

植物和微生物遗传学

大豆耐旱种质鉴定和相关根系性状的遗传与QTL定位

刘莹^{1,3}, 盖钧镒¹, 吕慧能¹, 王永军^{1,2}, 陈受宜²

1.南京农业大学大豆研究所, 国家大豆改良中心, 作物遗传与种质创新国家重点实验室, 南京210095; 2.中国科学院遗传与生物研究所植物生物技术开放实验室, 北京 100101; 3.河北工程学院, 邯郸 056038

收稿日期 2004-9-3 修回日期 2005-1-12 网络版发布日期 接受日期

摘要 从301份黄淮海和长江中下游地区代表性大豆地方品种和育成品种(系)中按根系类型选取59份, 在苗期干旱胁迫和非胁迫条件下对地上部和地下部性状进行2年重复鉴定, 发现材料间性状隶属函数值具有丰富遗传变异, 以株高、叶龄、根干重和茎叶干重隶属函数的算术平均数为抗旱综合指标从中筛选出汉中八月黄、晋豆14、科丰1号、圆黑豆等强耐旱型(1级)和临河大粉青、宁海晚黄豆等干旱敏感型(5级)材料。比根干重、比总根长、比根体积与耐旱隶属函数平均值均呈极显著正相关, 可作为耐旱性的根系性状指标。利用“科丰1号×南农1138-2”(1级×4级)衍生的RIL群体为材料, 对耐旱相关根系性状采用主基因+多基因混合遗传模型分离分析法进行遗传分析并进行QTL定位。结果表明, 该两亲本间比根干重、比总根长、比根体积的遗传均为两对主基因加多基因模型, 后两者主基因间有连锁(重组率分别为4.30%和1.93%); 主基因遗传率为62.26% - 91.81%, 多基因遗传率为2.99% - 24.75%; 耐旱相关根系性状各主要由1对主基因控制, 另1对效应较小。QTL分析检测到5、3、5个QTLs分别控制比根重、比根总长、比根体积, 位于N6-C2, N8-D1b+W, N11-E, N18-K连锁群上。3性状各有1个贡献率大的QTL(Dw1, R11, Rv1), 而且均位在N6-C2的STAS8_3T-STAS8_6T相同距离的区段上, 其他QTLs效应均较小。分离分析与QTL定位的结果相对一致。

关键词 [大豆](#); [耐旱性](#); [根系性状](#); [相关](#); [遗传](#); [数量性状分离分析](#); [QTL定位](#)

分类号

扩展功能

本文信息

- ▶ [Supporting info](#)
- ▶ [PDF\(355KB\)](#)
- ▶ [HTML全文\(0KB\)](#)
- ▶ [参考文献](#)

服务与反馈

- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)

▶ [复制索引](#)

▶ [Email Alert](#)

▶ [文章反馈](#)

▶ [浏览反馈信息](#)

相关信息

▶ [本刊中 包含 “大豆; 耐旱性; 根系性状; 相关; 遗传; 数量性状分离分析; QTL定位” 的相关文章](#)

▶ 本文作者相关文章

- [刘莹](#)
- [盖钧镒](#)
- [吕慧能](#)
- [王永军](#)
- [陈受宜](#)

Identification of Drought Tolerant Germplasm and Inheritance and QTL Mapping of Related Root Traits in Soybean (*Glycine max* (L) Merr.)

LIU Ying^{1, 3}, GAI Jun-Yi¹, LÜ, Hui-Neng¹, WANG Yong-Jun^{1,2}, CHEN Shou-Yi²

1.Soybean Research Institute of Nanjing Agricultural University/ National Center for Soybean Improvement/ National Key Laboratory for Crop Genetics and Germplasm Enhancement, Nanjing 210095, China;2.Plant Biotechnology Laboratory, Institute of Genetics and Developmental Biology, Chinese Academy of Science, Beijing 100101, China; 3. Hebei University of Engineering, Handan 056038, China

Abstract

Fifty nine accessions of soybean (*Glycine max* (L.) Merr.) selected from 301 ones from Huang-Huai-Hai and Middle-Lower Changjiang Valleys were tested in two years for their tolerance to drought by using the mean membership index value averaged over those of plant height, leave number, dry root weight and dry stem and leaf weight. Four most tolerant accessions (Rank 1) and two most sensitive ones (Rank 5) were identified. There existed very significant correlations between drought tolerance and relative values of dry

root weight, total root length, and root volume (per plant dry weight basis), respectively, which could be used as root indicators of drought tolerance. The RIL population derived from Kefeng 1 × Nannong 1138-2 was used to analyze the inheritance of the three relative root traits by using the segregation analysis of quantitative trait under the major gene plus polygene mixed inheritance model. The results showed that between the two parents (Rank 1 × Rank 4), the relative values of dry root weight, total root length and root volume were respectively controlled by two major genes (linked together for the latter two traits, recombination value being 4.30% and 1.93%, respectively) plus polygenes with their major gene heritability values 62.26%–91.81% and polygene heritability values 2.99%–24.75%, indicating that major gene, especially the one with larger effect, accounted for a major part of the genetic variation between the two parents. There identified were five, three, and five QTLs located on N6-C2, N8-D1b+W, N11-E, and N18-K linkage groups for relative dry root weight, total root length and root volume, respectively. Each of the traits appeared to have one locus (Dw1, R11, and Rv1) with relatively large effect in comparison with their other loci, and those major ones were located at about a same site of a same linkage group N6-C2. The results between segregation analysis and QTL mapping appeared pretty consistent, therefore could be used for verification each other.

Key words [soybean \(*Glycine max* \(L\) Merr.\)](#) [drought tolerance](#) [root trait](#) [correlation](#) [inheritance](#) [segregation analysis of quantitative trait](#) [QTL mapping](#)

DOI:

通讯作者 盖钧镒,陈受宜 sri@njau.edu.cn