

Comparing strategies of genomic selection to increase oil palm fresh fruit bunch yield

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Introduction

Genomic selection (GS) can increase hybrid performance in crossbred individuals. Heterosis in a complex trait can result from multiplicative interaction between more simple and additive components. In oil palm, the bunch production is the product of bunch weight (ABW) and bunch number (BN), two additive and negatively correlated traits. Oil palm breeding relies on reciprocal recurrent selection (RRS) between two complementary populations for ABW and BN, usually Deli and an African population like La Mé.

This study aimed at evaluating the potential of reciprocal recurrent genomic selection (RRGS) as an alternative to conventional RRS.

Material and methods

We simulated two realistic oil palm breeding populations (Fig. 1) and compared over four generations RRGs with RRS (Fig. 2). The goal of all breeding strategies was to select the best individuals in the 2 parental populations for hybrid performance on bunch production. For RRGs, we used 2500 SNP and the phenotypes of hybrids as data records in the GBLUP method to obtain the parental genomic estimated breeding values. We studied the effects of 4 parameters on the selection response in hybrids: (1) the molecular data used to calibrate the GS model: in RRGs_PAR, we only used parental genotypes and in RRGs_HYB we also used genotypes of hybrid individuals, taking into account the parental origin of marker alleles; (2) the frequency of calibration of GS model [every generation, every 2 or every 4 generations]; (3) for RRGs_HYB, the number of genotyped hybrids [300, 1000, 1700 individuals] and (4) the number of selection candidates [120, 300 individuals].

Results and discussion

With RRS the annual selection response in hybrid bunch production was 0.30% (Fig. 3). The highest annual selection response was made by RRGs_HYB with progeny-tests every four generations, 300 candidates and at least 1,000 genotyped hybrids. **The annual response was 0.49%, ie almost two thirds higher than annual response of RRS (P<0.01).**

With RRGs_HYB, the annual selection response was 0.06% higher when the selection was made among 300 individuals than 120 individuals (P<0.001). The annual selection response was similar with progeny-tests every 2 and every 4 generations, but 0.10% higher than with progeny-tests every generation (P<0.001). The annual selection response was similar with 1,000 and 1,700 genotyped hybrids, but 0.13% higher than with 300 genotyped hybrids (P<0.001).

With RRGs_PAR, the annual selection response was 0.05% higher when the selection was made among 300 individuals than 120 individuals (P<0.01). The annual selection response was similar with progeny-tests every 2 and every 4 generations, but 0.07% higher than with progeny-tests every generation (P<0.01).

Conclusion

Both RRGs_HYB and RRGs_PAR could lead to a much higher selection response for FFB in hybrids than RRS, because they allowed reducing the generation interval and increasing selection intensity.

The best strategy was RRGs_HYB with progeny-tests every 4 generations, 300 candidates and genotyping at least 1,000 hybrids. However, RRGs_PAR with progeny-tests every 2 or every 4 generations and 300 selection candidates was an interesting (and cheaper) alternative.

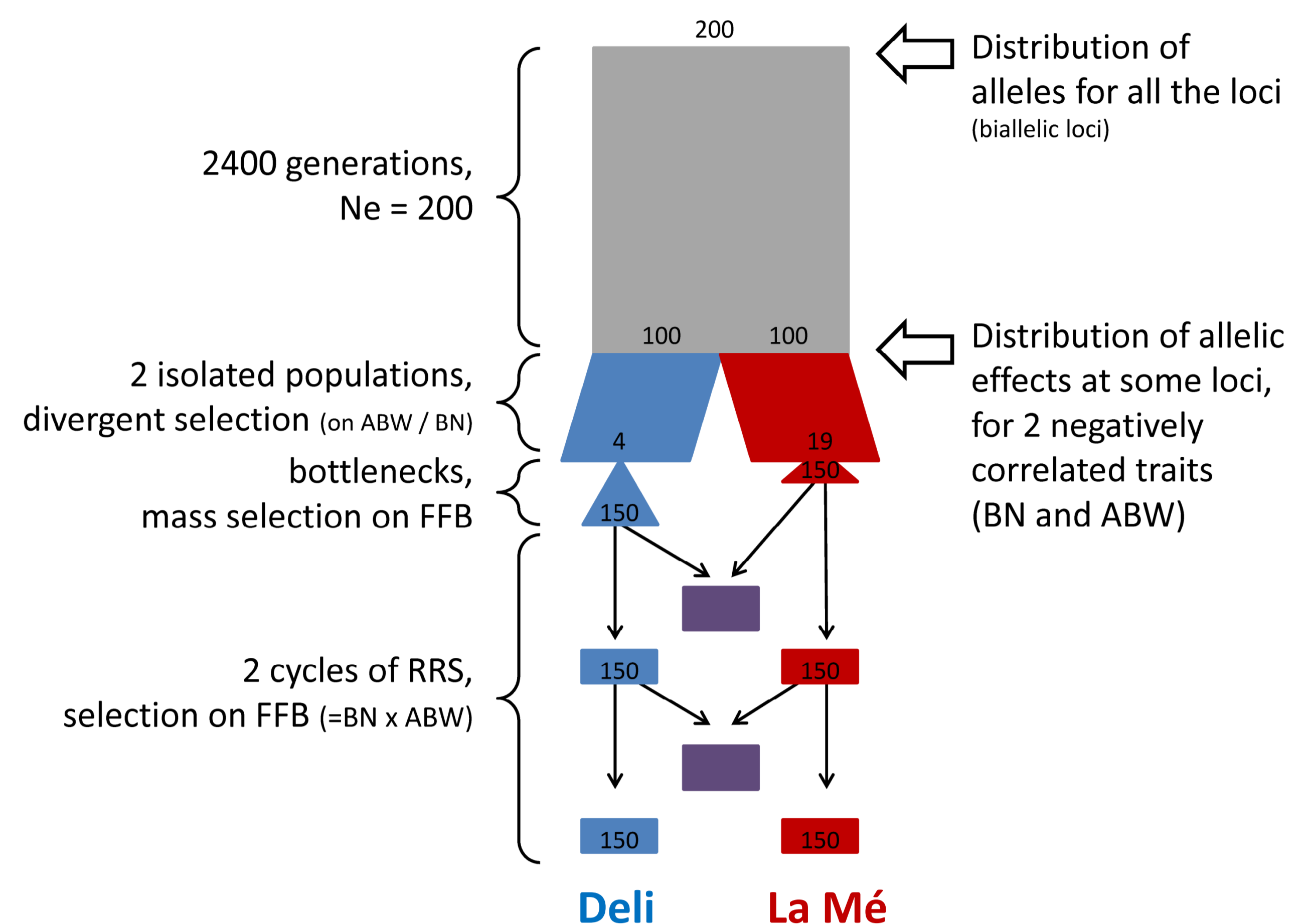


Fig. 1 Simulation of the initial breeding populations (generation 0).

Random mating allowed reaching mutation-drift equilibrium after 2400 generations. Natural selection was applied to increase bunch weight (ABW) in population A (in blue) and bunch number (BN) in population B (in red). Bottleneck events were at the origin of Deli and La Mé populations. In subsequent generations, artificial selection (mass selection and RRS) was applied to increase bunch production (FFB, which is the product of ABW by BN). QTL for ABW and BN were assigned after the first 2400 generations of random mating. RRS: reciprocal recurrent selection

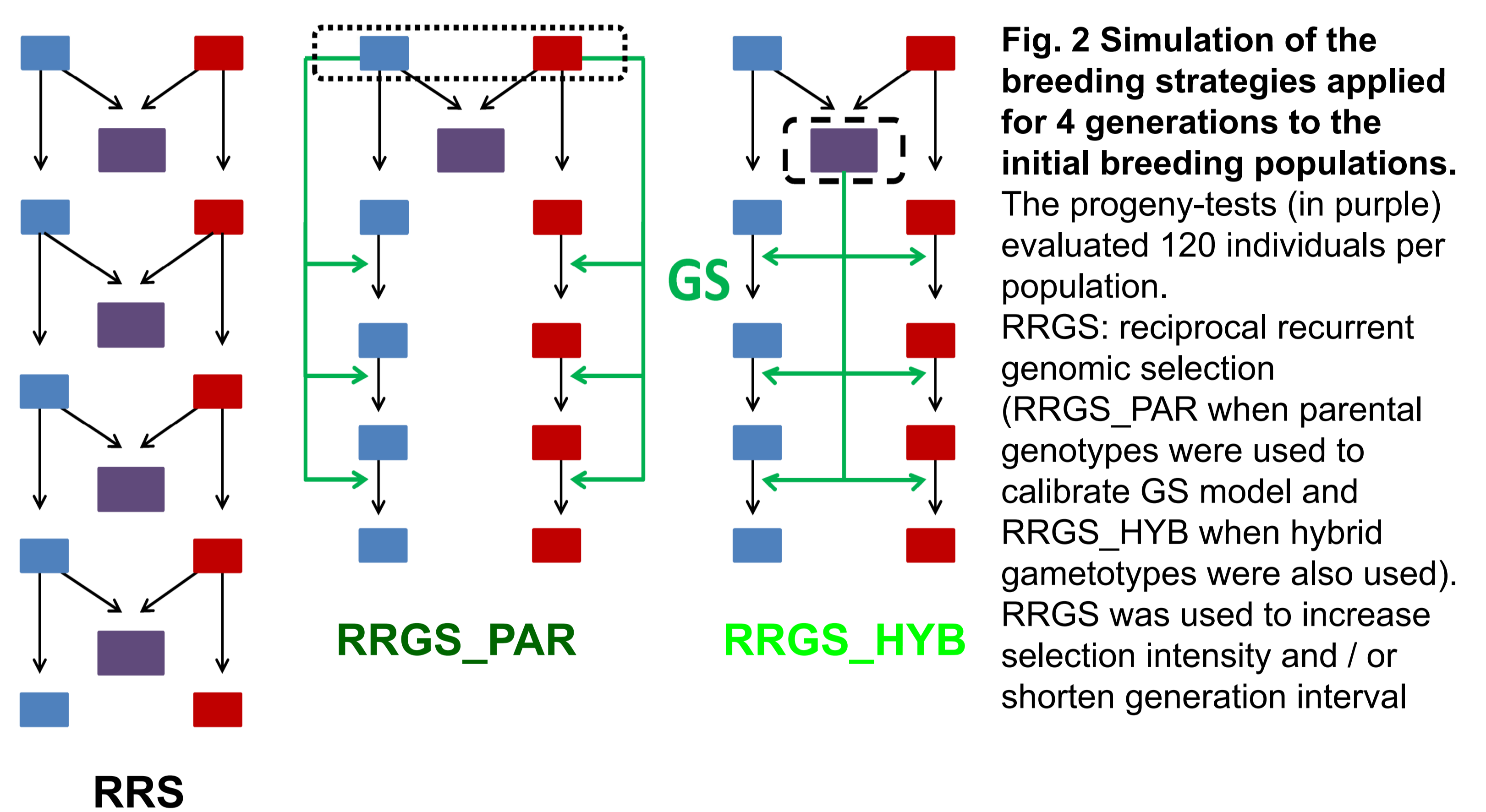


Fig. 2 Simulation of the breeding strategies applied for 4 generations to the initial breeding populations.

The progeny-tests (in purple) evaluated 120 individuals per population. RRGs: reciprocal recurrent genomic selection (RRGs_PAR when parental genotypes were used to calibrate GS model and RRGs_HYB when hybrid gametotypes were also used). RRGs was used to increase selection intensity and / or shorten generation interval

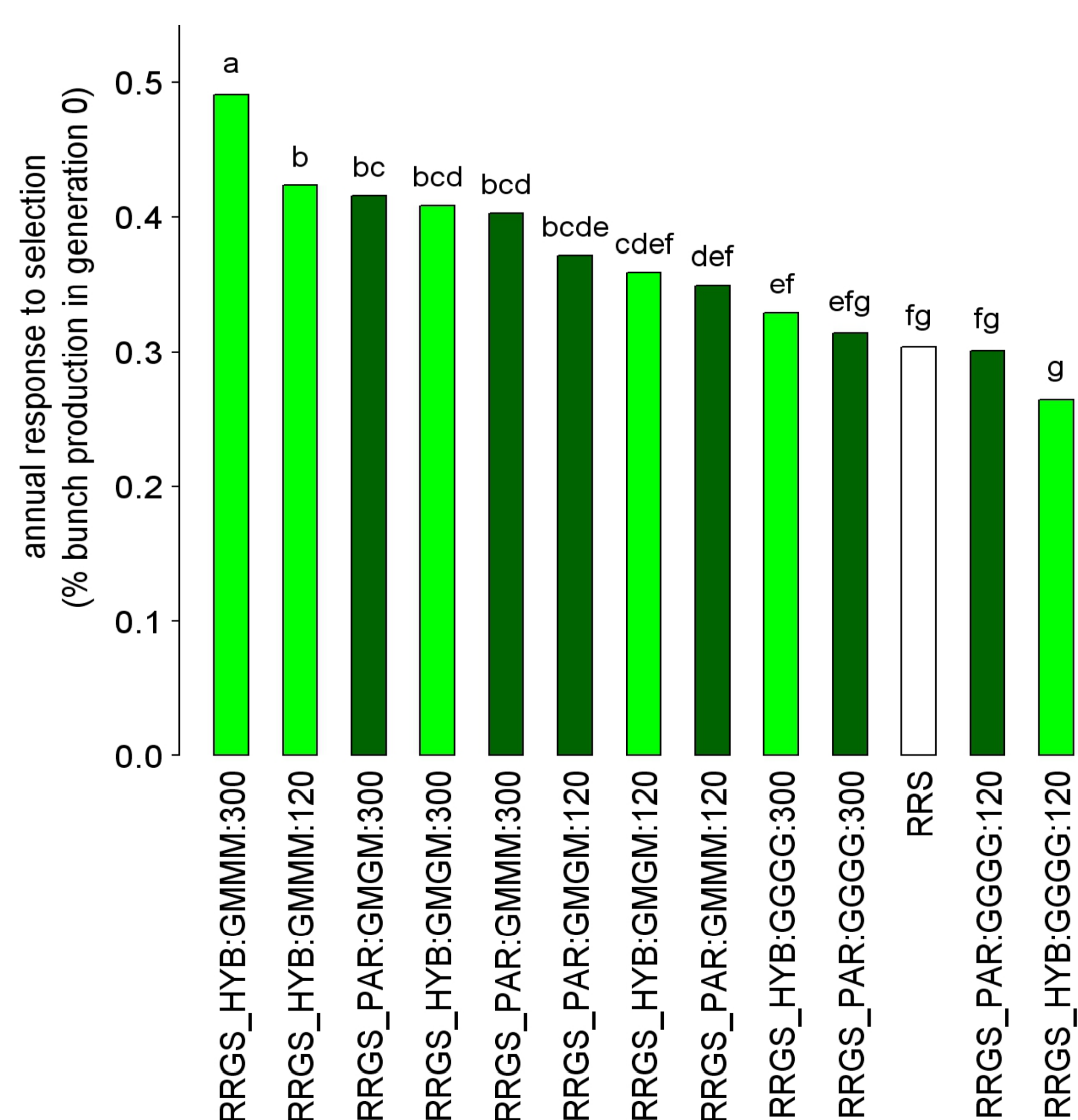


Fig. 3 Annual response to selection after four generations of selection (in percentage of bunch production of hybrids in generation 0).

For RRGs_HYB 1,700 hybrids were used to calibrate the GS model. GGGG: GS model calibrated every generation (with progeny-tests), GMGM: GS model calibrated every 2 generations and selection made only on markers in the other generations, GMM: GS model calibrated every 4 generations. 120 / 300: number of candidates per generation and population (in RRS the candidates were the 120 progeny-tested individuals per parental population). Values were means over 5 replicates. Values with the same letter were not significantly different at P=0.01