

TABLE 1

The parameters of the simulated genetic model

|  |                                  |
|--|----------------------------------|
|  |                                  |
| Map per chromosome <sup>a</sup>                      |                                  |
| Number of chromosomes is the total number of morgans | 10                               |
| Mutation rate of QTL                                 | $2.5 \times 10^{-3}$             |
| Distribution of additive mutational effects          | Gamma(1.66; 0.4)                 |
| Dominance of QTL effects                             | 0                                |
| Mutation rate of marker loci                         | $2.5 \times 10^{-3}$             |
| Population structure                                 |                                  |
| Generations 1–1000                                   | Ideal <sup>b</sup> , $N = 100$   |
| Generation 1001                                      | Ideal <sup>b</sup> , $N = 200$   |
| Generation 1002                                      | 20 half-sib families, $N = 2000$ |
| Generation 1003 and later                            | Ideal <sup>b</sup> , $N = 2000$  |
| Marker genotyping                                    | Generations 1001 and later       |
| Phenotypic recording                                 | Generations 1001 and 1002        |

<sup>a</sup> M, marker position; Q, QTL position.<sup>b</sup> Ideal denotes a population structure where the effective size equals the actual population size. This structure is simulated by giving every male (female) in generation  $t - 1$  an equal probability of becoming the sire (dam) of animal  $i$  in generation  $t$ , which implies no selection and random mating of males and females.