Theor Appl Genet (2007) 114:1019–1028
DOI 10.1007/s00122-006-0495-8

ORIGINAL PAPER

The use of MapPop1.0 for choosing a QTL mapping sample from an advanced backcross population

C. Birolleau-Touchard · E. Hanocq · A. Bouchez · C. Bauland · I. Dourlen · J. -P. Seret · D. Rabier · S. Hervet · J. -F. Allienne · Ph. Lucas · O. Jaminon · R. Etienne · G. Baudhuin · C. Giauffret

Received: 28 July 2006 / Accepted: 21 December 2006 / Published online: 14 February 2007

Abstract QTL detection is a good way to assess the genetic basis of quantitative traits such as the plant response to its environment, but requires large mapping populations. Experimental constraints, however, may require a restriction of the population size, risking a decrease in the quality level of QTL mapping. The purpose of this paper was to test if an advanced backcross population sample chosen by *MapPop 1.0* could limit the effect of size restriction and improve the QTL detection when compared to random samples. We used the genotypic and phenotypic data obtained for 280 genotypes, considered as the reference population. The "MapPop sample" of 100 genotypes was first compared to the reference population, and genetic maps, genotypic and phenotypic data and QTL results were analysed. Despite the increase in donor allele frequency in the MapPop sample, this did not lead to an increase of the genetic map length or a biased phenotypic distribution. Three QTL among the 10 QTL found in the reference population were also detected in the MapPop sample. Next, the MapPop sample results were compared to those from 500 random samples of the same size. The main conclusion was that the MapPop software avoided the selection of biased samples and the detection of false QTL and appears particularly interesting to select a sample from an unbalanced population.

Communicated by J.-L. Jannink.

C. Birolleau-Touchard · E. Hanocq · A. Bouchez · C. Bauland · I. Dourlen · J. -P. Seret · D. Rabier · S. Hervet · J. -F. Allienne · Ph. Lucas · O. Jaminon · R. Etienne · G. Baudhuin · C. Giauffret (✉)
INRA-USTL, UMR Stress abiotiques et différenciation des végétaux cultivés, Estrées-Mons, BP 50136, 80203 Péronne Cedex, France
e-mail: Catherine.Giauffret@mons.inra.fr

Present Address:
A. Bouchez
INRA, UMR CARRTEL, 75 av. de Corzent, BP 511, 74203 Thonon Cedex, France

Present Address:
C. Bauland
INRA-UPS-CNRS-INA.PG, UMR de Génétique Végétale, 91190 Gif-sur-Yvette, France

Introduction

The development of DNA markers and free QTL mapping software has largely facilitated QTL detection as an efficient tool to assess the genetic basis of quantitative traits such as the plant response to its environment, like abiotic stress. Field trials in various climatic conditions, and/or experiments under controlled conditions, are necessary to assess the variability of complex traits, and imply an increase in the number of measurements. The size of growth rooms or greenhouses limits the number of plants that can be studied at a time. In addition to a classical agronomic approach, the response of a plant to its environment should be evaluated by physiological and biochemical analyses to better understand the underlying mechanisms. These analyses are often costly and time consuming, and make a reduction of the size of the population under study desirable.

The detection power is an essential criterion for QTL mapping, and is defined by the number of true and false QTL detected (Charmet 2000). Reducing the

size of a QTL mapping population decreases the detection power (Charcosset and Gallais 1996), and as a consequence small effect (minor) QTL will not be detected in a small population. For example, a number of 100 doubled haploid (DH) lines seems to be a critical limit below which only large effect (major) QTL can be detected (Charmet 2000), and it is very difficult to detect minor QTL with less than 500 progenies (independently of markers density) (Tuberosa et al. 2003). Furthermore, reducing the population size increases the QTL confidence interval, as well as the risk of detecting false QTL. According to simulations by Bernardo (2004), for a trait controlled by ten QTL with an heritability of 0.50 and an alpha risk of 0.05, the false QTL detection rate is 0.33, 0.45 and 0.54 for mapping populations of, respectively, 2,000, 400 and 150 genotypes. The ability to locate a QTL according to its associated marker loci is limited by the effects of recombination (Soller et al. 1976), and the probability to observe recombinant events decreases with the number of individuals in the sample (Doerge 2002). The accuracy of QTL detection depends on the method of sampling individuals from a population. In a sample, the individuals can be chosen randomly, according to the phenotypic data (selective genotyping), or according to the genotypic data (selective phenotyping). Selective genotyping requires an 'a priori' decision on which trait to chose that represents the plant response, as only one trait at a time can be taken into account (Vales et al. 2005). In contrast, selective phenotyping does not imply such constrains, as shown by Vision et al. (2000) when developing the MapPop 1.0 software. This software was used by Doganlar et al. (2002) to construct a tomato core collection in order to keep as much as possible all genetic information from the total population. Recently, Vales et al. (2005) used it to choose a sample for barley rust tolerance QTL detection by selective phenotyping. Moreover, the interest of selective phenotyping to detect QTL was studied by simulation (Jin et al. 2004; Xu et al. 2005; Jannink et al. 2005).

The purpose of this paper is to evaluate the profit given by the MapPop1.0 software for QTL detection when sampling in an unbalanced population such as an advanced backcross (ABC) population. This kind of population is employed for QTL detection when one of the two parents presents some agronomic disadvantages that may hide its potential otherwise (Lewis and Goodman 2003). To minimise this kind of epistatic interactions, alleles from this parent are lowered to reduce their frequency. Since 1996, when Tanksley and Nelson first proposed this kind of population to study the genetic potential of exotic lines, ABC populations have been used for QTL detection in different species, for example tomato (Bernacchi et al. 1998a, b; Tanksley and Nelson 1996; Tanksley et al. 1996), rice (Moncada et al. 2001), and barley (Pillen et al. 2003, 2004). For our study we used genotypic and phenotypic data obtained from a maize ABC population of 280 genotypes, and MapPop 1.0 was used to select a smaller sample from this population. The QTL detection results in the MapPop sample were compared to those obtained in the reference population, as well as in 500 different random samples of the same size.

Materials and methods

Reference population

The ABC population of maize was obtained from crosses between two parental lines; F2 and F334. The recurrent parental line F2 is adapted to north-western European climate, whereas the donor line F334 is a highland tropical genotype which is late-flowering in temperate regions. The F_1 generation was backcrossed twice with the recurrent parental line to obtain a BC_2 generation. Then, the genotypes were self-pollinated once to obtain 280 lines of the BC_2S_1 generation.

The agronomic trait considered in this study was the number of days from sowing until female flowering. Since this trait is measured easily, reproducibly and at low cost, it allowed a phenotypic evaluation on the whole population in nine environments (six to two sites across France for 2 years), and showed an heritability of 0.83.

Reference genetic map

In the absence of software to directly construct a genetic map from genotypic data of a BC_2S_1 population, we used three different softwares to build our map. First, Mapmaker (Lander et al. 1987; Lincoln et al. 1992) was used to get a reliable order for markers. Unfortunately, distances based on "F_3 intercross mating" formulas were not well suited. Then QMap (by courtesy of JC Nelson) gave the LOD score and the recombination frequencies of pairs of loci (R^2) with appropriate BC_2S_1 formulas. Finally, Joinmap3.0 (Van Ooijen and Voorrips 2001) calculated the genetic distances directly from the Mapmaker marker order and from the QMap estimated LOD and R^2 values. These calculations are no longer dependent on the population type. The maps were drawn with MapChart 2.1 (Voorrips 2002). The reference map, obtained from the total ABC population, contained 128 SSR markers and its size was 1,551 cM (marker density of 12.11 cM).

Population sampling

The MapPop sample

MapPop 1.0 is a software designed to optimise the distribution of recombination points all over the genome when building high-density whole-genome maps. We used MapPop1.0 to select a sample supposedly containing as much genetic information as possible to construct a map or to detect QTL. The selection criterion used to choose the MapPop sample was the expected Maximum Bin Length (eMBL), the expected maximum distance between two recombination points. The closer the sample eMBL is to the reference population eMBL, the more the sample is representative for the reference population. The sample eMBL depends on the sample size desired and on the computational time used for sampling. In other words, the best sample selected by MapPop1.0 is the sample with the smallest eMBL given a defined computational time and a given sample size. After testing several computational times (data not shown), we chose the one after which the eMBL no longer improved. Sampling of several population sizes were tested with this optimum time. Sample sizes were chosen in order to minimise the eMBL with respect to experimental limits for phenotypic evaluation. Finally, we obtained what we considered as the best sample, named the "MapPop sample" in the following study.

Random samples

Five hundred sub-populations were generated by a random sampling of the reference population. The size of these samples was chosen according to the MapPop sample size, and genotypes were sampled without replacement.

QTL detection

In the absence of any Interval Mapping QTL detection software suited for the population type, we detected QTL by linear regression. With the genetic map and the genotypic data as basis, Grafgen software (Servin et al. 2002) enabled us to calculate for each individual the probabilities of the presence of each possible marker genotype (homozygous F2, homozygous F334 and heterozygous) at each 2 cM along the ten chromosomes. On the basis of these probabilities, we calculated the F334 donor allele dose at each 2 cM.

A linear regression model was applied each 2 cM with the PROC GLM procedure of the SAS software (version 8.1) (1991). The model is the additive model: $Y_i = \mu + \alpha_i + E_i$, where Y_i is the performance of the genotype i , μ is the general mean, α_i is the genotype main effect and E_i is the error. The phenotypic data were the mean data over all the environments. LOD values were calculated from the F values as proposed by Haley and Knott (1992) and Lander and Botstein (1989). The LOD threshold was determined with 500 permutations on the reference population and on the MapPop sample. The LOD threshold of the MapPop sample was also used for QTL detection in the equally sized populations sampled randomly. The LOD thresholds for alpha-risks of 5, 10 and 25% were, respectively, 2.82, 2.55 and 2.04 for the MapPop sample, and 2.76, 2.50 and 2.02 for the reference population. The confidence interval on a QTL position was determined by the 1 LOD unit drop-off method.

Comparison between the MapPop sample and the random samples

QTL detection was performed on the reference population (called standard QTL detection), the MapPop sample and the 500 random samples.

True and false QTL

Detection power was defined by the number of true and false QTL detected (Charmet 2000). A QTL was considered true or false when its LOD peak fell in or out the confidence interval of a QTL detected in the reference population, respectively.

Comparison of LOD patterns

Comparisons of LOD patterns were assessed by calculating the Pearson correlation coefficient (PROC CORR procedure of SAS, version 8.1, 1991) between the LOD values for reference population and those for the MapPop and random samples. High correlation coefficients are indicative for a high similarity of the LOD patterns, but allow no conclusions with respect to the detection of QTL.

Results

A sample size of 100 genotypes

The sample size was determined according to the MapPop1.0 results and the experimental constraints. The eMBL of the reference population was 4.43 cM. The eMBL of the MapPop sample varied from 13.62 to 5.57 cM for sample sizes of 25 to 150, respectively

(Fig. 1). Between 50 and 100 genotypes, the eMBL decreased from 9.42 to 6.36 cM, while between 100 and 150 genotypes, the eMBL decreased from 6.36 to 5.57 cM, a drop-off of less than 1 cM. Considering experimental constraints, especially when assessing metabolic functions, the most convenient sample size would be between 100 and 125 lines. We choose a sample of 100 genotypes for the MapPop sample and the random samples, about one-third of the reference population size.

Genotypic data

Donor allele frequency

In the reference population, distribution of the genotypes according to their percentage of donor alleles (Fig. 2a) revealed a peak at 10–12% and a mean of 13.2%. For the distribution of the percentages for homozygous donor alleles, the peak was at 8–10%, and the mean 6.95% (Fig. 2b). These values were close to the theoretical percentages of 12.5 and 6.25%, respectively. In the MapPop sample these values had moved to higher percentages (Fig. 2a, b); a peak at 14–16% for the donor allele percentage (mean 15.6%), and a peak at 8–10% for the homozygous donor allele percentage (mean 7.9%). Illustrated in Fig. 2 are also the donor allele percentages for the best and worst random samples (as determined according to the number of true and false QTL detected; see below). The peaks and the mean values were similar to those of the reference population, but the worst sampling resulted in a flat-topped donor allele percentage distribution caused by a decrease in the number of genotypes containing 10–14% donor alleles (Fig. 2a).

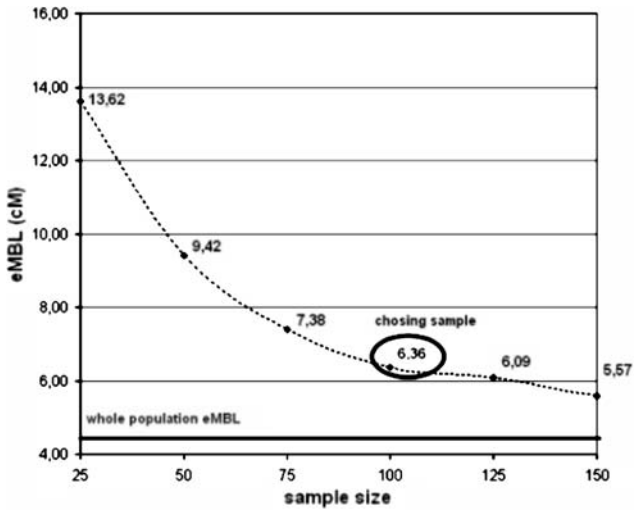

Fig. 1 eMBL as a function of the sample size (*dashed line*) compared to the reference population eMBL (*black line*)

Genetic map

The genetic map obtained with the MapPop sample was quite similar to the one obtained with the reference population (Fig. 3). The MapPop map was smaller (1,304 cM) than the reference map (1,551 cM), and had acquired a mean marker interval of 10.77 cM (12.11 for the reference map). Upon sampling, polymorphisms for seven markers located on three regions of the reference map (chromosomes 1, 2 and 6) were no longer detected. As a consequence, distances between markers flanking these regions were significantly decreased (chromosomes 1 and 2), or the linkage group was parted (chromosome 6). Moreover, linkage groups were broken due to the decrease in polymorphisms (chromosomes 3 and 7). A total of seven segments were lost; among them six had flanking markers separated by more than 20 cM. Without these seven segments, the reference map size would be 1,375 cM, similar to the MapPop map size. On the chromosomes 4, 5, 8, 9 and 10, all the markers were located in the same order, only changes in distances were observed. These results show that except for seven segments the map structure was conserved with the MapPop sample data.

The QTL detection was done on the reference map for the reference population as well as for the samples (MapPop and random).

Phenotypic data and QTL detection

The phenotypic distribution of the number of days until female flowering for the reference and sampling populations are shown in Fig. 4. The phenotypic distributions were similar between the reference population and the MapPop sample, even though in the MapPop sample the relative number of late-flowering genotypes had increased. In contrast, both the worst and the best random samples presented less late-flowering phenotypes, and the worst random sampling resulted in a higher peak with a restricted variance leading to a poor population representation.

LOD patterns for QTL detection in the reference and sample populations are shown in Fig. 5. The correlation value between the LOD patterns of the reference population and the MapPop sample was 0.74, whereas for the random samples this value varied from 0.27 to 0.84. Most of the 500 random samples (93.4%) had a correlation value smaller than the MapPop sample one.

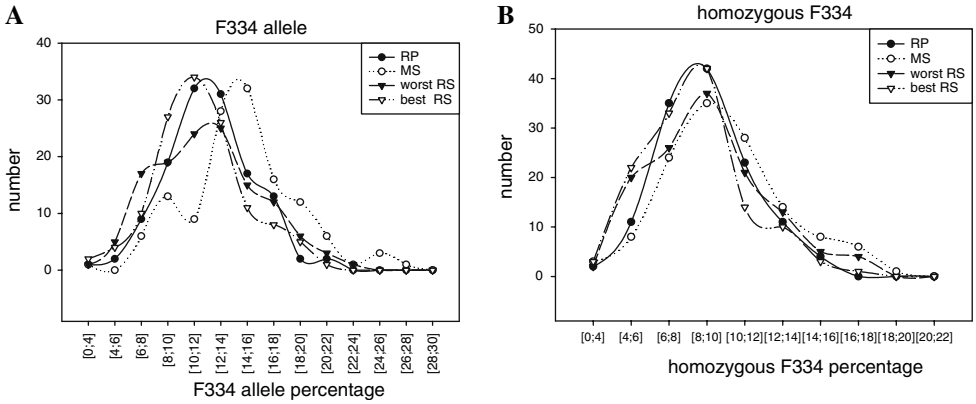

Fig. 2 Distribution of the genotypic data. **a** Percentage of donor allele and **b** percentage of homozygous donor alleles. *RP* reference population, *MS* MapPop sample, *RS* random sample

The standard QTL detection resulted in four QTL detected at a 5% threshold and six smaller QTL at a 25% threshold. The first ones were located on the chromosomes 3 (LOD = 3.41), 7 (3.98), 8 (2.88) and 10 (2.77), whereas the additional six were located on the chromosomes 1 (4 QTL) and 5 (2 QTL) with LOD values between 2.05 and 2.46.

In the MapPop sample, one QTL was detected at a 10% threshold on chromosome 7 whereas two QTL were detected at a 25% threshold on chromosomes 1 and 10, each corresponding to QTL already detected in the reference population. No false QTL were detected. Chromosome 1 represents a special case because of its high marker density (8.29 cM) and its LOD profile: four close QTL (at 30, 70, 100 and 110 cM) detected at a low threshold (25%) in the reference population. In the MapPop sample, only one QTL was detected on this chromosome (at 70 cM). On the other chromosomes, when the QTL were detected at a 25% threshold in the reference population, they were no longer detected in the MapPop sample. Among the four QTL detected at a 5% threshold in the reference population, two QTL were still detected on chromosomes 7 and 10, both with relative high marker densities of 10.71 and 11.16 cM, respectively. The two QTL on chromosomes 3 and 8, both with relative low marker densities of 18.07 and 16.08 cM, respectively, were no longer detected. When the QTL were detected in the MapPop sample, they were detected at a lower threshold (25 or 10%) than the 5% threshold for the reference population, but their location was the same.

In Fig. 6 the number of true and false QTL detected in the MapPop and random samples are shown. Among the 500 random samples, a maximum of seven true QTL were detected together with one to three false QTL. The maximum number of true QTL detected without detecting false QTL was five. There were 11 random samples in this case (Fig. 6). Among them, the best random sample had a LOD pattern showing a correlation value of 0.75 with the LOD pattern of the reference population. In 73 random samples no true QTL were detected and false QTL were between 0 and 4. Among them, the worst random sample had a low correlation value of 0.28, and allowed the detection of zero true and four false QTL (Fig. 5). At least one false QTL or only false QTL were detected in, respectively, 41.4 and 4.8% of the random samples. Neither true nor false QTL was detected in 9.8% of the random samples. On the whole, the mean number of QTL detected with random samples was 1.9 for true QTL and 0.7 for false QTL (2.2 when random samples with no QTL were not taken into account). QTL confidence intervals were similar among the reference population, the MapPop sample and the random samples. The best random sample showed a genotypic and phenotypic distribution that was closer to the reference population distributions than the worst sample (cf. Figs. 2, 4).

Discussion

The experimental design and the population size have an important influence on the accuracy of QTL detection, and this is particularly true for an ABC population. In this study, given the choice of the experimental constraints, the genetic map, and QTL detection characteristics, a sample size of 100 genotypes was considered as a good compromise. In the experimental studies, population sizes for QTL studies vary from 100 to over 400 progenies (Tuberosa et al. 2003), whereas 100 seems to be a commonly employed population size (Vales et al. 2005). From a theoretical point of view, 100 is a limited population size to detect QTL. To have the same detection power, a backcross population needs more individuals than an F_2 (Soller et al. 1976). Two populations of 300 F_2 individuals and 150 DH lines gave similar estimates of QTL position and effect

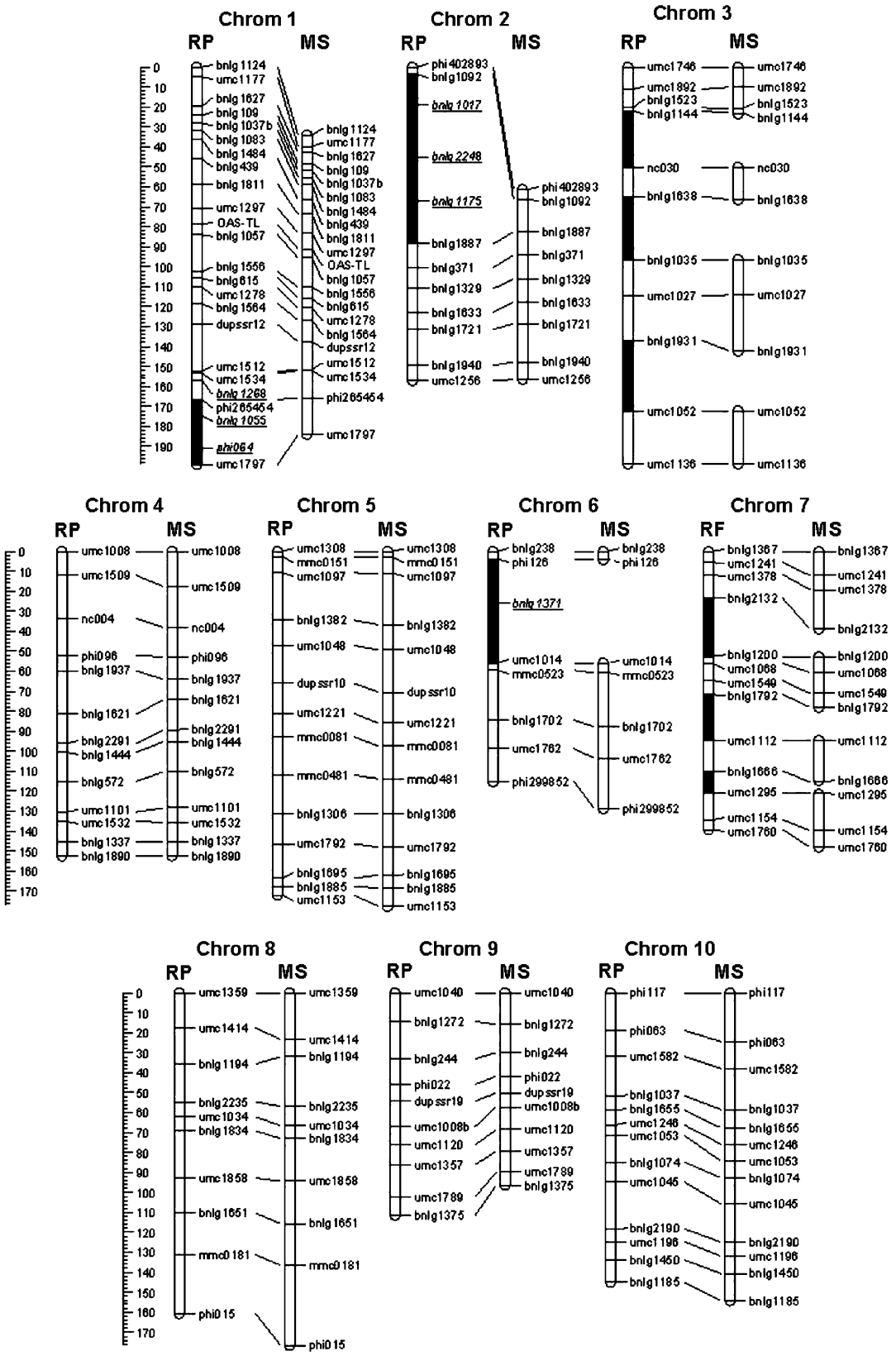

Fig. 3 Comparison of the genetic maps from the reference population and the MapPop sample. The scales are in cM. *RP* = reference population, *MS* = MapPop sample

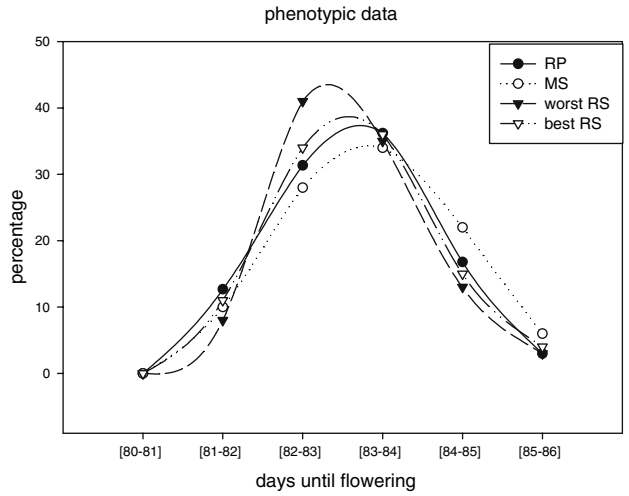

Fig. 4 Distribution of the phenotypic data. *RP* reference population, *MS* MapPop sample, *RS* random sample

(Hyne et al. 1995), whereas RILs could be used with smaller sample sizes than backcrosses (Asins 2002). A simulation study found that the optimal size was of 1050 F2 genotypes and 8400 BC genotypes (Soller et al. 1976).

We used the eMBL (expected maximum bin length) as criterion to choose the MapPop sample in order to reduce the size of the maximum interval between two recombination points and avoid the risk of loosing a QTL in those regions. However, the use of the SSBL (sum of squares of bin length) could improve the sample when the markers are widely spaced (Vision et al. 2000).

The BC_2S_1 population studied in this paper was unbalanced, presenting a low percentage of the donor alleles. In order to optimise the positions of recombination points, MapPop1.0 preferentially chooses from a population the genotypes with donor alleles which are sparse in the genome. The MapPop sampling resulted in an increase in the donor alleles frequencies, and as a consequence a longer genetic map could be expected. This was not the case. In fact, the map obtained from the MapPop sample was smaller and denser than the reference map. This was due to a loss of segments with relative low marker densities. Moreover, some single markers could not be mapped since genotypes allowing the detection of their polymorphism were not sampled (bnlg1175 on chromosome 2, bnlg1371 on chromosome 6). Interval distances between flanking markers were then increased or decreased. A decreased or increased map size reflects a smaller or higher number of recombination events, respectively. When the new distance computed within the sample population is above a given threshold considered to define linkage groups, the consequence is fragmentation of the chromosome. Adding a marker could be an easy way to improve the map, less time consuming and less expensive than phenotyping plants in a larger sample. When the new distance was shorter, this could be partly due to an increase of the number of markers having segregation distortion. Forty markers in the MapPop sample have distortion against 11 in the reference population. For example, in the MapPop sample, on chromosome 2, bnlg1092, bnlg1017, and bnlg2248 have distortion and an excess of homozygous donor alleles.

When the segments lost in the MapPop sample map were not taken into account, the size of the MapPop map was only slightly superior to the size of the reference map. This could be the consequence of the lower number of recombination events in the ABC population compared to a RIL population that limited the possibilities of optimisation.

A map density between 10 and 15 cM helps to maintain the detection power. This is the usual advice for QTL detection. Increasing the map beyond such a density does not improve QTL detection power (Asins 2002; Piepho 2000; Tuberosa et al. 2003). The QTL detected with LOD-thresholds of 5% on the reference population were also detected in the MapPop sample when the map region had a good marker density, i.e. lower than 12 cM (chromosomes 7 and 10), but were not detected when the map region had a marker density of more than 15 cM (chromosomes 3 and 8). According to Xu et al. (2005), marker spacing affects the precision with which crossing-over are detected in the reference population. A modest increase in marker density can counteract the effects of increased crossing-over and obtain equivalent power over the whole map.

An increase in the donor allele frequency might cause a bias in the phenotypic distribution, but it was not the case. In presence of such a bias, the QTL detection would not be valid. This is exemplified by the worst random sample showing a phenotypic distribution dissimilar from that of the reference population. The sampling effect on the phenotypic distribution would probably have been higher in the case of a major QTL. In that case, the increase of the donor allele percentage at the major locus would have induced a strongly biased phenotypic distribution toward the donor phenotype value.

In an unbalanced backcross population, the QTL detection relies on the number of donor alleles bringing polymorphism. In the MapPop sample, the increase in donor allele percentage corresponded to a decrease in the number of markers with a deficiency of donor alleles compared to the theoretical percentage,

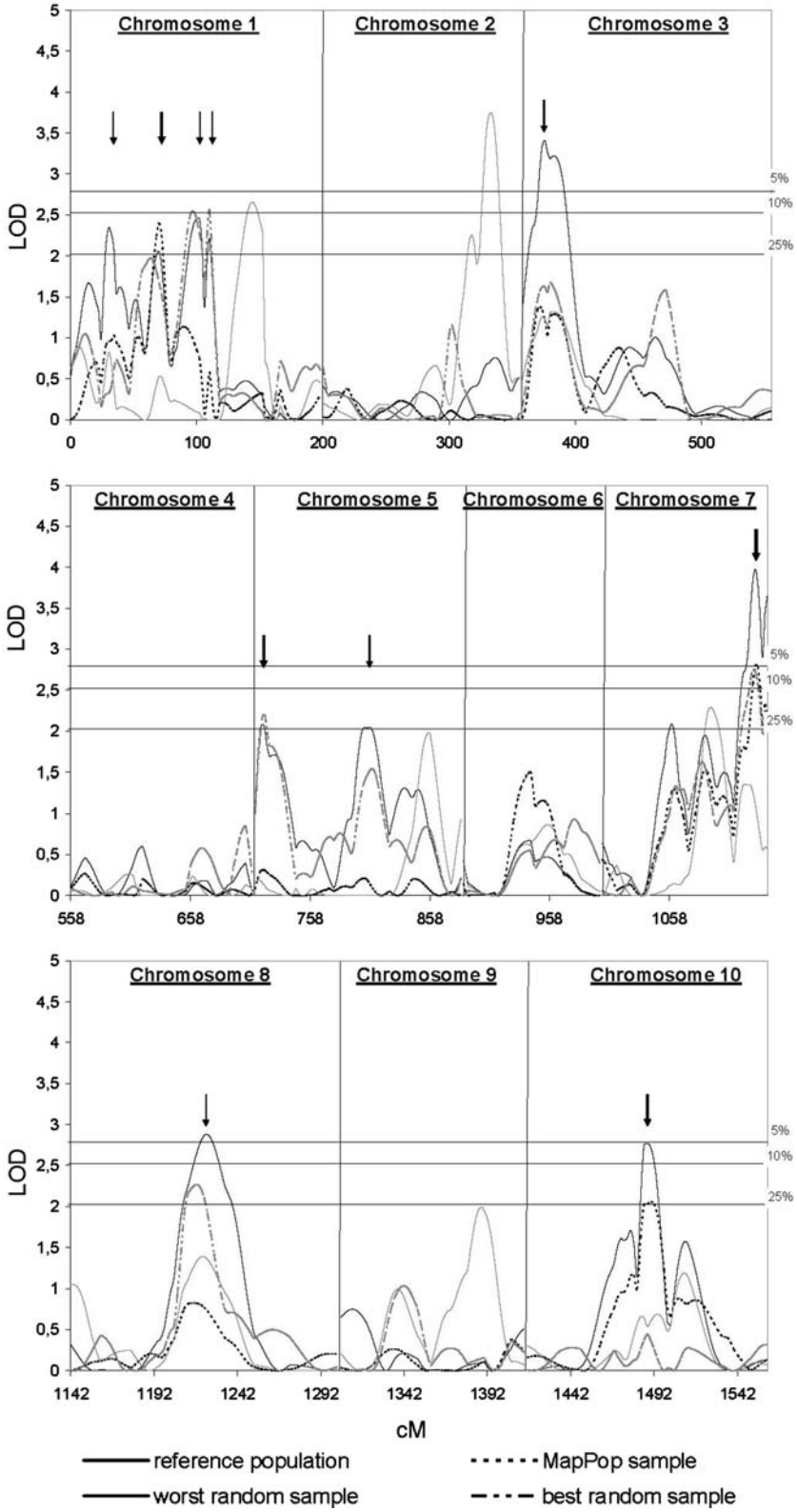

Fig. 5 Comparison of the LOD profiles of the reference population, MapPop sample, the best random sample and the worst random sample. *Arrows* show the QTL detected with the reference population and the *biggest arrows* show the QTL both detected with the reference population and the MapPop sample

whereas these markers increased in the best and the worst random samples. Among the 128 markers, there are 26 markers presenting a deficiency of donor alleles in the MapPop sample, against respectively 52, 56 and 64 markers in the reference population, the worst random sample, and the best random samples. The MapPop sampling could minimise the risk of having markers with small numbers of donor alleles, and thus

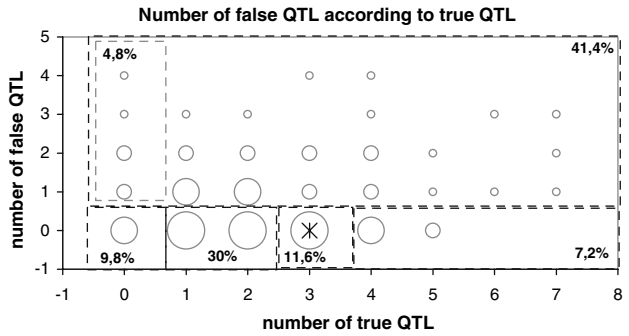

Fig. 6 Number of false QTL as a function of true QTL for the MapPop sample (*cross*) and the random samples (*spots*). Spots' sizes represent the number of random samples with the described combination of false versus true QTL

the risk of detecting false QTL. When the detection of QTL relies on one or two individuals carrying the donor allele compared to the rest of the population, the phenotypic evaluation has to be highly reliable.

The trait we studied was an agronomic trait with a high heritability: it was easy to measure on the large reference population and its evaluation was highly reliable. However, the more heritable a trait is, the smaller the risk of loosing QTL (Gallais and Rives 1993) and the smaller the risk of detecting a false QTL (Charcosset and Gallais 1996). The results with a low heritable trait should not have been the same. This could be the case with physiological and biochemical measurements, which are employed to assess metabolism and need to be studied on small populations because they are expensive and/or time-consuming, as they are often less heritable than agronomic ones (between 0.36 and 0.62 according to Fracheboud et al. 2004 and Paterson et al. 2003).

For the standard QTL detection, we choose a high alpha-risk of 25%, which is a prospecting threshold. All the QTL detected have to be confirmed, but it means that 25% of the QTL may be false. In a first attempt we took the same alpha-risk for the reference population and the samples. However, because of their size, the power of the test is lower in the samples, and the alpha-risk had to be lowered to detect QTL. Among the three QTL detected in the MapPop sample, two QTL (on chromosomes 1 and 10) were also found in a study where several flowering trait QTL were analysed together by a meta-analysis approach (Chardon et al. 2004). The QTL found by this method are probably reliable and confirm two of the three QTL we found in the MapPop sample.

Other risks related to small population sizes are shifted or increased confidence intervals for QTL positions (Hyne et al. 1995). It was not the case in this study, not for the MapPop sample and neither for the best and the worst random sample. Estimations of the genetic effect have not been checked, but there is a risk of overestimating them (Utz et al. 2000).

In a balanced population the increase in one allele and the lack of polymorphism at some markers would be much reduced. The risk of allele loss in RILs is almost absent, but increases as the population gets more unbalanced. According to Vales et al. (2005), the number of QTL detected in a DH population did not change in random samples or in a selective phenotyping sample chosen by MapPop1.0 when sample sizes were between 50 and 100. The selective approach became superior to the random sampling when the sample size increased above 100. This suggests that the use of MapPop 1.0 would be more valuable for sample selection from an unbalanced population than from a balanced population.

In conclusion, the MapPop 1.0 software can be applied successfully to sample unbalanced populations for prospective QTL analysis, provided a genetic map with a marker density of at least 10 cM is available. This may be of particular interest when long and expensive measurements are considered to further investigate a trait of interest.

Acknowledgments The data collection was supported by Genoplante, the French consortium for plant genomics (http://www.genoplante.com). The data analysis was part of a PhD work granted by the Conseil Régional de Picardie (http://www.cr-picardie.fr) We thank A.-L. Lainé and N. Bahrman for their technical advises for genotyping. We thank P. Barre of INRA, Lusignan, France and J.C. Nelson of Department of Plant Pathology, Kansas State University, USA for their technical and scientific help for the genetic mapping. J.C. Nelson supplies the QMap software. We thank S. Carof, X. Charrier, D. Denoue, M. Dupin, F. Lardière, and G. Leau for their contribution to the phenotyping of the population in the different locations. We thank Theo Hendricks for his valuable comments and suggestions on the manuscript.

References

Asins MJ (2002) Present and future of quantitative trait locus analysis in plant breeding. Plant Breed 121:281–291

Bernacchi D, Beck-Bunn T, Emmatty D, Eshed Y, Inai S, Lopez J, Petiard V, Sayama H, Uhlig J, Zamir D, Tanksley S (1998a) Advanced backcross QTL analysis of tomato. II. Evaluation of near-isogenic lines carrying single-donor introgressions for desirable wild QTL-alleles derived from Lycopersicon hirsutum and L. pimpinellifolium. Theor Appl Genet 97:170–180

Bernacchi D, Beck-Bunn T, Eshed Y, Lopez J, Petiard V, Uhlig J, Zamir D, Tanksley S (1998b) Advanced backcross QTL analysis in tomato. I. Identification of QTLs for traits of agronomic importance from Lycopersicon hirsutum. Theor Appl Genet 97:381–397

Bernardo R (2004) What proportion of declared QTL in plants are false? Theor Appl Genet 109:419–24

Charcosset A, Gallais A (1996) Estimation of the contribution of quantitative trait loci (QTL) to the variance of a quantitative trait by means of genetic markers. Theor Appl Genet 93:1193–1201

Chardon F, Virlon B, Moreau L, Falque M, Joets J, Decousset L, Murigneux A, Charcosset A (2004) Genetic architecture of flowering time in maize as inferred from quantitative trait loci meta-analysis and synteny conservation with the rice genome. Genetics 168:2169–2185

Charmet G (2000) Power and accuracy of QTL detection: simulation studies of one-QTL models. Agronomie 20:309–323

Doerge R (2002) Mapping and analysis of quantitative trait loci in experimental populations. Nat Rev Genet 3:43–52

Doganlar S, Frary A, Ku H, Tanksley S (2002) Mapping quantitative trait loci in inbred backcross lines of Lycopersicon pimpinellifolium (LA1589). Genome 45:1189–1202

Fracheboud Y, Jompuk C, Ribaut J, Stamp P, Leipner J (2004) Genetic analysis of cold-tolerance of photosynthesis in maize. Plant Mol Biol 56:241–253

Gallais A, Rives M (1993) Detection, number and effects of QTLs for a complex character. Agronomie 13:723–738

Haley C, Knott S (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. Heredity 69:315–324

Hyne V, Kearsey M, Pike D, Snape J (1995) QTL analysis: unreliability and bias in estimation procedures. Mol Breed 1:273–282

Jannink JL (2005) Selective phenotyping to accurately map quantitative trait loci. Crop Sci 45:901–908

Jin C, Lan H, Attie AD, Churchill GA, Bulutuglo D, Yandell BY (2004) Selective phenotyping for increased efficiency in genetic mapping study. Genetics 168:2285–2293

Lander E, Botstein D (1989) Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. Genomics 121:185–199

Lander E, Green P, Abrahamson J, Barlow A, Daly M, Lincoln S, Newburg L (1987) MAPMAKER: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. Genomics 1:174–181

Lewis RS, Goodman MM (2003) Incorporation of tropical maize germplasm into inbred lines derived from temperate x temperate-adapted tropical line crosses: agronomic and molecular assessment. Theor Appl Genet 107:798–805

Lincoln S, Daly M, Lander E (1992) Constructing genetic maps with MAPMAKER/EXP3.0, 3rd edn. Whitehead Institute Technical Reports

Moncada P, Martínez CP, Borrero J, Chatel M, Guimaraes HGJrE, Tohme J, McCouch SR (2001) Quantitative trait loci for yield and yield components in an Oryza sativa × Oryza rufipogon BC2F2 population evaluated in an upland environment. Theor Appl Genet 102:41–52

Paterson A, Saranga Y, Menz M, Jiang C, Wright R (2003) QTL analysis of genotype × environment interactions affecting cotton fiber quality. Theor Appl Genet 106:384–396

Piepho H (2000) Optimal marker density for interval mapping in a backcross population. Heredity 84:437–440

Pillen K, Zacharias A, Leon J (2003) Advanced backcross QTL analysis in barley (Hordeum vulgare L.). Theor Appl Genet 107:340–352

Pillen K, Zacharias A, Leon J (2004) Comparative AB-QTL analysis in barley using a single exotic donor of Hordeum vulgare ssp spontaneum. Theor Appl Genet 108:1591–1601

SAS institute Inc (1991) SAS user's guide: release 8.1 eds SAS Institute, Cary, North Carolina

Servin B, Dillmann C, Decoux G, Hospital F (2002) MDM: a program to compute fully informative genotype frequencies in complex breeding schemes. J Hered 93:227–228

Soller M, Brody T, Genizi A (1976) On the power of experimental designs for the detection of linkage between marker loci and quantitative loci in crosses between inbred lines. Theor Appl Genet 47:35–39

Tanksley S, Nelson J (1996) Advanced backcross QTL analysis: a method for the simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. Theor Appl Genet 92:191–203

Tanksley SD, Grandillo S, Fulton TM, Zamir D, Eshed T, Petiard V, Lopez J, Beck-Bunn T (1996) Advanced backcross QTL analysis in a cross between an elite processing line of tomato and its wild relative L. pimpinellifolium. Theor Appl Genet 92:213–224

Tuberosa R, Salvi S, Sanguineti M, Maccaferri M, Giuliani S, Landi P (2003) Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. Plant Soil 255:35–54

Utz H, Melchinger A, Schon C (2000) Bias and sampling error of the estimated proportion of genotypic variance explained by quantitative trait loci determined from experimental data in maize using cross validation and validation with independent samples. Genetics 154:1839–1849

Vales M, Schon C, Capettini F, Chen X, Corey A, Mather D, Mundt C, Richardson K, Sandoval-Islas J, Utz H, Hayes P (2005) Effect of population size on the estimation of QTL: a test using resistance to barley stripe rust. Theor Appl Genet 111:1260–1270

Van Ooijen J, Voorrips R (2001) Joinmap 3.0, software for the calculation of genetic linkage maps. Plant Research International, Wageningen

Vision T, Brown D, Shmoys D, Durrett R, Tanksley S (2000) Selective mapping: a strategy for optimizing the construction of high-density linkage maps. Genetics 155:407–420

Voorrips R (2002) MapChart: software for the graphical presentation of linkage maps and QTLs. J Hered 93:77–78

Xu Z, Zou F, Vision T (2005) Improving quantitative trait loci mapping resolution in experimental crosses by the use of genotypically selected samples. Genetics 170:401–408