

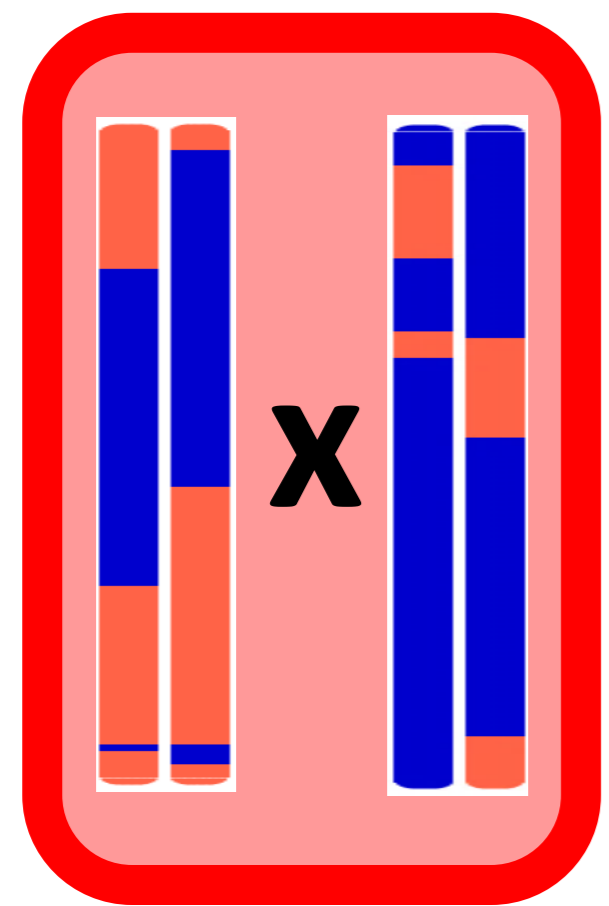
Maximizing future gain

Exploiting variance of descendants for optimized selection decisions

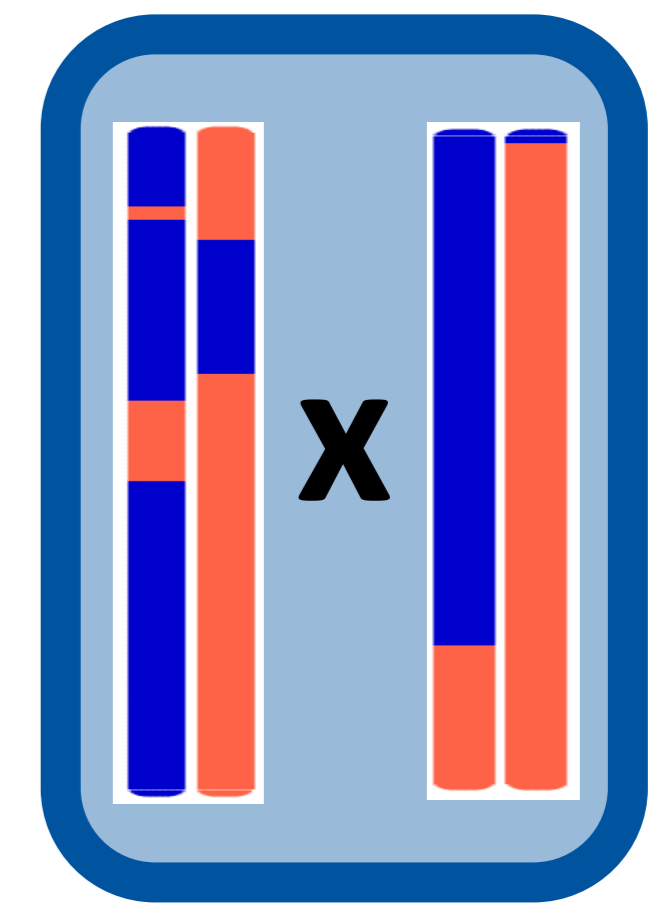
Tobias A. M. Niehoff¹, Jan ten Napel¹, Piter Bijma¹, Torsten Pook¹, Yvonne C. J. Wientjes¹, Bernadett Hegedűs¹, Mario P. L. Calus¹

¹Animal Breeding and Genomics, Wageningen University and Research, NL

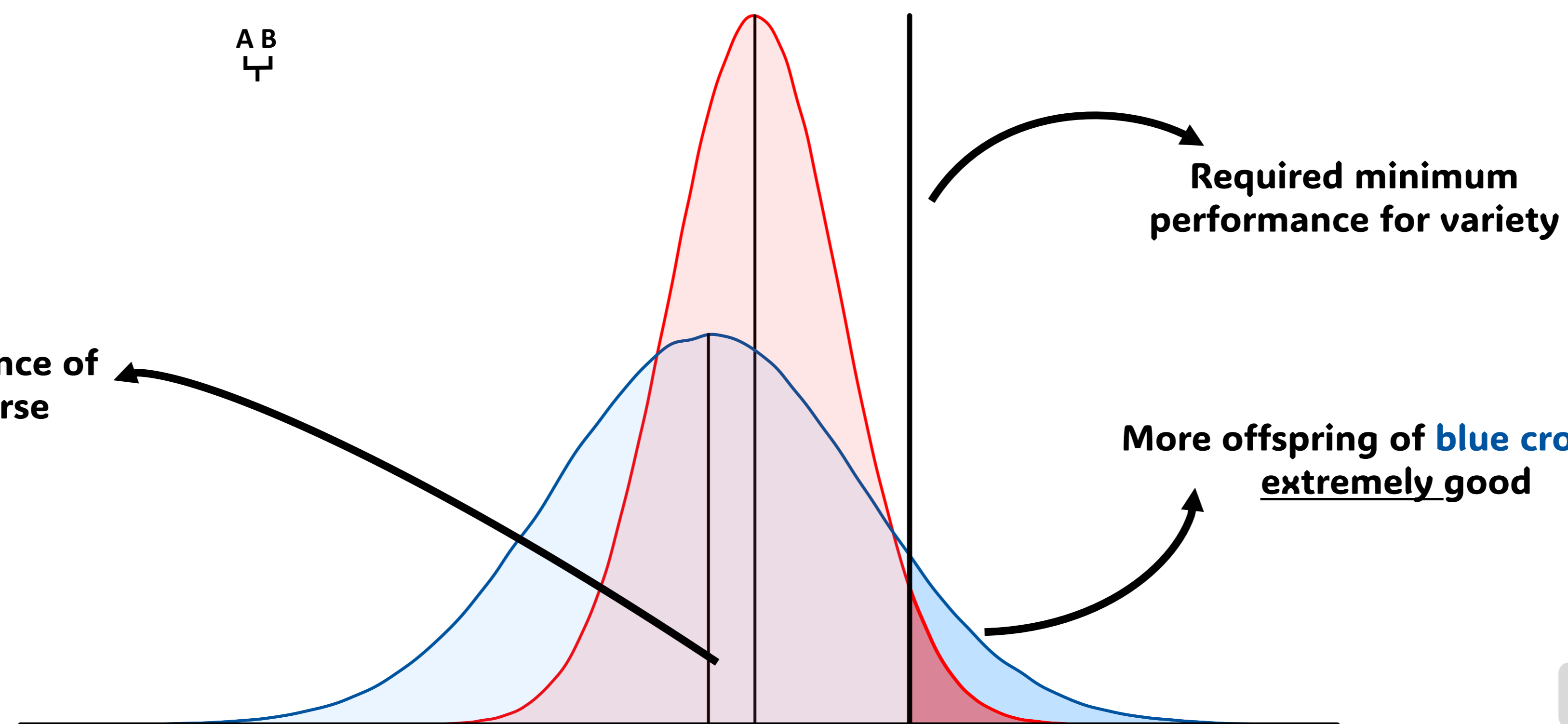
Looking 1 generation ahead



Generate 100 offspring of **red** or **blue** cross.
Which cross do you choose?

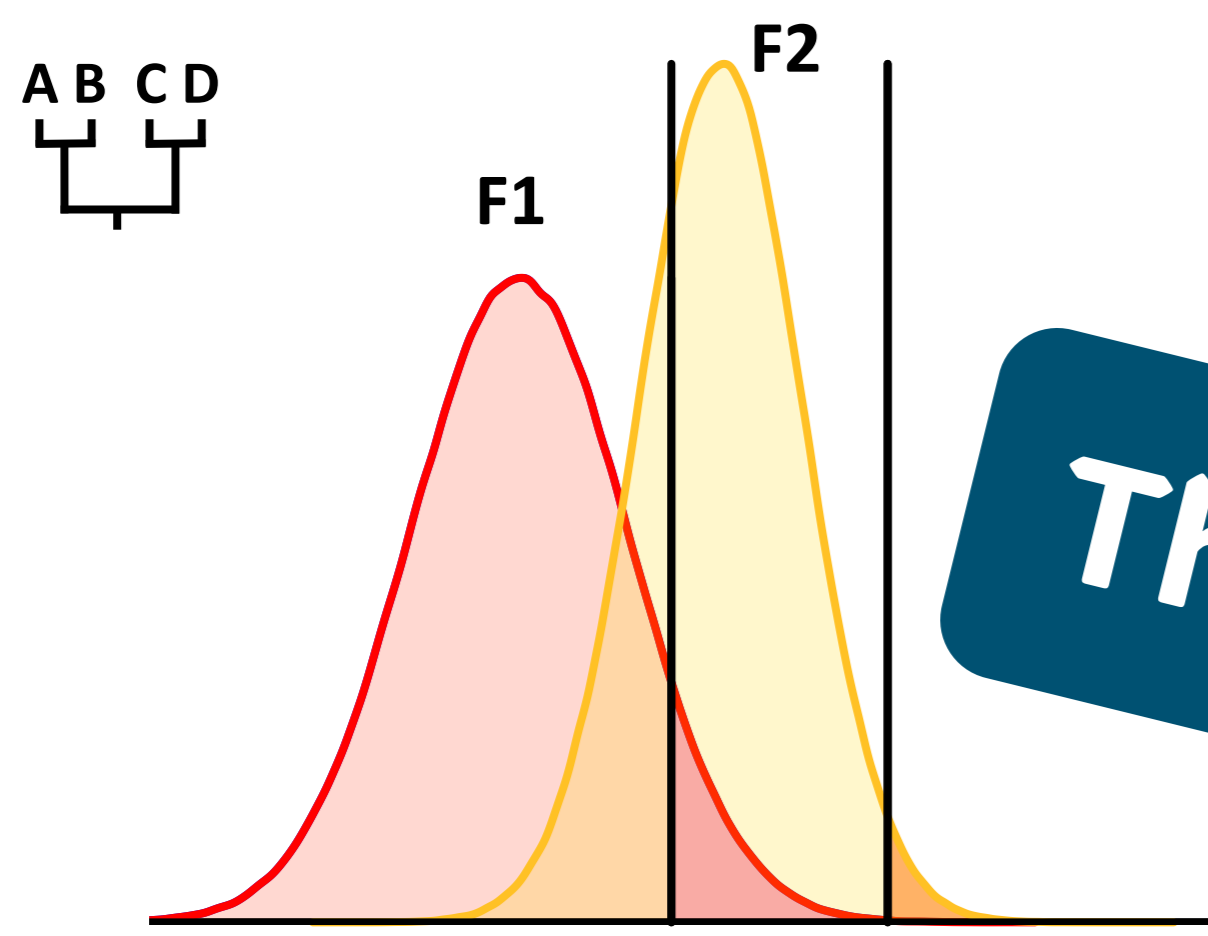


Average performance of blue cross is worse



This problem is addressed by the Usefulness criterion (Schnell & Utz, 1975)

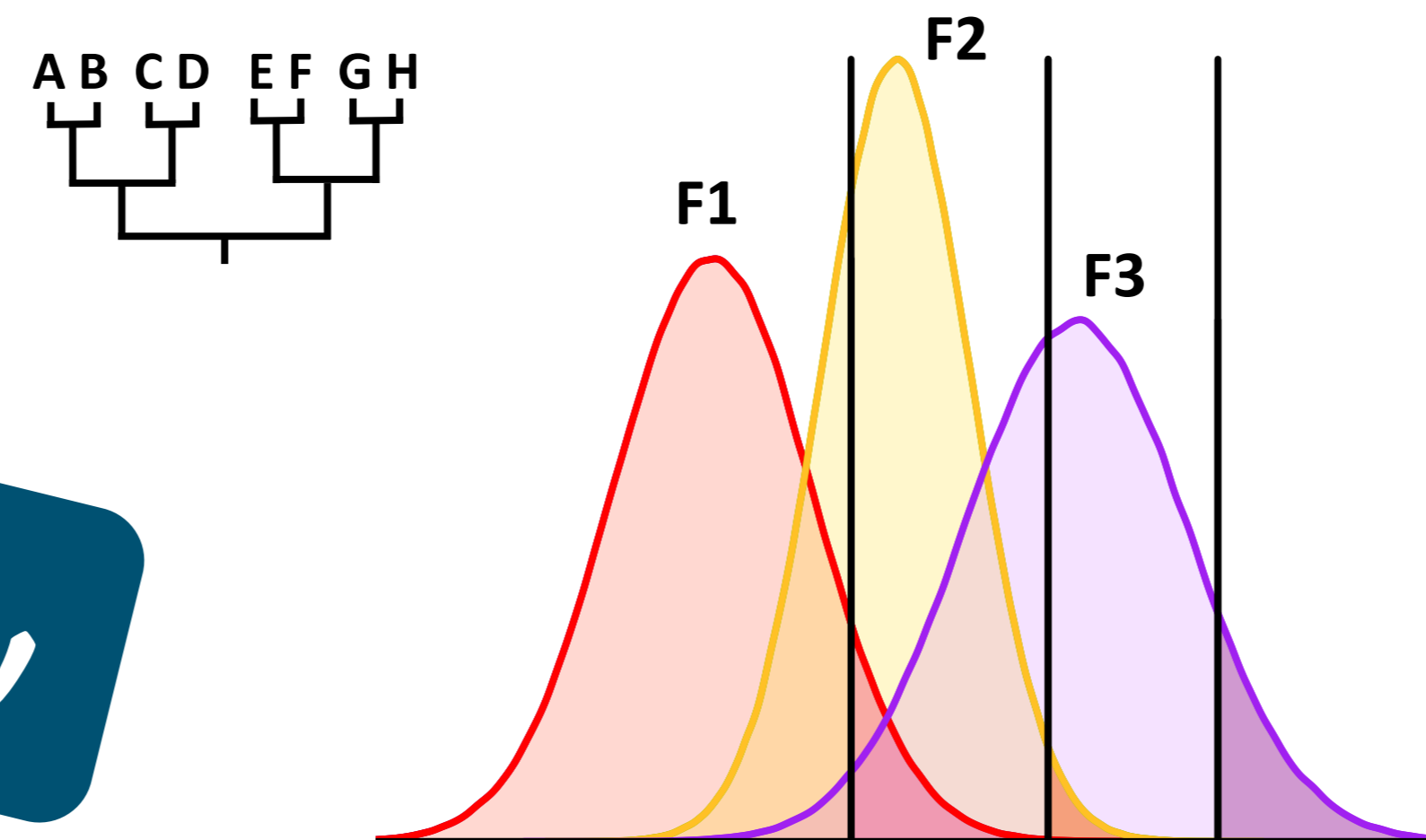
Looking 2 generations ahead



1 generation: probability F1
2 generations: probability F2

$$\text{Prob}_{F_2} = \text{Prob}_{F_1} \times \text{Prob}(F_2 | \text{selected } F_1)$$

Looking 3 generations ahead



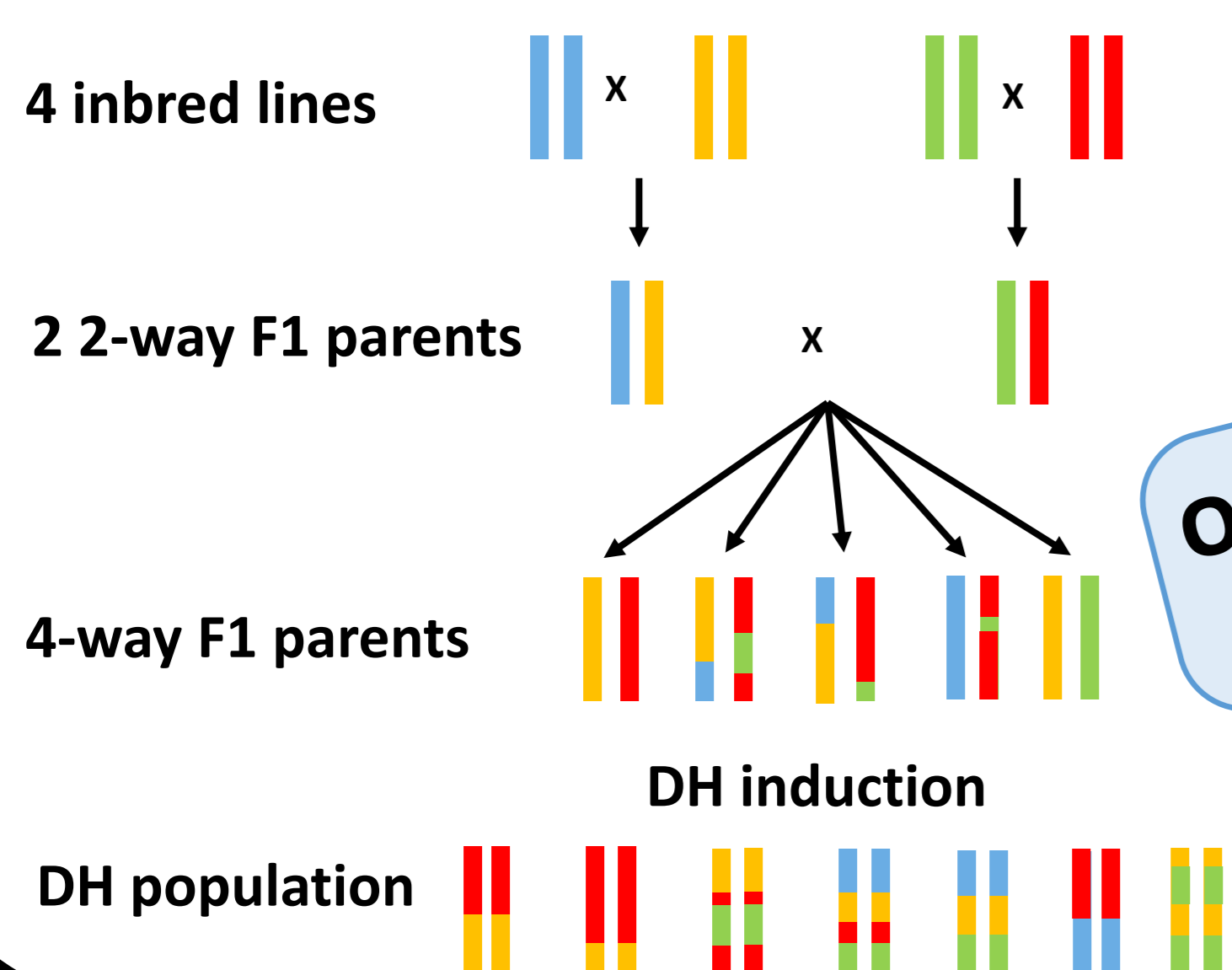
1 generation: probability F1
2 generations: probability F2
3 generations: probability F3

$$\text{Prob}_{F_3} = \text{Prob}_{F_1} \times \text{Prob}_{F_2} \times \text{Prob}(F_3 | \text{selected } F_2)$$

...extendable to any generation

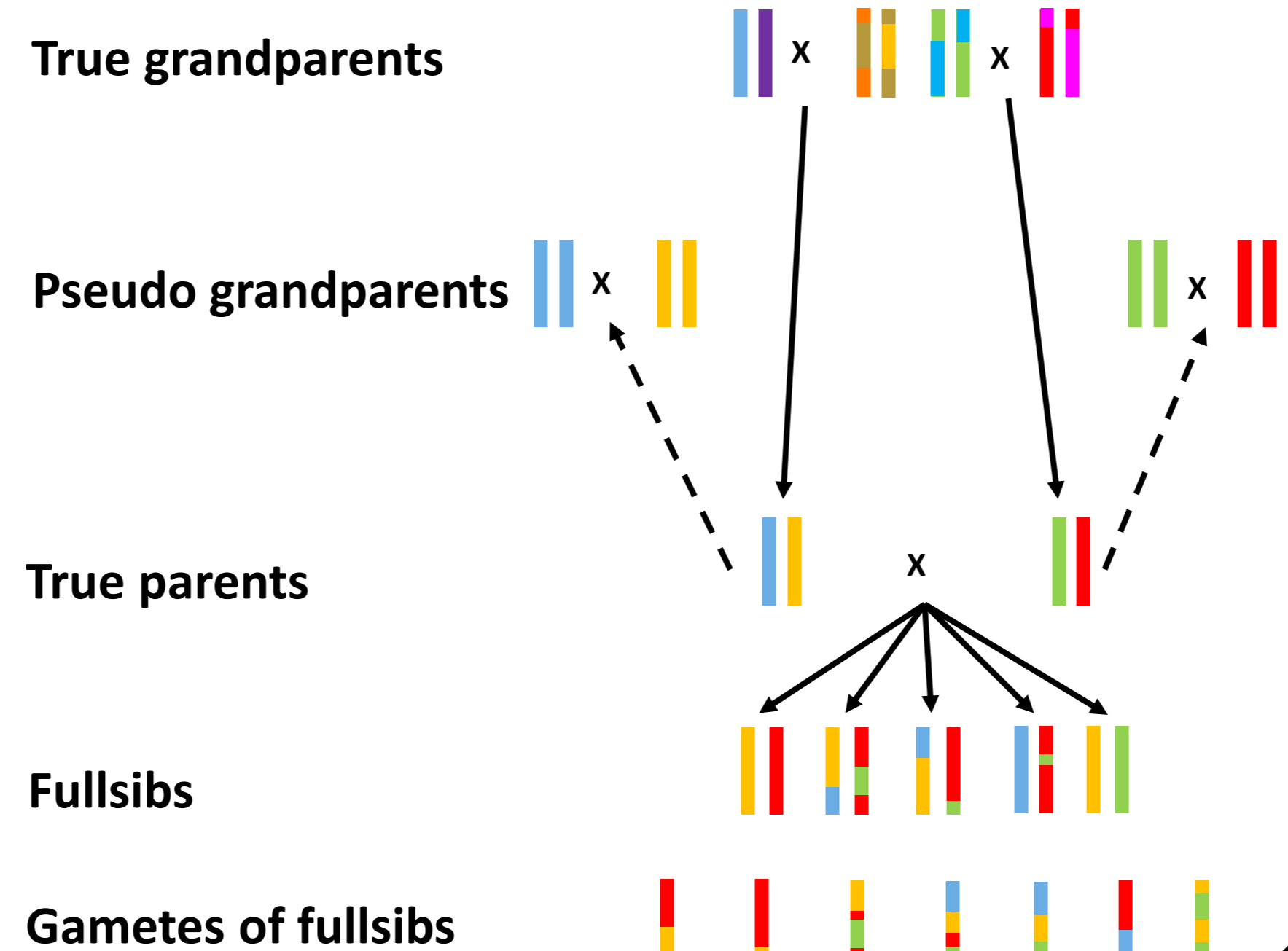
Works for all diploid species

Line breeding
e.g. barley

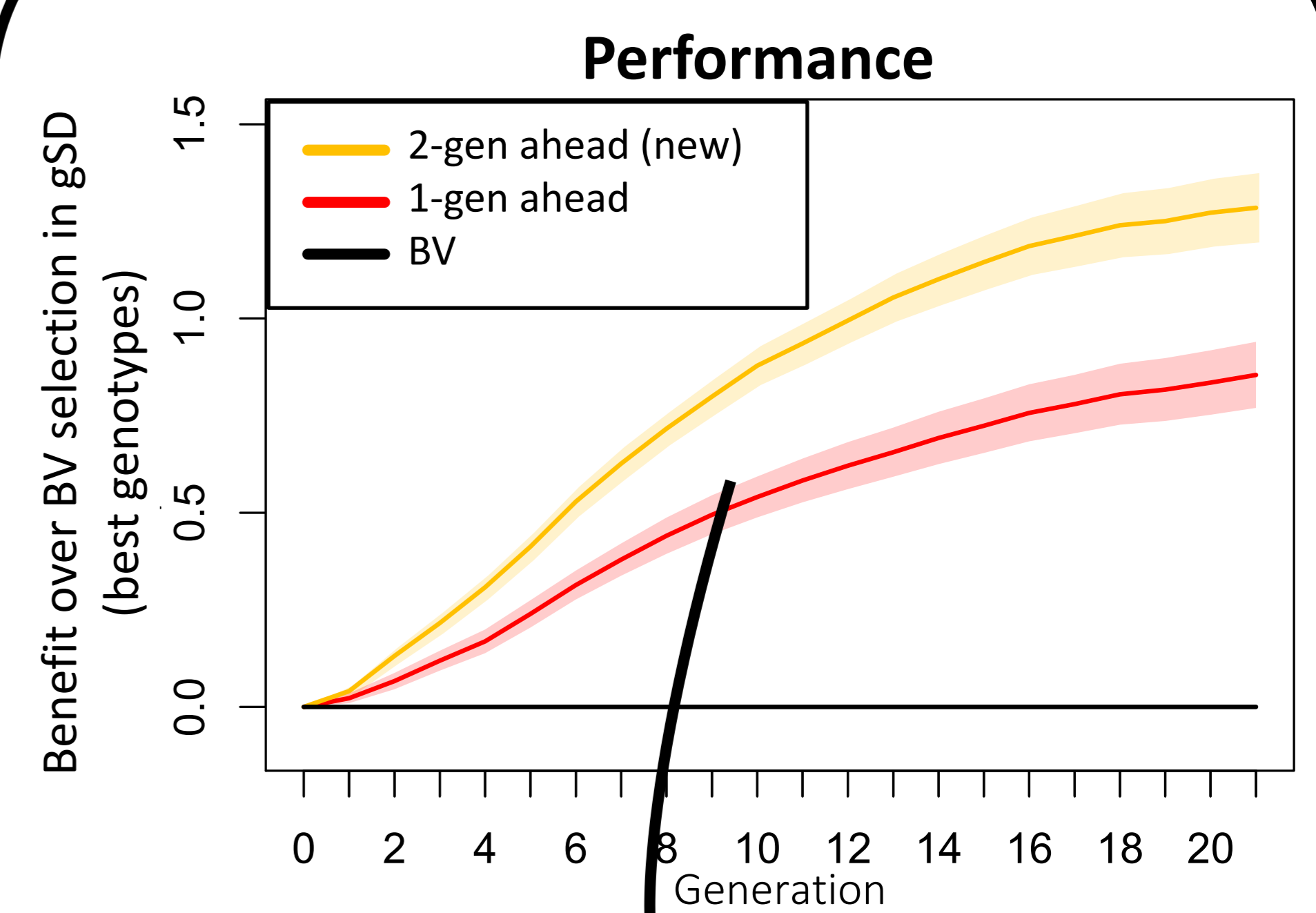


Only different in ploidy!

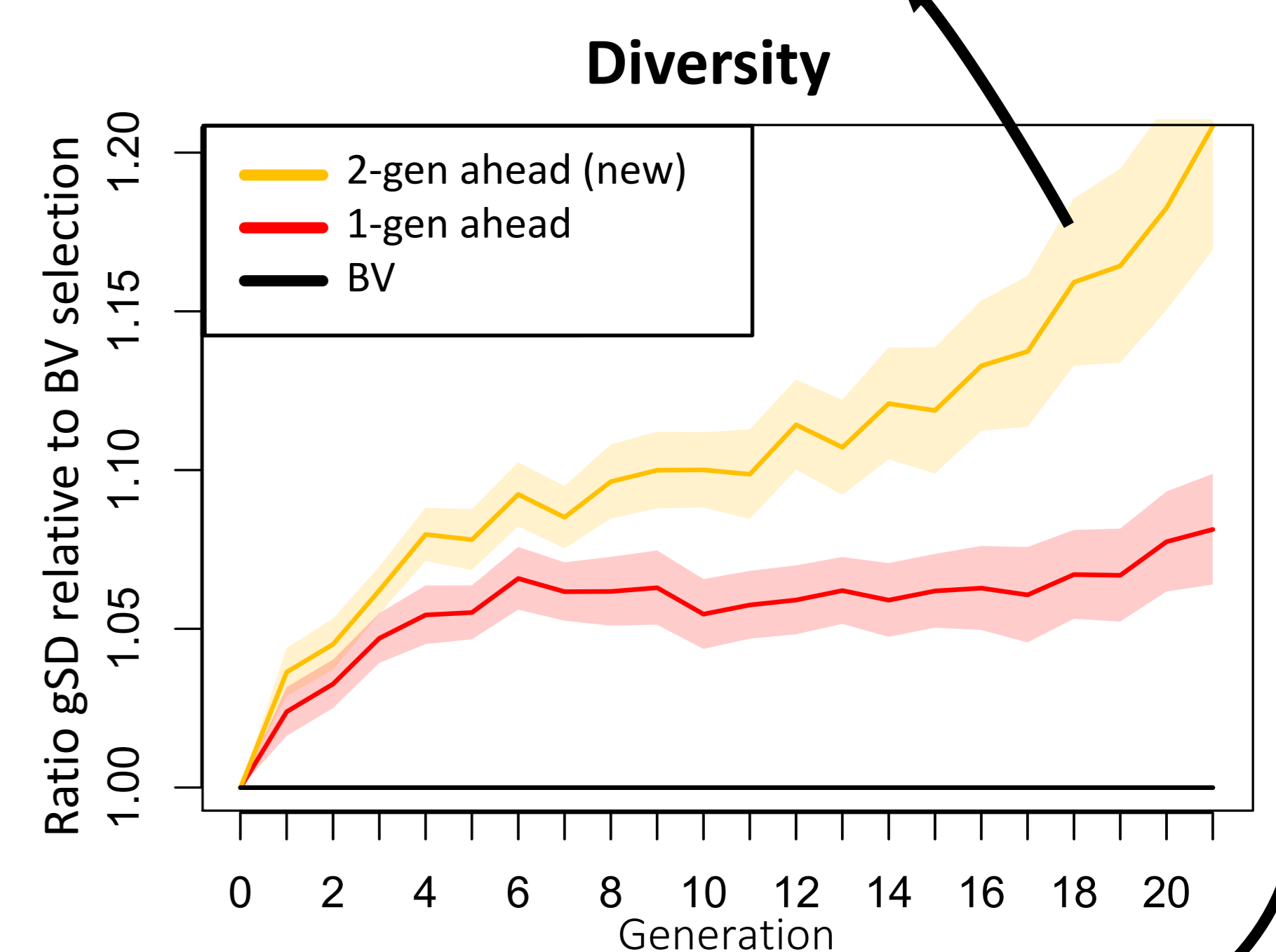
Outcross species
e.g. animals, apples



Selection experiment (simulated)



More gain
+ more variation



Prediction of progeny variances

◆ 2-way cross: Lehermeier et al. (2017), Osthusenrich et al. (2017)

$$V_{DH_{2\text{-way}}} = \sum_{j=1}^n \sum_{l=1}^n 4(1-2c_{jl})D_{jl}^{AB} * \alpha_j \alpha_l$$

◆ 4-way cross: Allier et al. (2019)

$$V_{DH_{4\text{-way}}} = \sum_{j=1}^n \sum_{l=1}^n \left((1-2c_{jl})^2 (D_{jl}^{AB} + D_{jl}^{CD}) + (1-2c_{jl})(D_{jl}^{AC} + D_{jl}^{AD} + D_{jl}^{BC} + D_{jl}^{BD}) \right) * \alpha_j \alpha_l$$

◆ N-way cross: Niehoff et al. (new)

$$V_{DH_{N\text{-way}}} = \left(\frac{4}{N}\right)^2 \sum_{i=1}^N \sum_{k>l}^N \sum_{j=1}^n \sum_{l=1}^n (1-2c_{jl})^{m_{ik}} D_{jl}^{ik} * \alpha_j \alpha_l$$

DH variance can be partitioned into gametic Mendelian sampling variance of ancestors.

→ This gametic MSV can be used to derive variance of non-inbred offspring

→ Extension of Usefulness criterion (Schnell & Utz, 1975) to any generation

$$\sigma_{\text{gamMS 4-way } F_1}^2 = (\sigma_{2\text{-way } DH}^2 - \sigma_{4\text{-way } F_1}^2) * 0.25$$

n: number loci
c: recombination frequency
α: average effect
j, l: locus j, locus l
D: LD in haplotypes
m: number of meioses that reduce D of parents

N: number haplotypes (2, 4, 8, 16, ...)
i, k: haplotype i, haplotype k

Required input:

- ◆ Genetic map
- ◆ Phased genotypes
- ◆ Estimates of marker effects (e.g., rrBLUP)



tobias.niehoff@wur.nl
www.wageningenur.nl/abg



This work is part of the Breed4Food project and financially supported by:

