dabaicha and

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通讯作者: 陈亮, E-mail: liangchen@mail.tricaas.com; Tel: 0571-86652835

作者简介:

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