植物遗传资源学报
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苦瓜亚种间遗传图谱构建及果实相关性状 QTL 定位

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摘要：苦瓜是我国传统的瓜类蔬菜，品种资源遗传背景十分狭窄，因此，在选育种应用中亟需拓宽种质资源的利用范围。本研究以小果型野生亚种 *Momordica charantia* ssp.*macroloba* ‘NJ’为母本、普通亚种 *M. charantia* ssp. *charantia* ‘Tan’为父本，基于重测序及 bin 标记基因分型构建苦瓜亚种间遗传图谱，并利用 multiple-QTL model（MQM）方法对果实相关性状进行 QTL 定位。结果表明，构建的苦瓜亚种间遗传图谱包含 1563 个 bin 标记，覆盖 11 条染色体，总遗传距离为 1556.91 cM，标记间平均距离为 1.00 cM，遗传与物理图谱间比较显示苦瓜两个亚种在 MC08 号染色体存在一个约 11 Mb 的倒位区域。QTL 定位结果显示，共有 7 个 QTL 达到了 LOD 检测阈值，其中果长 2 个（*qFL5.1*、*qFL7.1*）、果形指数 2 个（*qFSI1.1*、*qFSI4.1*）、果重 2 个（*qFW5.1*、*qFW6.1*）、果形 1 个（*qFS5.1*）；果长 *qFL5.1*、果形 *qFS5.1*、果重 *qFW5.1* 形成一个一致性的主效 QTL 区间，贡献率分别为 23.00%、30.20%、24.80%；果形指数的 2 个 QTL（*qFSI1.1*、*qFSI4.1*）均与果形 *qFS5.1* 不同，贡献率分别为 22.80%、14.60%。本研究结果有助于揭示苦瓜两个亚种基因组的变异特征以及为亚种间种质创新和果实相关性状基因挖掘奠定基础。

关键词：苦瓜亚种；遗传图谱；果实相关性状；QTL

Construction of Inter-subspecific Genetic Map of Bitter Gourd (*Momordica charantia* L.) and QTL Mapping for Fruit-related Traits

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Abstract: Bitter gourd is a traditional melon vegetable in China, characterized by a very narrow genetic background of variety resources. Consequently, there is an urgent need to broaden the utilization of germplasm resources in breeding applications. In this

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study, we used the small-fruited wild subspecies *Momordica charantia* ssp. *macroloba* ‘NJ’ as the maternal parent and the common subspecies *M. charantia* ssp. *charantia* ‘Tan’ as the paternal parent. Based on resequencing and bin marker genotyping, we constructed a genetic map of inter-subspecies in bitter gourd, and employed the multiple-QTL model (MQM) method to map quantitative trait loci (QTL) associated with fruit-related traits. The results showed that the constructed genetic map of inter-subspecies in bitter gourd comprised 1,563 bin markers, spanning 11 chromosomes with a total genetic distance of 1,556.91 cM and an average marker interval of 1.00 cM. A comparison of the genetic and physical maps revealed an inversion region of approximately 11 Mb on chromosome MC08 between the two subspecies of bitter gourd. The QTL mapping results indicated that a total of seven QTL reached the LOD detection threshold, including two for fruit length (*qFL5.1* and *qFL7.1*), two for fruit shape index (*qFSI1.1* and *qFSI4.1*), two for fruit weight (*qFW5.1* and *qFW6.1*), and one for fruit shape (*qFS5.1*). The fruit length QTL *qFL5.1*, fruit shape QTL *qFS5.1*, and fruit weight QTL *qFW5.1* colocalized to form a major-effect QTL interval, with contribution rates of 23.00%, 30.20%, and 24.80%, respectively. The two QTLs for fruit shape index (*qFSI1.1* and *qFSI4.1*) were different from the fruit shape QTL *qFS5.1*, with contribution rates of 22.80% and 14.60%, respectively. The findings of this study contribute to our understanding of the genomic variation between the two subspecies of bitter gourd and provide the foundation for inter-subspecific germplasm innovation and gene mining of fruit-related traits.

Key words: bitter gourd subspecies; genetic map; fruit-related traits; QTL

苦瓜（*Momordica charantia* L.）属于葫芦科一年生攀援草本植物，是我国夏季重要的瓜类蔬菜。苦瓜起源于非洲[1]，目前，种质资源主要分布在非洲和亚洲的热带地区[1-2]。苦瓜包括两个亚种，分别为小果型野生亚种 *M. charantia* ssp. *macroloba*（简称 *macroloba*）和普通亚种 *M. charantia* ssp. *charantia*；其中普通亚种又包含两个变种，即栽培变种 *M. charantia* ssp. *charantia* var. *charantia*（简称 *charantia*）和野生变种 *M. charantia* ssp. *charantia* var. *muricata*（简称 *muricata*），后者野生变种被认为是栽培变种的直接野生祖先[3-7]。苦瓜小果型野生亚种 *macroloba* 通常处于纯野生状态，相比于普通亚种，表现为叶小茎细、果实与种子较小、常具有较强的生长势和抗逆性，是进行苦瓜种质扩增和创新的重要种质资源。

在长期的育种过程中，由于受到持续、高强度的人工选择，主要作物都面临种质资源遗传多样性减少、品种同质化严重等问题[8-9]。野生资源通常作为新的遗传多样性来源，在作物的种质遗传改良过程中发挥重要作用[10-12]。在模式植物水稻中，研究人员从多个野生水稻种中鉴定了大量的生物与非生物胁迫抗性、产量、品质相关的优异基因[13]。在另一个模式植物番茄中，研究人员利用野生番茄 *Solanum pimpinellifolium* 和栽培番茄 *S. lycopersicum* 构建种间遗传图谱，并定位了果形、果重等性状 QTL 位点[14-16]。在葫芦科模式植物黄瓜中，国内外学者利用哈氏黄瓜（*Cucumber sativus* var. *hardwickii*）[17-18]、西双版纳黄瓜（*C. sativus* var. *xishuangbannanesis*）[19-22]等黄瓜野生变种和酸黄瓜（*C. hystrix*）[23-27]、西印度黄瓜（*C. anguria*）[28]等近缘野生种资源，开展了一系列优异基因位点的发掘工作。以上研究为相关作物种质扩增和遗传改良提供了额

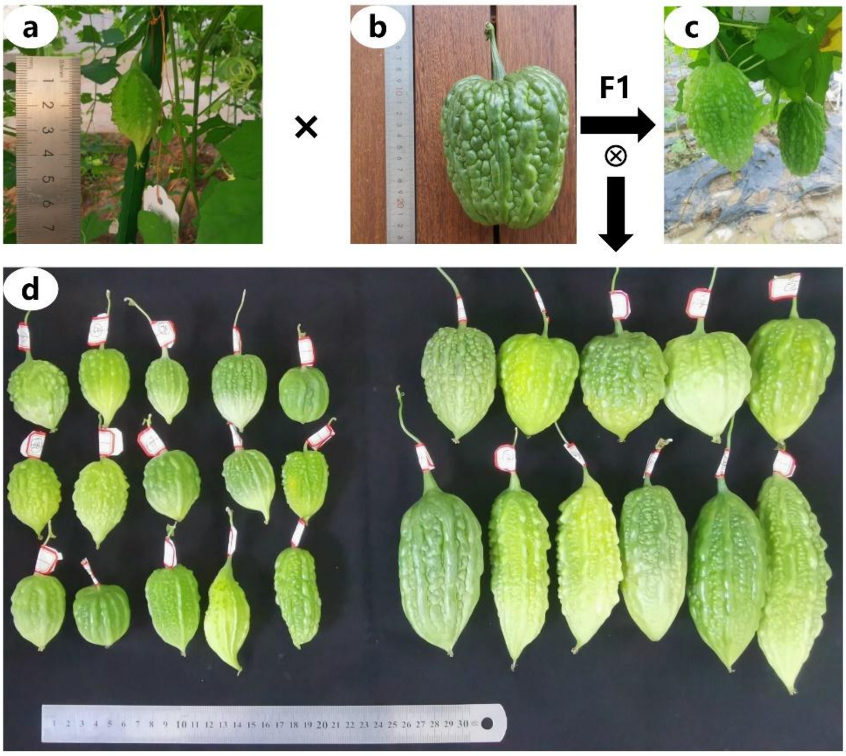
外的优异基因资源。

有关苦瓜野生资源的利用，目前主要集中在核型分析[29]、形态特征[29-31]、营养成分[29]、光合特性[31]等方面的鉴评，但相关研究使用的野生材料类型（*macroloba* 或者 *muricata*）并不清楚。张长远等[32]利用野生变种 *muricata* 与栽培变种 *charantia* 杂交获得 F_2 后代，并初步观察到单株产量等 6 个性状表现为数量遗传特点。野生亚种 *macroloba* 与 *charantia* 或 *muricata* 的遗传距离较远[6]，是拓宽苦瓜种质遗传背景的理想种质资源。迄今，有关苦瓜两个亚种间杂交的遗传图谱构建及性状遗传定位的研究尚鲜见报道。本研究以小果型野生亚种自交系‘NJ’为母本，栽培变种自交系‘Tan’为父本构建 F_2 群体，通过重测序进行基因分型并构建亚种间 bin 标记[33]遗传图谱，然后对苦瓜果实相关性状进行 QTL 定位，旨在为苦瓜亚种间杂交育种提供理论参考。

1 材料与方法

1.1 试验材料

苦瓜母本‘NJ’收集于福建省漳州市南靖县，属于小果型野生亚种 *M. charantia* ssp.*macroloba*，果形为纺锤形，果长、果径、果形指数、果重分别为 7.84±0.32 cm、3.69±0.27 cm、2.12±0.08、7.47±1.12 g；父本‘Tan’选自广东省佛山市地方种‘谭边大顶’，属于普通亚种 *M. charantia* ssp. *charantia*，果形为圆锥形，果长、果径、果形指数、果重分别为 11.44±1.24 cm、10.71±0.48 cm、1.07±0.12、540.37±52.60 g，两个亲本经连续多代自交已形成稳定自交系，亲本间果长（$F = 23.20^{**}$）、果径（$F = 537.95^{**}$）、果形指数（$F = 180.49^{**}$）、果重（$F = 942.50^{**}$）存在极显著差异（图 1）。通过‘NJ’与‘Tan’杂交及 F_1 自交获得 154 份‘NJ’×‘Tan’ F_2 植株。2022 年秋季，将 F_2 植株种植于佛山大学园艺教学试验基地，种植密度为 1.5 m 包沟、单行种植、株距 80 cm，采用“人字形”搭架方式，按照常规栽培方式进行统一管理。



a：母本自交系‘NJ’，b：父本自交系‘Tan’，c：F_1果实，d：代表性 F_2果实

a: maternal inbred line ‘NJ’, b: paternal inbred line ‘Tan’, c: F_1 fruit, d: representative F_2 fruit

图 1 苦瓜自交系‘NJ’与‘Tan’及其 F_1、F_2果实

Fig.1 Fruits of bitter gourd inbred lines ‘NJ’, ‘Tan’ and their F_1 and F_2

1.2 性状调查

待植株抽蔓后对 F_2代单株分别编号，坐果后对苦瓜果实相关性状进行调查和测量。在植株生长中前期，选择主蔓上第二个或以上生长正常的果实，经人工辅助授粉并标记日期，在授粉后 18 d，利用游标卡尺测量果长（苦瓜果顶至果尾的长度；Fruit Length，FL）、果径（果实最粗位置横截面的直径；Fruit Diameter，FD），并计算果形指数（Fruit Shape Index，FSI），利用电子天平测量单个苦瓜果重（Fruit Weight，FW），每个植株测量三个果实。在商品果期（授粉后 15-20 d）观察果实形状（Fruit Shape，FS），果形似‘NJ’，表现为纺锤形的记录为‘B’，果形似‘Tan’，表现为圆锥形的记录为‘D’。

1.3 重测序及基因分型

待植株长出侧蔓后，采集 F_2植株侧蔓嫩叶用于 DNA 提取。利用试剂盒（VAHTS Universal Plus DNA Library Prep Kit for Illumina, Vazyme）构建 DNA 文库。利用高通量测序平台 GenoLab M 进行 DNA 文库测序。对原始 read 进行一系列过滤后，利用 BWA 软件[34]进行 clean reads 与‘Dali-11’参考基因组[6]的序列比

对，并利用 GATK 软件[35]对 F_2 单株进行 SNP 鉴定。通过扫描全基因组 SNP，采用滑动窗口方法进行 bin 标记基因型鉴定[33]。首先，扫描 15 个 SNP 大小的窗口，根据 SNP 比率来指定基因型。然后，计算每个窗口中‘NJ’与‘Tan’之间 SNP 数量比例，如果窗口中有 70%或更多来自父母本一方的 SNP，则被认为是与父母本一致的纯合基因型，否则，该窗口被认为是杂合基因型。通过比较 F_2 个体在 100 kb 区间内的基因型来构建 bin 标记基因型。

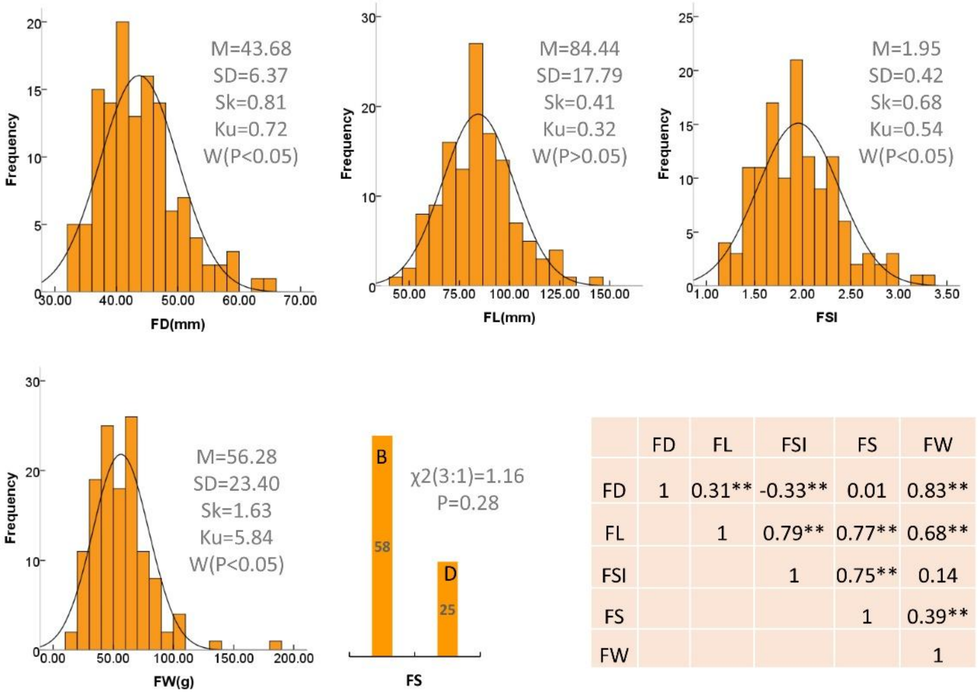
1.4 遗传图谱构建及 QTL 检测

将获得的 1921 个 bin 标记基因型数据导入 JoinMap4.1 软件[36]，经卡方检验过滤掉极端偏分离位点后剩余 1680 个。利用回归作图算法及 Kosambi’s 函数进行遗传作图。根据作图结果获得遗传图谱文件（.map），再将基因型文件（.loc）和表型文件（.qua）一起导入 MapQTL6 软件[37]。利用 MQM（multiple-QTL model）作图方法进行 QTL 检测。利用排列检验（Permutation test）确定 LOD 显著性阈值（P=0.05），通过‘one-LOD support interval’划定置信区间[38-39]。

2 结果与分析

2.1 果实相关性状表型分析

‘NJ’×‘Tan’ F_2 植株果实在大小和果形上发生了剧烈分离（图 1）。除果长表型数据呈正态分布，果径、果形指数、果重的都呈正偏态分布（图 2）。选择易于区分果形的 83 株植株进行调查，果形为纺锤形（B）植株有 58 株，圆锥形（D）植株有 25 株，经卡方检验符合 3:1 分离规律。相关性分析表明果径与果长、果重呈显著正相关，与果形指数呈显著负相关；果长与果形指数、果形、果重呈显著正相关；果形指数与果形呈显著正相关；果形与果重呈显著正相关。



	FD	FL	FSI	FS	FW
FD	1	0.31**	-0.33**	0.01	0.83**
FL		1	0.79**	0.77**	0.68**
FSI			1	0.75**	0.14
FS				1	0.39**
FW					1

M、SD、Sk、Ku、W 分别表示平均数、标准差、偏度、峰度、Shapiro-Wilk 检验；B、D 分别表示纺锤形、圆锥形；FD、FL、FSI、FW、FS 分别表示果径、果长、果形指数、果重、果形

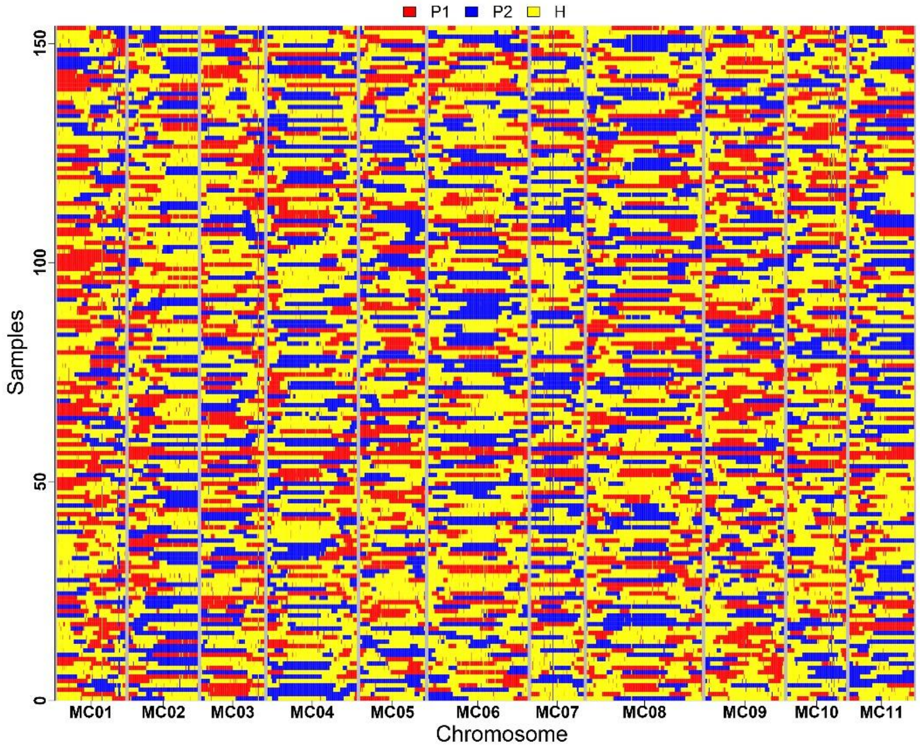
M, SD, Sk, Ku, and W represent mean, standard deviation, skewness, kurtosis, and Shapiro-Wilk test respectively. B and D represent spindle or stick shape and conical shape respectively. FD, FL, FSI, FW, and FS represent fruit diameter, fruit length, fruit shape index, fruit weight, and fruit shape, respectively

图 2 F_2 群体果实相关性状频次分布及相关性分析

Fig.2 Frequency distribution and correlation analysis of fruit-related traits in F_2 population

2.2 测序数据与基因型分析

对 154 个 F_2 个体进行重测序，经过滤后总共产生了 404.39 Gb 的数据（约 28.62 亿 read；详见 https://doi.org/10.13430/j.cnki.jpgr. 20241126002，附表 1）。F_2 各样本的测序深度范围为 5.34 ~ 18.82，平均为 7.58；以‘Dali-11’作为参考基因组比对的平均覆盖率为 87.97%；各样本测序数据的平均 Q20 为 94.39%，显示了较高的测序质量（详见 https://doi.org/10.13430/j.cnki.jpgr. 20241126002，附表 1）。对 F_2 各样本 SNP 位点数量进行统计（详见 https://doi.org/10.13430/j.cnki.jpgr. 20241126002，附表 2），结果显示各样本平均纯合 SNP 位点数量为 899758，平均杂合位点数量为 950674。通过滑动窗口进行基因分型，最终在 11 条染色体上获得 1921 个 bin 标记（图 3）。



红色（P_1）表示‘NJ’基因型，蓝色（P_2）表示‘Tan’基因型，黄色（H）表示 F_1 杂合基因型

Red (P_1) indicates the ‘NJ’ genotype, blue (P_2) indicates the ‘Tan’ genotype, and yellow (H) indicates the F_1 heterozygous genotype

图 3 苦瓜 bin 标记图谱

Fig.3 Bin marker map of bitter gourd

2.3 亚种间遗传图谱特征分析

将上述 1921 个 bin 标记基因型数据导入到 Joinmap 4.0 软件，构建遗传图谱。经连锁分析，最终获得一张包含 1563 个 bin 标记的苦瓜亚种间遗传图谱，所有 bin 标记分布于 11 个连锁群上，对应在 11 条染色体上（表 1）。该图谱总遗传距离为 1556.91 cM，平均遗传距离为 1.00 cM，平均重组率为 6.22 cM/Mb。通过对全基因组范围遗传和物理位置进行比对，发现在 MC08 号染色体 23.35 Mb 到 34.35 Mb 区间（约 11 Mb）存在一个较大的染色体倒位片段（图 4）。

表 1 苦瓜亚种间遗传图谱基本信息

Table 1 Basic information of inter-subspecific genetic map of bitter gourd

染色体 Chr.	Bin 数量 Number of bins	遗传距离(cM) Genetic distance	密度(cM/marker) Density	重组率(cM/Mb) Recombination rate
MC01	97	143.27	1.48	6.85
MC02	129	120.97	0.94	5.75
MC03	122	118.52	0.97	6.14

MC04	163	177.72	1.09	6.60
MC05	129	141.84	1.10	7.16
MC06	207	178.54	0.86	5.97
MC07	84	96.98	1.15	5.95
MC08	221	125.21	0.57	3.63
MC09	169	178.58	1.06	7.48
MC10	117	141.58	1.21	7.86
MC11	125	133.7	1.07	6.75
总计 Total	1563	1556.91	1.00	6.22

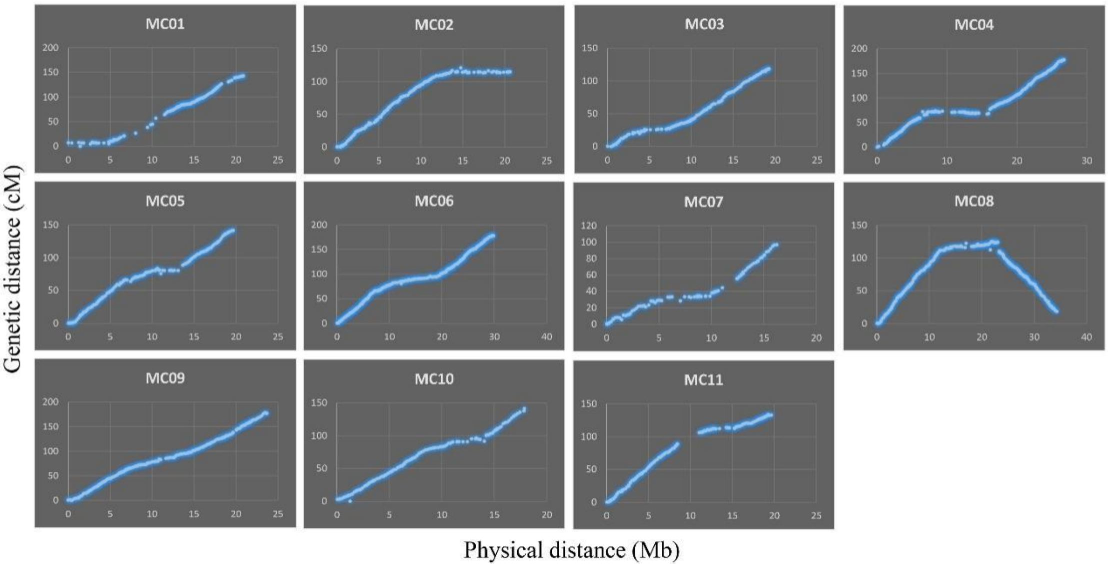
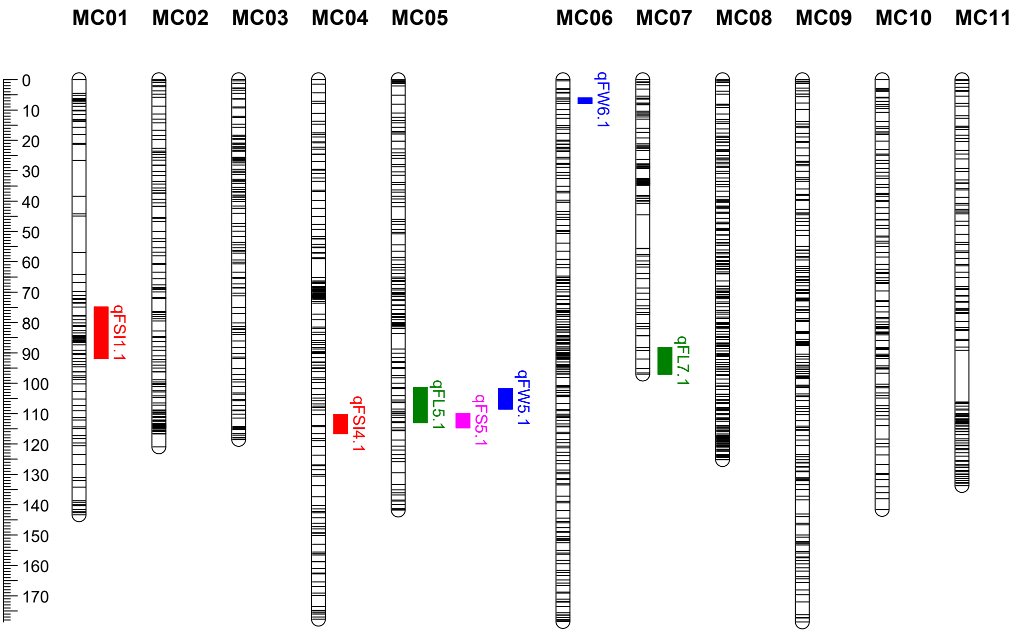


图 4 苦瓜亚种间遗传图谱与物理图谱比较

Fig.4 Comparison of genetic map and physical map between subspecies of bitter gourd

2.4 果实相关性状 QTL 定位

结合遗传图谱与果实相关性状表型进行 QTL 检测，通过排列检验确定果长、果径、果形指数、果形、果重的 LOD 阈值分别为 4.1、4.1、4.0、4.3、3.9，结果显示果径无 QTL 被检测到，果形被检测到 1 个 QTL 位点，其他三个性状分别被检测到 2 个 QTL 位点，所有位点分布在 MC01、MC04、MC05、MC06、MC07 五条染色体上（图 5、表 2）。其中，果长 2 个 QTL 为 *qFL5.1*、*qFL7.1*，贡献率分别为 23.00%、14.70%，加性效应分别为 11.25、9.54，显性效应分别为-3.67、1.30；果形指数 2 个 QTL 为 *qFSI1.1*、*qFSI4.1*，贡献率分别为 22.80%、14.60%，加性效应分别为-0.26、-0.23，显性效应分别为-0.13、0.04；果重 2 个 QTL 为 *qFW5.1*、*qFW6.1*，贡献率分别为 24.80%、13.90%，加性效应分别为 15.45、12.96，显性效应分别为-4.22、-6.40；果形 QTL 为 *qFS5.1*，贡献率为 30.20%，加性效应为-0.30，显性效应为-0.20。



红色条表示果形指数 QTL，绿色条表示果长 QTL，蓝色条表示果重 QTL，紫色条表示果形 QTL

Red bars indicate the QTL of fruit shape index, green bars indicate the QTL of fruit length, blue bars indicate the QTL of fruit weight, purple bar indicates the QTL of fruit shape.

图 5 苦瓜亚种间遗传图谱及果实相关性状 QTL 位点

Fig. 5 Inter-subspecific genetic map and QTL loci for fruit-related traits in bitter gourd

表 2 苦瓜果实相关性状 QTL 位点信息统计

Table 2 QTL of fruit-related traits identified in bitter gourd

性状/数量性状位点 Traits/QTL	连锁群 Linkage group	最近标记 Nearest marker	位置 (cM) Position	LOD 值 LOD score	贡献率(%) Phenotypic variation explained	遗传区间 (cM) Genetic interval	物理区间 (Mb) Physical interval	加性效应 Additive	显性效应 Dominance
果长 Fruit Length									
qFL5.1	MC05	MC05_156	106.25	7.28	23.00	11.68	1.70	11.25	-3.67
qFL7.1	MC07	MC07_153	88.28	4.43	14.70	8.70	1.04	9.54	1.30
果形指数 Fruit Shape Index									
qFSI1.1	MC01	MC01_140	84.91	7.18	22.80	16.94	2.53	-0.26	-0.13
qFSI4.1	MC04	MC04_207	113.90	4.38	14.60	6.23	0.31	-0.23	0.04
果形 Fruit Shape									
qFS5.1	MC05	MC05_165	111.33	6.49	30.20	4.71	0.61	-0.30	-0.20
果重 Fruit Weight									
qFW5.1	MC05	MC05_156	106.25	7.90	24.80	6.67	0.81	15.45	-4.22
qFW6.1	MC06	MC06_10	7.15	4.17	13.90	1.91	0.30	12.96	-6.40

3 讨论

一方面主要农作物商业品种面临严重的同质化问题，另一方面仅有有限的种质资源被用于品种遗传改良[40]。许多未开发的野生资源包含大量的遗传多样性，因此如何从野生资源中重新获得丢失的有益遗传多样性将在优异种质培育过程中发挥更关键的作用[11-12]。苦瓜小果型野生亚种 *macroloba* 主要分布在非洲、南亚、东南亚等地区，在我国台湾、福建、广东、广西等地也有少量分布[6-7]。野生亚种 *macroloba* 单果质量通常低于 10 g，果实和种子大小都显著低于普通亚种 *charantia* 和 *muricata*[6, 7, 41]。*macroloba* 与普通亚种的遗传分化时间约在 190 万年以前，两者基因组变异较大[6]。本研究亚种间遗传图谱结果发现 *macroloba* 与 *charantia* 在 MC08 号染色体存在一个约 11 Mb 大小的片段倒位，首次揭示了苦瓜两个亚种在染色体水平的大片段结构变异，该结构变异可能是推动两个亚种分化的重要变异因素。

虽然两个亚种遗传距离较远，但二者杂交亲和性较高，‘NJ’×‘Tan’ F_1 育性正常且表现出较强的杂种优势，与前人报道一致[41]；还发现 F_2 代性状出现剧烈分离且几乎无亲本类型，再次反映苦瓜两个亚种在遗传背景上的巨大差异。本研究苦瓜亚种间 F_2 群体无亲本类型出现可能与群体较小有关，建议今后在进行类似研究时适当扩大 F_2 群体数量。构建的苦瓜亚种间遗传图谱总遗传距离为 1556.91 cM，低于类似基于全基因组 SNP 标记的亚种内遗传图谱的总距离，如已报道的 2203.95 cM[42]、2329.20 cM[43]、2415.20 cM[44]，亚种间遗传图谱相对于亚种内较低的重组率[42]可能是引起二者差异的主要因素。

通常，选择用于构建作图群体的亲本应尽可能在目标性状上具有差异。本试验两个亲本的果径存在极显著差异，然而并无果径 QTL 被定位，说明果径遗传可能受微效多基因控制；果长、果形指数、果重也均存在极显著差异，总共有 7 个主效 QTL 位点（贡献率 > 10%）被发现。其中，果形 *qFS5.1* 与果重 *qFW6.1* 的遗传区间分别为 4.71 cM 和 1.91 cM，说明这两个 QTL 位点标记具有较高的应用潜力，下一步通过精细定位和开发更紧密的分子标记将有助于这些 QTL 的实际育种应用。另外，本研究在 MC05 号染色体上发现一个一致性的主效 QTL 位点（*qFL5.1*、*qFS5.1*、*qFW5.1*），相关几个性状间的显著相关性说明该 QTL 位点可靠性程度较高且可能存在多效性。与之相比，国内外部分学者也对苦瓜果长、果形指数、果重等性状进行了 QTL 遗传定位[43-46]，然而并没有发现一致性的主效位点。值得一提的是，本研究在 MC01（*qFSI1.1*）和 MC04（*qFSI4.1*）上各检测到的 1 个果形指数（FSI）QTL 位点，均不同于果形（FS）的位点（*qFS5.1*）。遗传分析表明果形指数呈数量性状分布，而在易于区分果形的 F_2 群体中，果形表现为质量性状分布特征，这与该两个性状 QTL 定位的结果比较一致。迄今，多个影响果形的变异位点在其他葫芦科作物中已被鉴定[47-48]，因此，基于本研究结果推测苦瓜果形的遗传变异位点也具有多样性。

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附表 1 154 个 F_2 样本重测序数据统计

Attached Table 1 The statistics of sequencing data for 154 F_2 samples

样本号 Sample ID	总 read 数 Total reads	总碱基数 Total bases	GC 含量 (%)GC	Q20 值 (%)Q20	平均深度 Mean depth	覆盖率(%) Coverage rate
DN-1	16233986	2238088396	36.59	94.63	6.33	85.17
DN-2	20878162	3034566740	35.15	95.04	9.1	90.91
DN-3	20731516	2981734556	35.32	94.85	8.89	89.91
DN-4	20961466	2943965531	36.15	94.81	8.45	90.04
DN-5	20876316	3041605544	35.19	94.9	9.08	89.56
DN-6	20776164	2881752707	36.65	94.55	8.13	87.82
DN-7	20918892	2898723237	36.73	94.42	8.22	89.08
DN-8	19143456	2769882949	35.64	94.77	8.09	90.78
DN-9	20627450	2954827926	35.6	94.69	8.11	90.16
DN-11	20769968	2862726212	36.29	94.73	8.03	89.29
DN-12	19126708	2722809915	35.73	94.54	7.92	88.47
DN-13	18191544	2527883372	36.36	94.48	7.18	86.24
DN-14	22395742	3126186115	35.96	94.64	8.81	89.71
DN-15	20283700	2911308772	35.49	94.71	8.55	90.09
DN-16	18657688	2583492387	36.97	94.65	7.41	89.27
DN-17	19276644	2739697895	36.19	94.34	8.1	90.09
DN-18	22268738	3188895493	35.54	94.58	9.4	92.19
DN-19	20827666	2942264109	36.04	94.66	8.6	90.17
DN-20	21661524	3029233543	36.38	94.46	8.53	88.77
DN-21	22324314	3110665185	36.43	94.81	8.75	89.63
DN-22	20832726	2996753563	35.66	94.75	8.89	91.3
DN-23	21035682	2935851815	36.96	94.4	8.31	89.38
DN-24	19440816	2720284800	36.56	94.54	7.69	88.27
DN-25	22101286	3120359745	36.54	94.4	9.1	90.87
DN-26	21284728	3008664351	35.97	94.47	8.63	88.62
DN-27	21535324	3012940101	36.26	94.51	8.65	89.83
DN-28	20353518	2876927547	36.09	94.46	8.29	88.55
DN-29	20920268	2980615208	35.41	94.53	8.82	90.84
DN-30	21018982	2972350539	36.48	94.72	8.64	89.51
DN-31	40492300	5537987808	36.73	94.13	14.94	92.42
DN-32	17223608	2437616346	36.65	94.45	6.96	86.88
DN-33	19212360	2784274078	35.39	94.68	8.45	91.92
DN-34	20531728	2924949820	36.16	94.69	8.56	89.36
DN-35	24494642	3430262214	36.66	94.53	9.79	90.9
DN-36	25201510	3582432617	36.33	94.71	10.2	91.33
DN-37	23262228	3267258510	36.56	94.68	9.49	93
DN-38	21470004	2983621122	36.96	94.64	8.53	89.58
DN-39	23393800	3328969895	36.46	94.84	9.78	92.47
DN-40	21280898	2990916609	36.61	94.66	8.57	88.53
DN-41	20650992	2759555921	37.66	94.06	7.56	89.66

DN-42	21898718	3125338102	36.1	94.79	8.26	89.13
DN-43	19942534	2788604130	36.91	94.61	7.94	86.92
DN-44	19866368	2739642663	36.76	94.59	7.79	89.77
DN-45	21733712	2987086059	37.04	94.67	8.34	89.23
DN-46	19569672	2771097276	36.6	94.59	8.08	90.42
DN-47	21650742	3102930305	36.31	94.8	9.17	92.12
DN-48	20797182	2903399974	36.94	94.58	8.25	89.27
DN-49	18381666	2626929375	36.34	94.85	7.76	89.69
DN-50	20281522	2843605881	36.76	94.71	8.17	89.26
DN-51	18816402	2616446465	36.84	94.87	7.53	88.88
DN-52	45667762	6586636945	35.96	94.72	18.82	95.03
DN-53	18676326	2613903486	37	94.78	7.49	87.5
DN-54	20266296	2770124011	37.33	94.78	7.74	88.86
DN-55	20316768	2808629371	37.12	94.58	7.92	87.49
DN-56	16712454	2359202343	36.59	94.55	6.86	86.16
DN-57	16860068	2387209778	36.08	94.71	7.02	88.53
DN-58	17500020	2476439938	36.11	94.72	7.28	88.58
DN-59	20407608	2994013596	35.14	94.82	7.96	89.6
DN-60	16094478	2312418440	35.7	94.76	6.9	86.21
DN-61	16618492	2414687956	35.68	94.97	7.25	88.74
DN-62	14407176	2053945718	36.27	94.82	6.06	84.31
DN-63	17256930	2479826607	36.1	94.8	7.32	88.93
DN-64	16095580	2359204928	35.17	94.81	7.13	90.69
DN-65	15876658	2302394917	35.25	94.63	6.96	88.3
DN-66	18502196	2672537067	35.26	94.89	8.05	90.1
DN-67	18012170	2582943154	35.39	94.92	7.72	89.96
DN-68	14944550	2056444797	36.43	94.61	5.82	83.51
DN-69	19918676	2908195831	35.12	94.72	8.83	92.27
DN-70	13325678	1878633122	35.86	94.71	5.52	82.9
DN-71	16480768	2334834640	35.84	94.61	6.92	89.02
DN-72	17987356	2544919493	35.87	94.73	7.35	87.23
DN-73	17408416	2471756648	35.92	94.79	7.28	88.25
DN-74	15502920	2092895498	36.82	94.46	5.82	84.4
DN-75	16612614	2340250680	35.84	94.78	6.8	86.38
DN-76	17681734	2519710379	35.52	94.8	7.48	90.2
DN-77	17495028	2350863592	36.98	94.26	6.45	86.11
DN-78	16196772	2297792873	35.88	94.84	6.79	87.83
DN-79	16596944	2332794081	36.21	94.72	6.8	86.82
DN-80	17336844	2467383946	35.33	93.99	7.28	86.97
DN-81	15069612	2172587622	35.05	94.19	6.51	86.96
DN-82	15710242	2248252318	35.39	94.05	6.68	88.22
DN-83	16909854	2427612786	35.05	94.29	7.29	88.03
DN-84	17470718	2511504198	34.79	94.16	7.56	88.72
DN-85	16969660	2406932350	35.88	93.74	7	85.88

DN-86	15405222	2215832844	36.43	93.75	6.55	83.91
DN-87	15791300	2230614655	35.97	93.92	6.47	86.81
DN-88	17198360	2434839917	35.59	93.92	7.21	88.85
DN-89	16145576	2322192982	35.54	94.08	6.87	86.82
DN-90	16044504	2306394607	35.19	94	6.93	87.68
DN-91	19792940	2832238469	35.37	93.89	8.37	89.35
DN-92	17551238	2520374524	35.06	94.27	7.55	88.85
DN-93	18558424	2640541395	35.56	94.05	7.69	86.51
DN-94	18288706	2638875312	34.98	94.2	7.84	90.13
DN-95	17594342	2529211156	35.86	94.1	7.54	89.17
DN-96	16565504	2322957782	36.08	93.93	6.66	85.44
DN-97	15590714	2214467010	35.98	93.99	6.56	86.6
DN-98	16635294	2353224492	35.73	93.98	6.79	86.53
DN-99	20397794	2964630642	34.68	94.35	9.06	92.59
DN-100	17565264	2523664483	35.21	94.15	7.49	88.69
DN-101	21085266	2930484765	35.95	94.15	8.27	89.8
DN-102	17293892	2512647209	34.87	94.15	7.57	88.67
DN-103	18742798	2641912250	36.36	93.8	7.55	89.2
DN-104	15688148	2213624481	36.7	93.71	6.44	85.35
DN-105	16231518	2350406050	35.88	94.13	6.99	87.46
DN-106	22567776	3095029521	36.23	94.06	8.69	89.95
DN-107	17606736	2406341255	37.04	93.83	6.72	85.96
DN-108	16989794	2400903156	36.43	93.76	7.01	87.36
DN-109	15267826	2132745800	37.07	93.73	6.06	83.89
DN-110	16740122	2345478402	36.72	93.87	6.74	85.87
DN-111	16984792	2444378503	35.97	93.9	7.34	88.33
DN-112	15688180	2192237935	36.94	93.9	6.33	84.9
DN-113	16471206	2307078747	36.65	93.56	6.68	86.67
DN-114	16051978	2241902524	36.81	93.78	6.49	85.94
DN-115	15723930	2222716923	36.1	93.95	6.53	87.22
DN-116	18526190	2526616191	36.77	93.67	7.1	88.69
DN-117	14283054	1966086646	36.92	94.12	5.54	80.51
DN-118	15406678	2172701867	36.29	94.11	6.28	83.58
DN-119	21324968	2918264374	37.36	93.61	8.06	86.7
DN-120	15114894	2043388920	37.55	93.55	5.62	83.01
DN-121	16150156	2238153458	37.04	93.64	6.5	87.69
DN-122	16712556	2296129918	37.24	93.59	6.41	83.61
DN-123	14498132	1957383702	37.32	93.59	5.36	82.83
DN-124	16182414	2238536270	36.91	93.66	6.34	85.04
DN-125	15713040	2183820725	36.96	93.71	6.09	84.93
DN-126	16276818	2281808255	36.9	93.91	6.6	85.16
DN-127	14212500	1970611855	37.03	93.4	5.34	82.74
DN-128	17847234	2528892019	36.45	94.36	7.4	88.59
DN-129	17179426	2478709758	36.13	94.31	7.44	89.5

DN-130	17522774	2508352323	35.5	94.65	7.47	88.68
DN-131	15400488	2161689538	36.52	94.42	6.29	84.39
DN-132	18966718	2721482954	35.59	94.66	7.95	87.16
DN-133	17144676	2444940380	35.98	94.59	7.16	86.83
DN-134	20234468	2820880176	36.14	94.6	8	89.85
DN-135	22281030	3253249322	35.63	94.59	9.14	92.4
DN-136	17008098	2438972021	35.84	94.57	7.25	87.23
DN-137	13698744	1911550847	37.04	94.15	5.46	80.02
DN-138	17222726	2479339511	36.25	94.56	5.43	83.13
DN-139	17246614	2438004541	35.81	94.6	7.12	86.77
DN-140	14394916	2001943399	37.12	94.33	5.75	83.87
DN-143	18887648	2634591502	36.43	94.57	6.99	86.17
DN-144	14481946	2084596196	35.9	94.46	6.22	85.33
DN-145	31071106	4499272194	35.54	94.65	12.57	92.78
DN-146	18254016	2569145977	36.22	94.6	7.46	88.29
DN-147	17470776	2517504901	35.92	94.7	7.55	89.83
DN-148	17652608	2529597071	36.17	94.61	7.45	88.03
DN-149	15458030	2176904911	36.21	94.69	6.39	86.39
DN-150	16654734	2406893364	34.93	94.11	7.21	88.66
DN-151	14441044	2044832688	35.94	94.12	6.05	85.57
DN-152	14250754	1923552906	37.3	94.49	5.35	81.65
DN-153	17387448	2395975642	36.49	94.48	6.82	86.66
DN-154	16557508	2368211771	35.8	94.45	7.18	91.04
DN-155	13699246	1915995383	36.51	93.93	5.57	82.96
DN-156	17502232	2461103199	35.88	93.94	7.13	86.4
DN-157	15116462	2204051820	35.09	94.07	6.16	85.52
总数 Total	2862190944	404387152818				
平均 Average			36.16	94.39	7.58	87.97

附表 2 154 个 F_2 样本 SNP 数据统计

Attached Table 2 The statistics of SNP data for 154 F_2 samples

样本号 SampleID	总 SNP 数 Total SNP	纯合 SNP Homozygous SNP	杂合 SNP Heterozygous SNP	纯合率(%) Homozygous rate	杂合率(%) Heterozygous rate
DN-1	1468497	762016	706481	51.89	48.11
DN-2	2166245	818014	1348231	37.76	62.24
DN-3	2214916	1114287	1100629	50.31	49.69
DN-4	1893324	853673	1039651	45.09	54.91
DN-5	2257667	1313685	943982	58.19	41.81
DN-6	2252634	1141843	1110791	50.69	49.31
DN-7	2047723	1090650	957073	53.26	46.74
DN-8	1688177	753131	935046	44.61	55.39
DN-9	1822746	821644	1001102	45.08	54.92
DN-11	1587008	662392	924616	41.74	58.26
DN-12	1787343	822379	964964	46.0	53.99
DN-13	1866720	991010	875710	53.09	46.91
DN-14	1641765	886500	755265	54.00	46.00
DN-15	2146110	958561	1187549	44.67	55.33
DN-16	1601653	645444	956209	40.30	59.70
DN-17	2070329	903105	1167224	43.62	56.38
DN-18	1607453	633327	974126	39.40	60.60
DN-19	1860335	916336	943999	49.26	50.74
DN-20	2220106	1161465	1058641	52.32	47.68
DN-21	1819144	868057	951087	47.72	52.28
DN-22	2035575	691445	1344130	33.97	66.03
DN-23	1749312	801715	947597	45.83	54.17
DN-24	1687915	798001	889914	47.28	52.72
DN-25	2195608	1082971	1112637	49.32	50.68
DN-26	2270017	1133196	1136821	49.92	50.08
DN-27	2035113	944600	1090513	46.42	53.58
DN-28	1972458	1052815	919643	53.38	46.62
DN-29	1993962	902909	1091053	45.28	54.72
DN-30	2073099	1178867	894232	56.86	43.14
DN-31	2758749	1475041	1283708	53.47	46.53
DN-32	1775336	845077	930259	47.60	52.40
DN-33	1816444	791154	1025290	43.56	56.44
DN-34	2213643	1142536	1071107	51.61	48.39
DN-35	2207026	1019658	1187368	46.20	53.80
DN-36	2442524	1146432	1296092	46.94	53.06
DN-37	1687016	572243	1114773	33.92	66.08
DN-38	2066050	1200970	865080	58.13	41.87
DN-39	2259478	831662	1427816	36.81	63.19

DN-40	2303713	1267616	1036097	55.02	44.98
DN-41	1489136	648504	840632	43.55	56.45
DN-42	2037312	886785	1150527	43.53	56.47
DN-43	2345890	1353278	992612	57.69	42.31
DN-44	1687016	743747	943269	44.09	55.91
DN-45	1962715	871168	1091547	44.39	55.61
DN-46	1966866	796440	1170426	40.49	59.51
DN-47	2094309	718239	1376070	34.29	65.71
DN-48	1989945	912309	1077636	45.85	54.15
DN-49	2035939	856515	1179424	42.07	57.93
DN-50	2100826	1183204	917622	56.32	43.68
DN-51	1803320	917900	885420	50.90	49.10
DN-52	2815734	839510	1976224	29.81	70.19
DN-53	1909081	957658	951423	50.16	49.84
DN-54	1858604	762305	1096299	41.01	58.99
DN-55	2163887	1222461	941426	56.49	43.51
DN-56	2038880	1112682	926198	54.57	45.43
DN-57	1461985	706806	755179	48.35	51.65
DN-58	1589047	752483	836564	47.35	52.65
DN-59	2013916	1015059	998857	50.40	49.60
DN-60	2051917	1349092	702825	65.75	34.25
DN-61	1972746	868182	1104564	44.01	55.99
DN-62	1792314	946827	845487	52.83	47.17
DN-63	1742536	672287	1070249	38.58	61.42
DN-64	1492898	609934	882964	40.86	59.14
DN-65	1955620	874199	1081421	44.70	55.30
DN-66	2273773	990521	1283252	43.56	56.44
DN-67	1688962	755764	933198	44.75	55.25
DN-68	1841646	934733	906913	50.76	49.24
DN-69	1658377	558849	1099528	33.70	66.30
DN-70	1486438	902278	584160	60.70	39.30
DN-71	1766722	719009	1047713	40.70	59.30
DN-72	2039951	1165416	874535	57.13	42.87
DN-73	1720336	858143	862193	49.88	50.12
DN-74	1629998	811086	818912	49.76	50.24
DN-75	1593352	1047614	545738	65.75	34.25
DN-76	1883973	685465	1198508	36.38	63.62
DN-77	1627001	666519	960482	40.97	59.03
DN-78	1840662	920523	920139	50.01	49.99
DN-79	1935086	1012535	922551	52.33	47.67
DN-80	2094227	1250050	844177	59.69	40.31
DN-81	1354276	690385	663891	50.98	49.02
DN-82	1438855	605158	833697	42.06	57.94
DN-83	2128556	1055168	1073388	49.57	50.43

DN-84	2041734	963444	1078290	47.19	52.81
DN-85	2001859	1173179	828680	58.60	41.40
DN-86	1761474	1045858	715616	59.37	40.63
DN-87	1461887	703043	758844	48.09	51.91
DN-88	1471967	669064	802903	45.45	54.55
DN-89	1484835	688893	795942	46.40	53.60
DN-90	1728918	845658	883260	48.91	51.09
DN-91	2022914	996246	1026668	49.25	50.75
DN-92	1954275	880420	1073855	45.05	54.95
DN-93	2105970	1308022	797948	62.11	37.89
DN-94	1686612	723598	963014	42.90	57.10
DN-95	1871736	766392	1105344	40.95	59.05
DN-96	1726158	957284	768874	55.46	44.54
DN-97	1754345	945085	809260	53.87	46.13
DN-98	1959451	1060327	899124	54.11	45.89
DN-99	1994189	703834	1290355	35.29	64.71
DN-100	2072927	924595	1148332	44.60	55.40
DN-101	1820500	693830	1126670	38.11	61.89
DN-102	1990565	965225	1025340	48.49	51.51
DN-103	1909743	1007918	901825	52.78	47.22
DN-104	1758300	939975	818325	53.46	46.54
DN-105	1791855	1010671	781184	56.40	43.60
DN-106	2041153	1007760	1033393	49.37	50.63
DN-107	1720313	851082	869231	49.47	50.53
DN-108	1705658	756184	949474	44.33	55.67
DN-109	1523272	744677	778595	48.89	51.11
DN-110	1698030	954884	743146	56.23	43.77
DN-111	2218379	1101335	1117044	49.65	50.35
DN-112	1683226	832922	850304	49.48	50.52
DN-113	1736763	855955	880808	49.28	50.72
DN-114	1728685	754698	973987	43.66	56.34
DN-115	1802794	844612	958182	46.85	53.15
DN-116	1684320	775184	909136	46.02	53.98
DN-117	1603201	1067693	535508	66.60	33.40
DN-118	1720669	959814	760855	55.78	44.22
DN-119	2219128	1323397	895731	59.64	40.36
DN-120	1644732	997508	647224	60.65	39.35
DN-121	1118269	598319	519950	53.50	46.50
DN-122	1719227	983502	735725	57.21	42.79
DN-123	1444300	694695	749605	48.10	51.90
DN-124	1721457	748723	972734	43.49	56.51
DN-125	1370207	557046	813161	40.65	59.35
DN-126	1797527	880077	917450	48.96	51.04
DN-127	1419664	719696	699968	50.69	49.31

DN-128	1652431	754618	897813	45.67	54.33
DN-129	1545280	776880	768400	50.27	49.73
DN-130	2039988	958805	1081183	47.00	53.00
DN-131	1596296	912576	683720	57.17	42.83
DN-132	2139094	1203507	935587	56.26	43.74
DN-133	1779689	864032	915657	48.55	51.45
DN-134	2076400	870665	1205735	41.93	58.07
DN-135	2038836	557394	1481442	27.34	72.66
DN-136	2118747	1064162	1054585	50.23	49.77
DN-137	1660389	946684	713705	57.02	42.98
DN-138	1498024	769616	728408	51.38	48.62
DN-139	1992463	1159533	832930	58.20	41.80
DN-140	1418312	652142	766170	45.98	54.02
DN-143	2085275	1020125	1065150	48.92	51.08
DN-144	1564056	723161	840895	46.24	53.76
DN-145	2491633	1095759	1395874	43.98	56.02
DN-146	1761433	721785	1039648	40.98	59.02
DN-147	1829055	665107	1163948	36.36	63.64
DN-148	1853280	898990	954290	48.51	51.49
DN-149	1945517	998102	947415	51.30	48.70
DN-150	1498190	689953	808237	46.05	53.95
DN-151	1560673	777498	783175	49.82	50.18
DN-152	1583099	992129	590970	62.67	37.33
DN-153	2014803	998667	1016136	49.57	50.43
DN-154	227974	136524	91450	59.89	40.11
DN-155	1556150	889848	666302	57.18	42.82
DN-156	1837461	1123784	713677	61.16	38.84
DN-157	1971280	1155198	816082	58.60	41.40
平均 Average	1850432	899758	950674	48.71	51.29