Supplementary Information

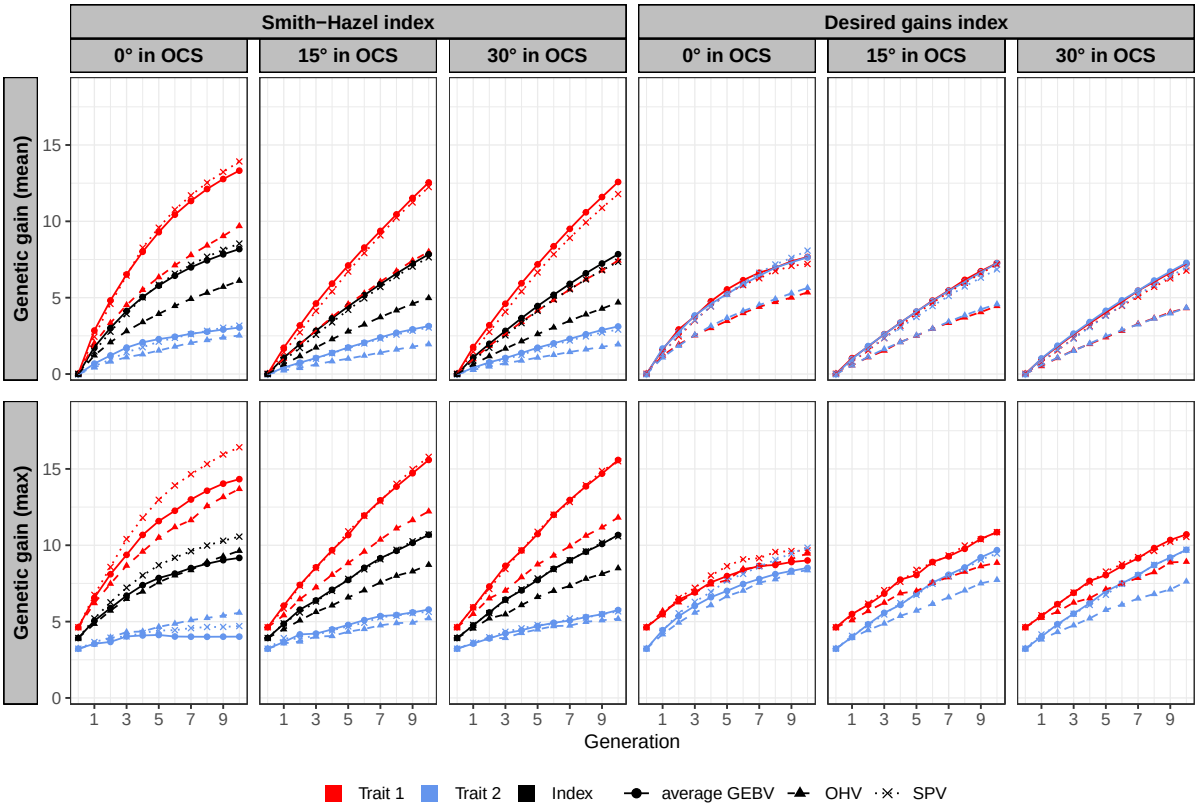
CrossingTools: Scalable cross evaluation and mating-plan optimisation for multiple traits

S. E. Weber, D. L. Waters, C. R. Werner and D. J. Tolhurst

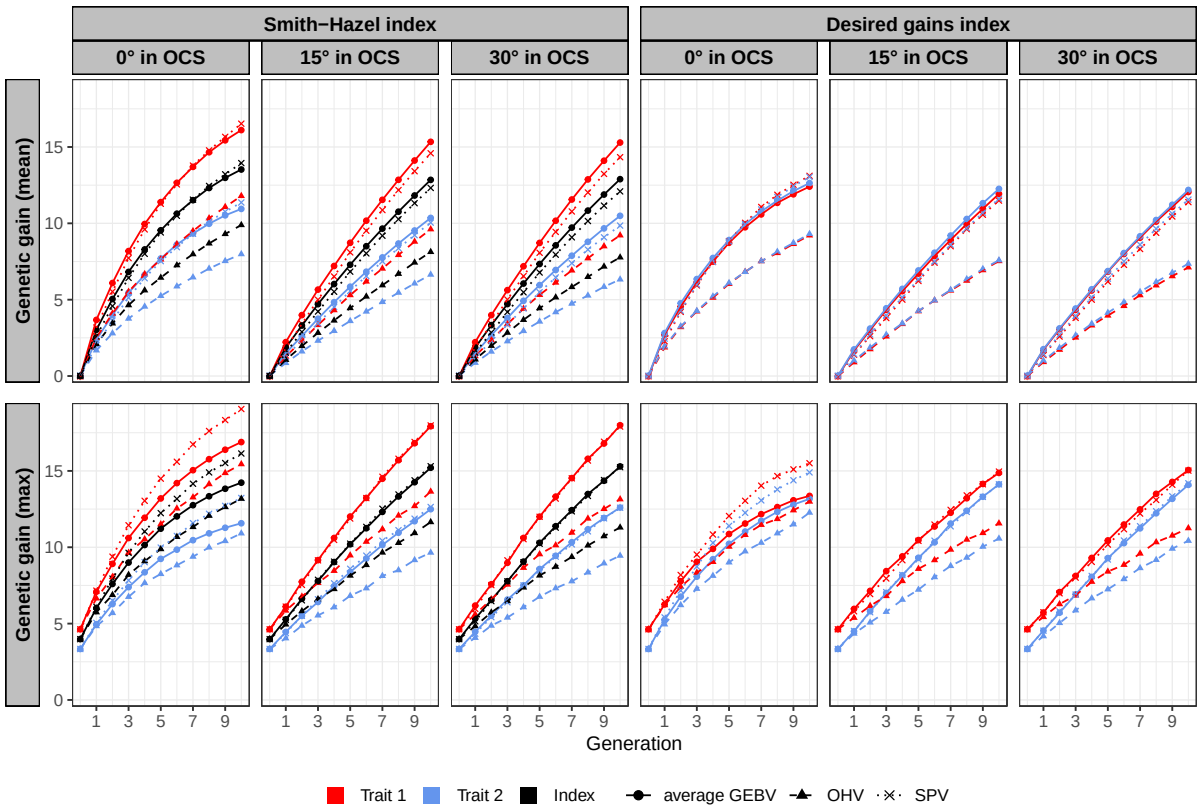
Theoretical and Applied Genetics

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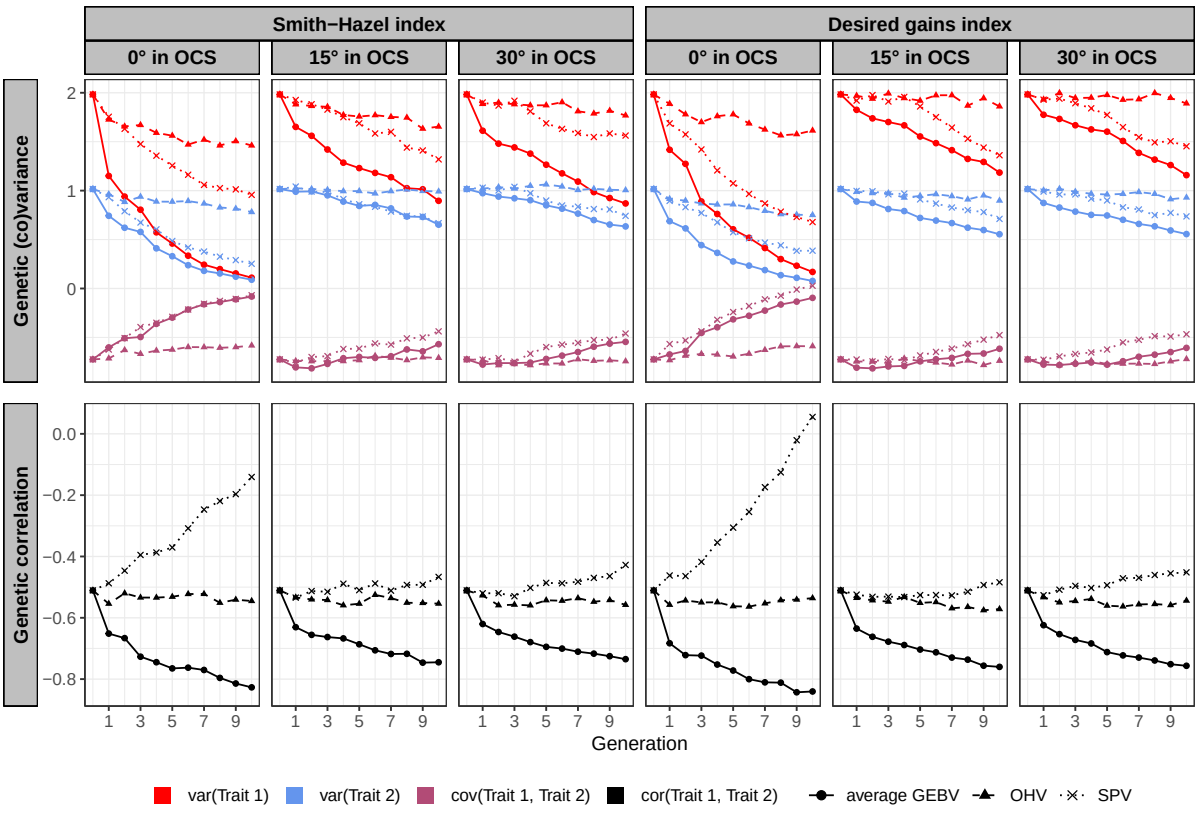
Supplementary figures



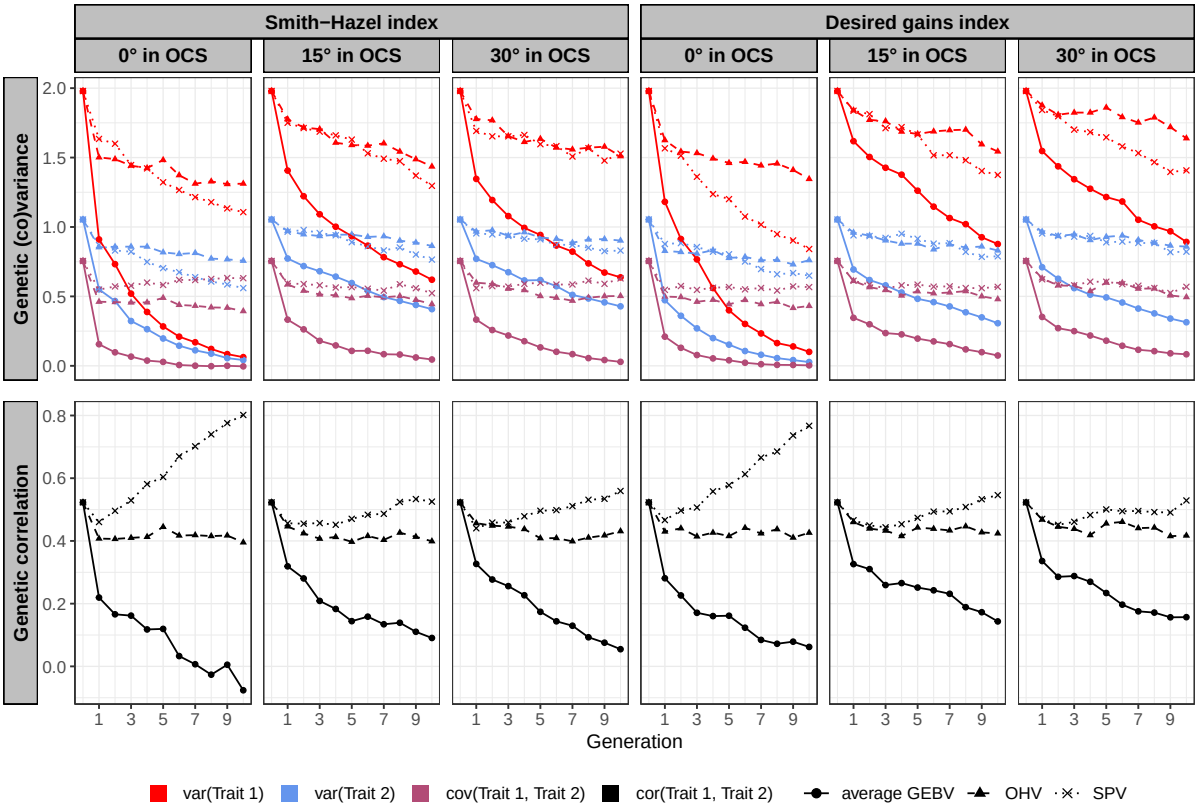
Supplementary Fig. S1: Mean (top row) and commercialisable (maximum) (bottom row) genetic gain over ten generations of mating based on true QTL effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic gain is shown for Trait 1 (red) and Trait 2 (blue), with the index shown in black. Selection was based on average breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of -0.5.



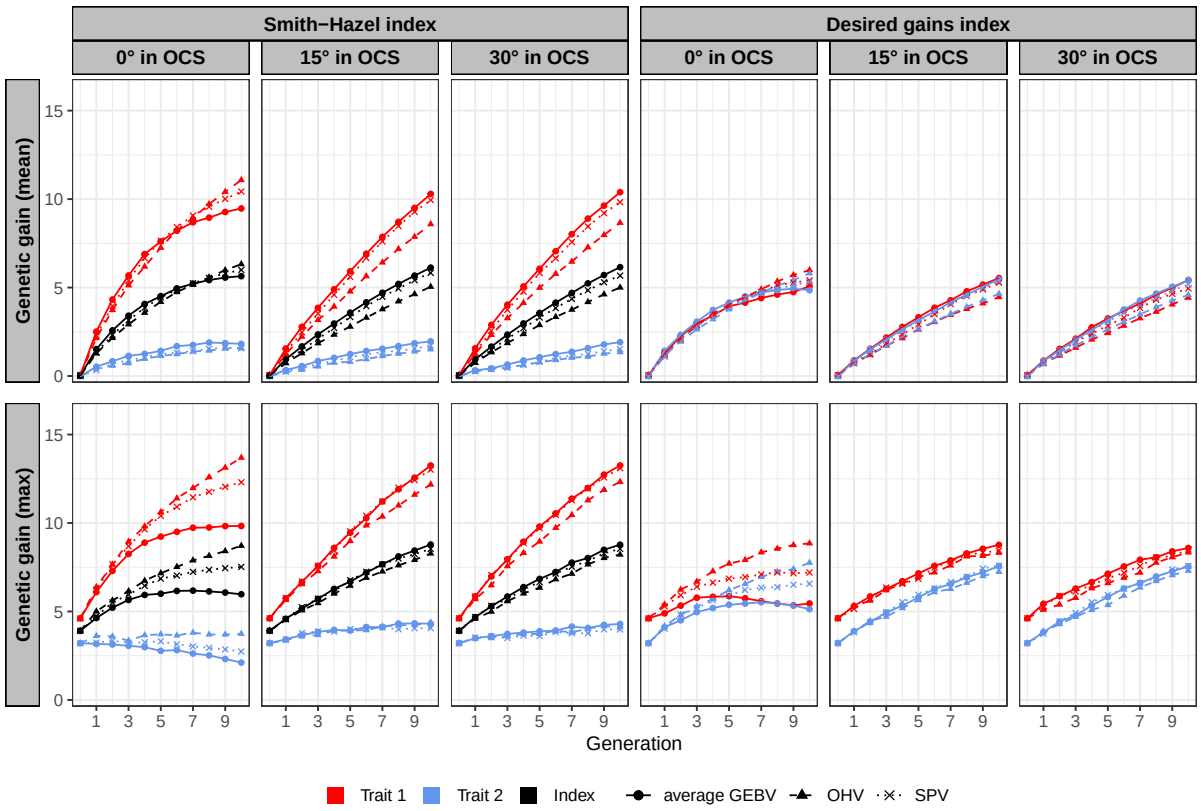
Supplementary Fig. S2: Mean (top row) and commercialisable (maximum) (bottom row) genetic gain over ten generations of mating based on true QTL effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic gain is shown for Trait 1 (red) and Trait 2 (blue), with the index shown in black. Selection was based on average breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of 0.5.



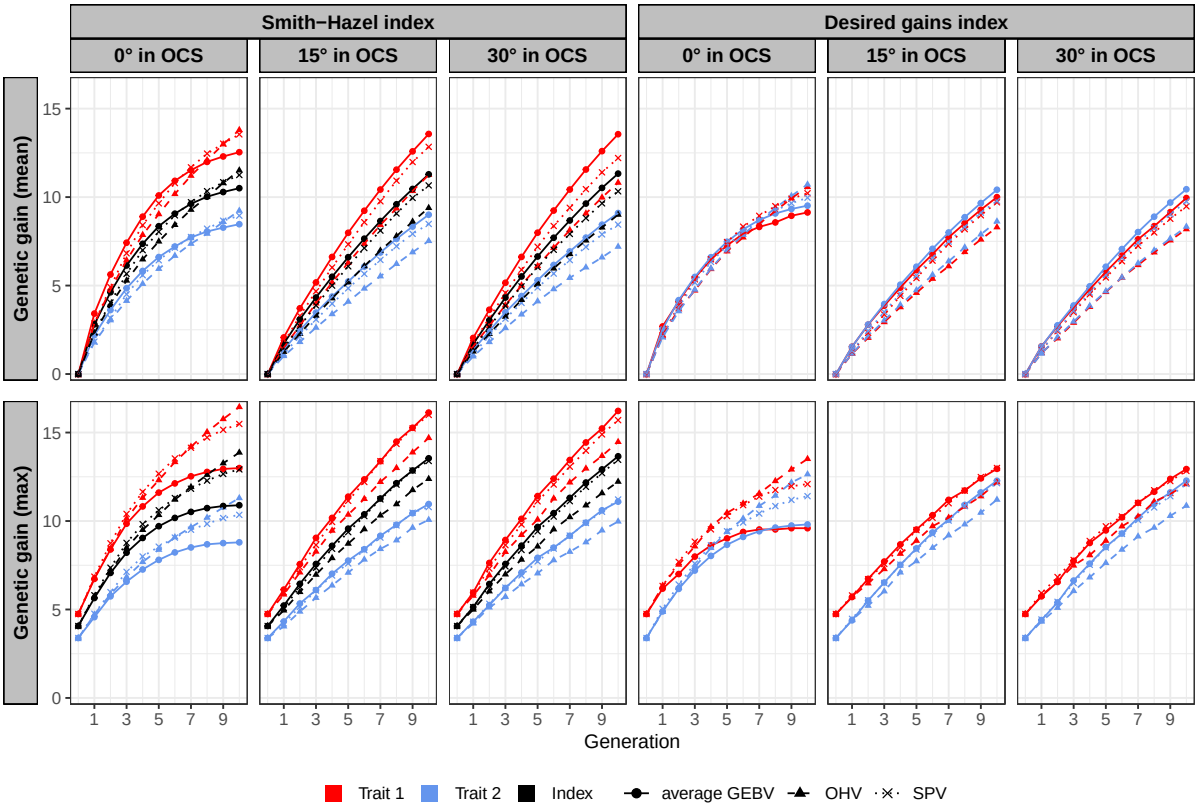
Supplementary Fig. S3: Genetic (co)variances (top row) and genetic correlation (bottom row) over ten generations of mating based on true QTL effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic variance is shown for Trait 1 (red), Trait 2 (blue), and their covariance (purple) and correlation (black). Selection was based on average breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of −0.5.



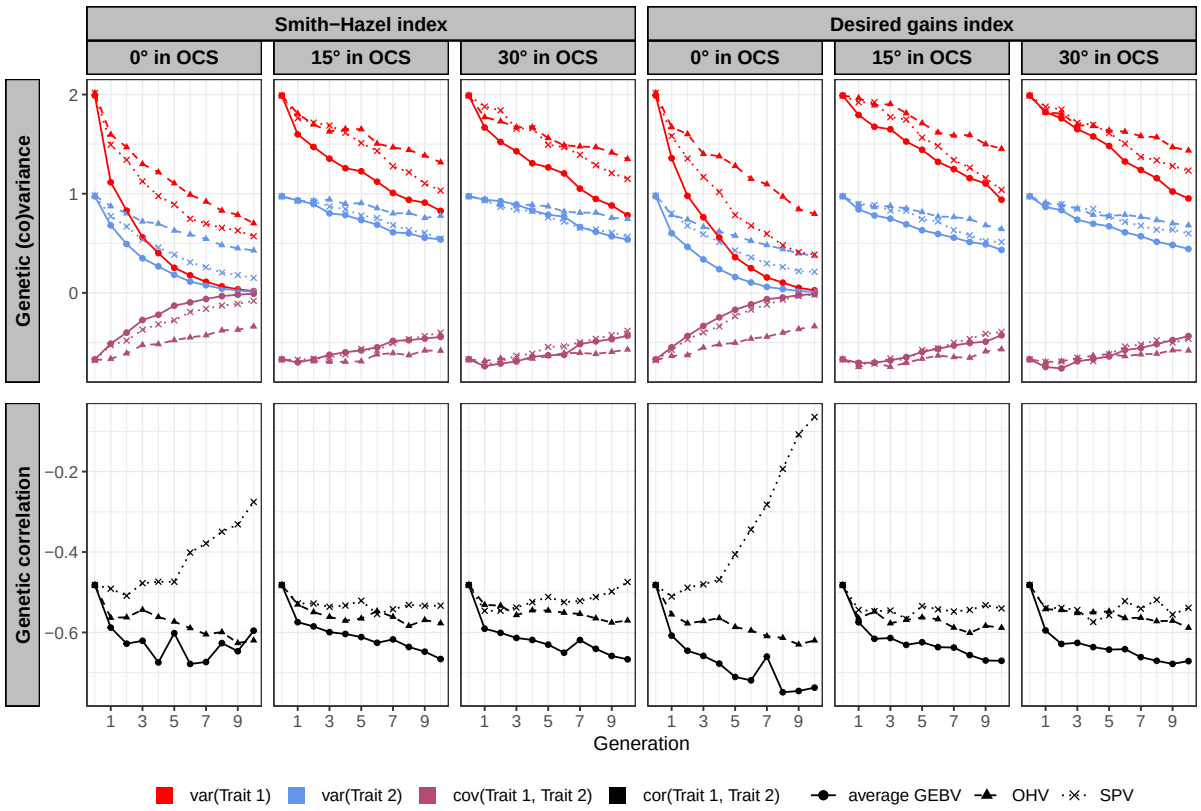
Supplementary Fig. S4: Genetic (co)variances (top row) and genetic correlation (bottom row) over ten generations of mating based on true QTL effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic variance is shown for Trait 1 (red), Trait 2 (blue), and their covariance (purple) and correlation (black). Selection was based on average breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of 0.5.



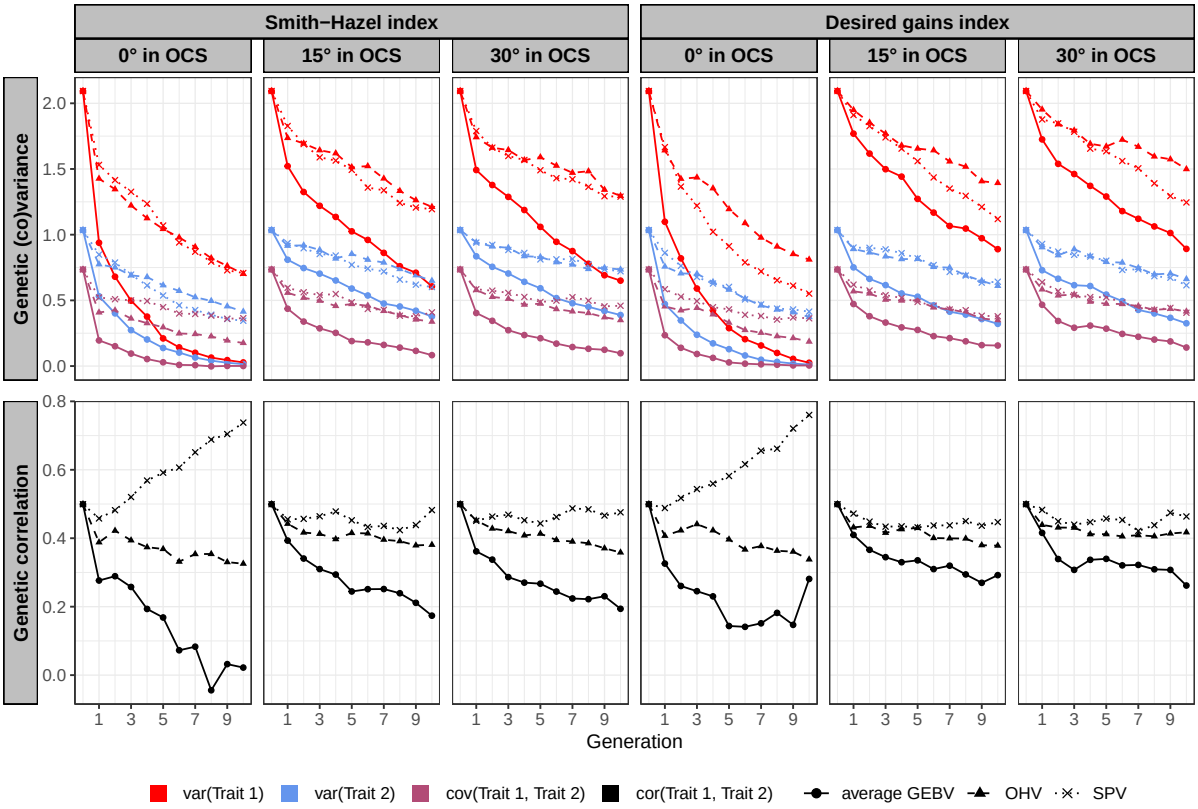
Supplementary Fig. S5: Mean (top row) and commercialisable (maximum) (bottom row) genetic gain over ten generations of mating based on estimated marker effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic gain is shown for Trait 1 (red) and Trait 2 (blue), with the index shown in black. Selection was based on average genomic estimated breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of −0.5.



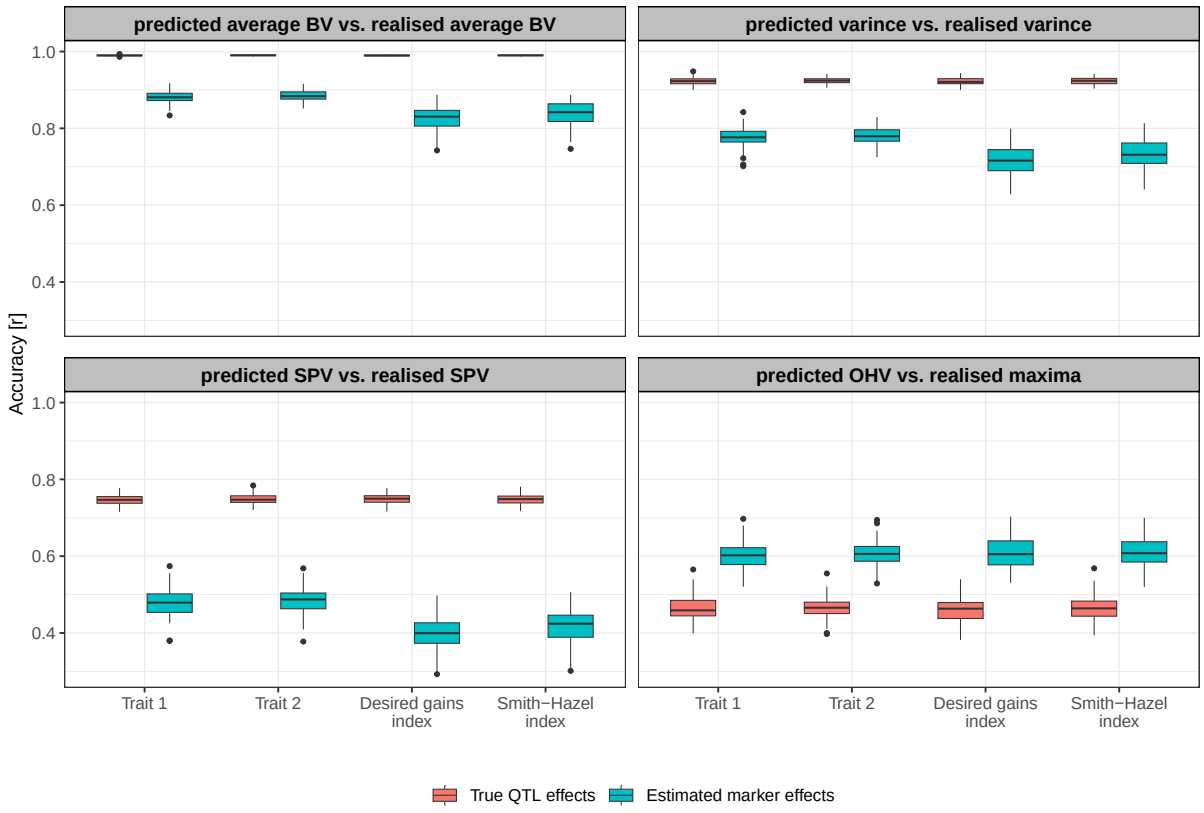
Supplementary Fig. S6: Mean (top row) and commercialisable (maximum) (bottom row) genetic gain over ten generations of mating based on estimated marker effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic gain is shown for Trait 1 (red) and Trait 2 (blue), with the index shown in black. Selection was based on average genomic estimated breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of 0.5.



Supplementary Fig. S7: Genetic (co)variances (top row) and genetic correlation (bottom row) over ten generations of mating based on estimated marker effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic variance is shown for Trait 1 (red), Trait 2 (blue), and their covariance (purple) and correlation (black). Selection was based on average genomic estimated breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of −0.5.



Supplementary Fig. S8: Genetic (co)variances (top row) and genetic correlation (bottom row) over ten generations of mating based on estimated marker effects under the Smith–Hazel index (left block) and Desired Gains index (right block). Columns show OCS angles of 0°, 15°, and 30°. Genetic variance is shown for Trait 1 (red), Trait 2 (blue), and their covariance (purple) and correlation (black). Selection was based on average genomic estimated breeding values (average GEBV; circles and solid lines), optimal haploid values (OHV; triangles and dashed lines), or superior progeny value (SPV; crosses and dotted lines). Results are shown for an initial genetic correlation of 0.5.



Supplementary Fig. S9: Accuracy of cross-performance criteria calculated from true QTL effects (red) or estimated marker effects (blue). Accuracy was measured as the Pearson correlation between predicted and realised values across 5,000 biparental crosses. For expected cross mean, segregation variance, and superior progeny value (SPV), predictions were compared with their corresponding realised family values, whereas optimal haploid value (OHV) was compared with the maximum genetic value realised among 50 DH progeny per cross. Results are shown for both individual traits and the two selection indices.