Optimal cross selection for long-term genetic gain in a twopart genomic selection strategy

Supplementary Material S2: Additional results

Gregor Gorjanc*, R. Chris Gaynor, John M. Hickey

G. Gorjanc, R.C. Gaynor, and J.M. Hickey The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush Research Centre, Midlothian EH25 9RG, UK

*Corresponding author (gregor.gorjanc@roslin.ed.ac.uk)

Fig. S2.1: Genetic mean of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints; two-part programs used four recurrent selection cycles per year

Fig. S2.2: Genic standard deviation of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints; two-part programs used four recurrent selection cycles per year

Fig. S2.3: Genetic standard deviation of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints (mean and 95% confidence interval); two-part programs used four recurrent selection cycles per year

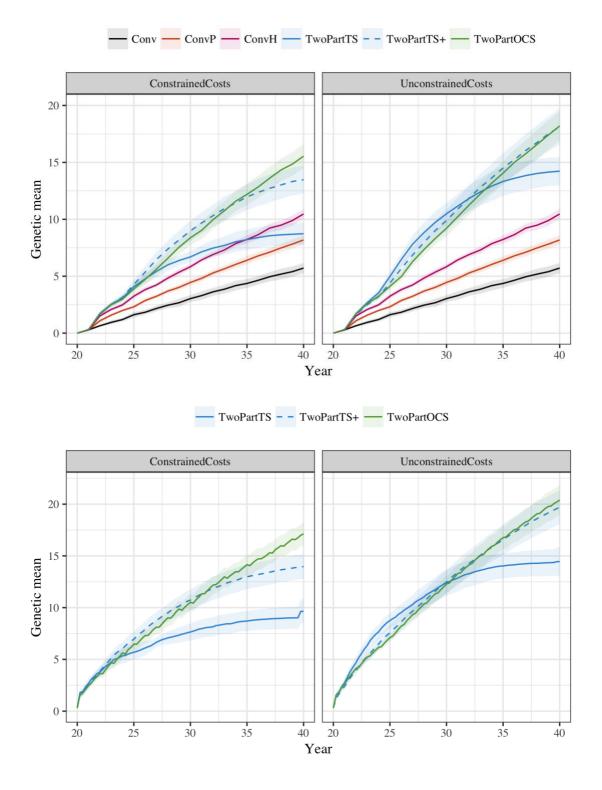


Fig. S2.1: Genetic mean of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints; two-part programs used four recurrent selection cycles per year

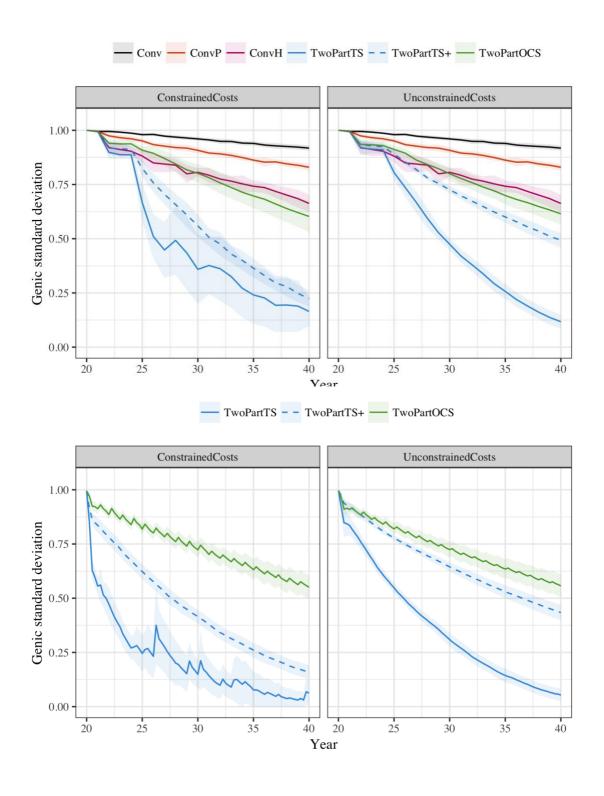


Fig. S2.2: Genic standard deviation of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints; two-part programs used four recurrent selection cycles per year

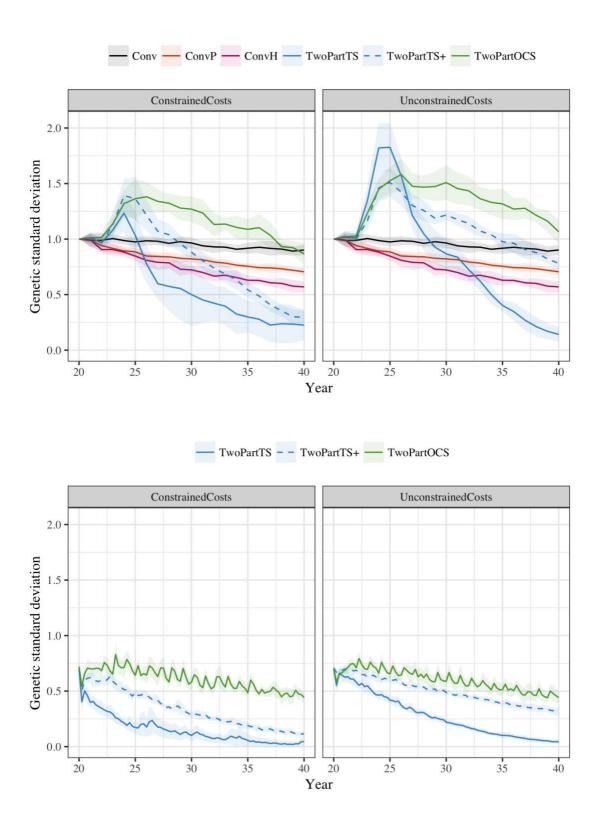


Fig. S2.3: Genetic standard deviation of doubled-haploid lines (top) and population improvement component (bottom) over 20 years of selection by breeding program and cost constraints (mean and 95% confidence interval); two-part programs used four recurrent selection cycles per year