Genomic breeding programs realize larger benefits in the presence of G×E than conventional breeding programs

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Genotype × environment interaction

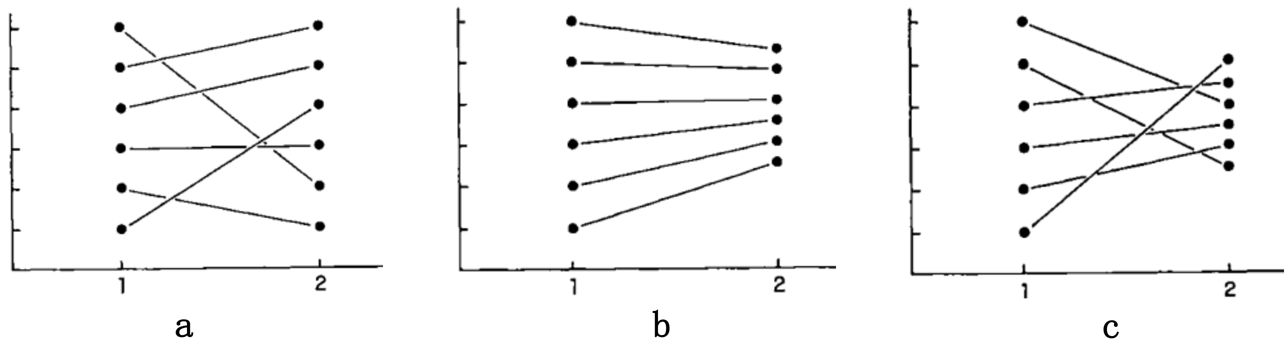


Fig. G x E involves changes : a) in rank; b) in variance; c) in rank and variance.

(J. C. Bowman, 1972)

a). Reranking $\Rightarrow r_g < 1$ (e.g. 0.6~1, milk production triats)

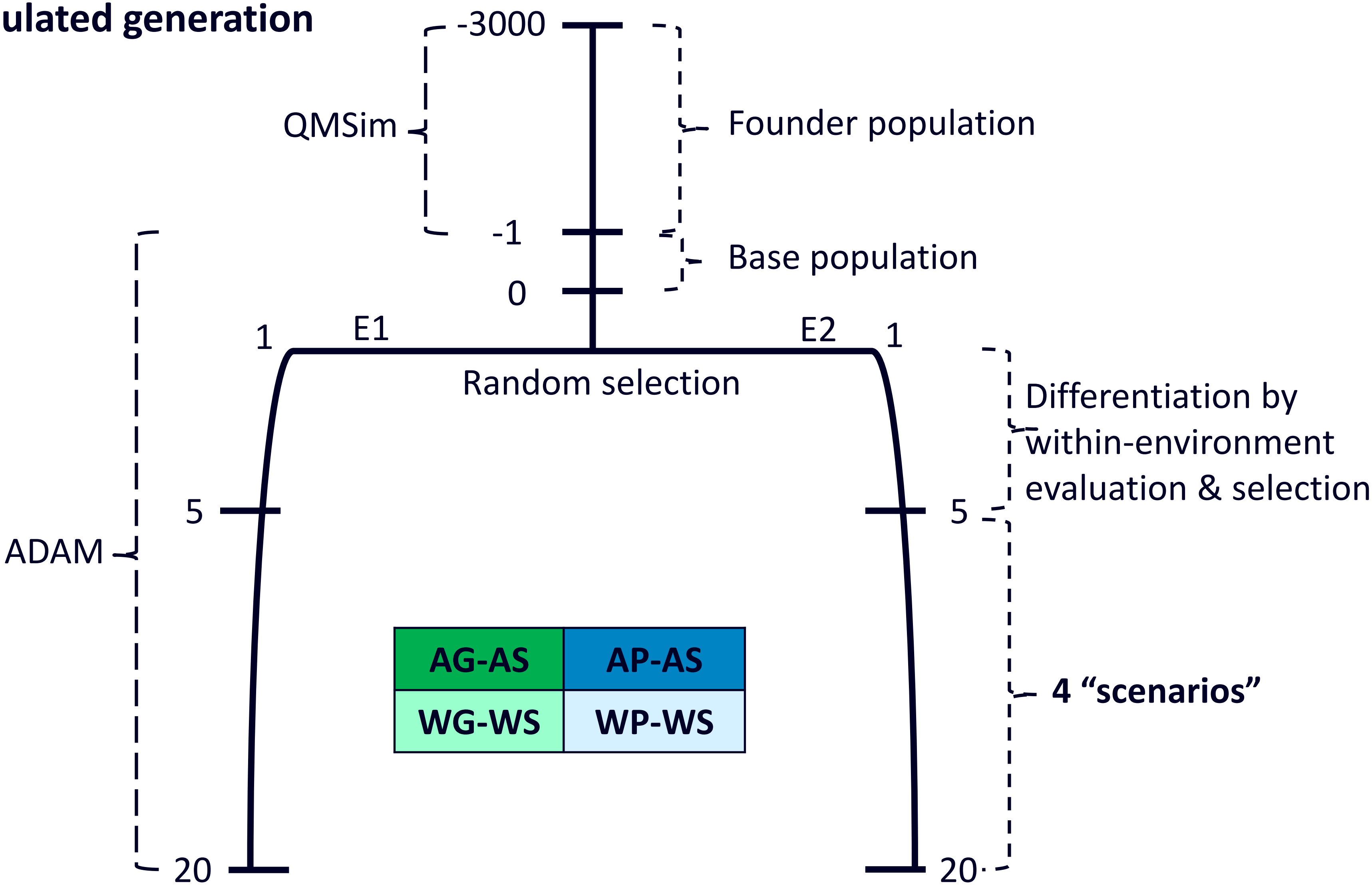
G×E

($r_g < 1$)

Hypothesis

GS breeding programs would realize larger benefits regarding genetic gain and rate of inbreeding by cooperation, and more probability for long-term cooperation in the presence of G×E than conventional PS breeding programs.

☐ Simulated generation



4 “scenarios”

AG-AS (cooperative GS)	**A**cross-environment ss**G**BLUP & **A**cross-environment selection for **S**ire
WG-WS (independent GS)	**W**ithin-environment ss**G**BLUP & **W**ithin-environment selection for **S**ire
AP-AS (cooperative PS)	**A**cross-environment **P**BLUP & **A**cross-environment selection for **S**ire
WP-WS (independent PS)	**W**ithin-environment **P**BLUP & **W**ithin-environment selection for **S**ire

Other parameters

- 2,000 QTL, 40,000 SNP , 30 chromosomes
- r_g (G×E) : 0.5~0.9
- h^2 of the goal trait: 0.1~0.5
- Initial genetic level, 0; initial genetic variance, 1
- Truncation selection
- Number of selected

	♂ ; ♀	generation t = 1~5	generation t = 6~20
Equal sizes	E1	50; 1000	50; 1000
	E2	50; 1000	50; 1000
Unequal sizes	E1	20; 400	80; 1600
	E2	50; 400	50; 1600

- 3 offspring per dam
- 50 replicates

Genetic evaluation

$$\begin{bmatrix} \boldsymbol{y}_1 \\ \boldsymbol{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \boldsymbol{e}_1 \\ \boldsymbol{e}_2 \end{bmatrix}$$

$\boldsymbol{y}_\mathbf{i}$: vector of observations in *i* th environment, *i* =1, 2

$\boldsymbol{\beta}_\mathbf{i}$: vector of herd-year-season fixed effects in *i* th environment

$\mathbf{a}_\mathbf{i}$: vector of additive genetic effects in *i* th environment

$\mathbf{e}_\mathbf{i}$: vector of residual effects of in *i* th environment

$\mathbf{X}_\mathbf{i}$ and $\mathbf{Z}_\mathbf{i}$: incidence matrices connecting $\boldsymbol{\beta}_\mathbf{i}$ and $\mathbf{a}_\mathbf{i}$ to y_i, respectively.

$$\begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} \sim N\left(0, \begin{bmatrix} \sigma^2_{a_1} & \boldsymbol{r_g}\sigma_{a_1}\sigma_{a_2} \\ & \sigma^2_{a_2} \end{bmatrix} \otimes \mathbf{H}\right), \quad \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} \sim N\left(0, \begin{bmatrix} \sigma^2_{e_1} & 0 \\ & \sigma^2_{e_2} \end{bmatrix} \otimes \mathbf{I}\right)$$

$\mathbf{H}$: matrix of additive genetic relationships among pedigree individuals (PBLUP), unified genetic relationship matrix of all genotyped and non-genotyped pedigree animals (ssGBLUP)

☐ G&F (equal sizes)

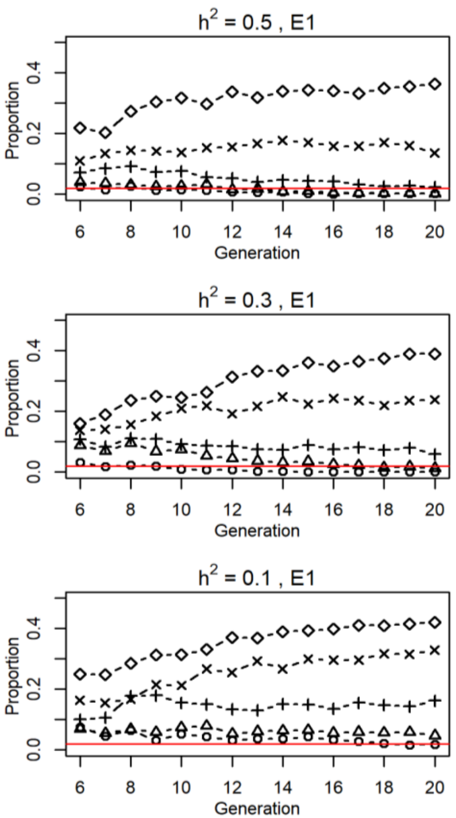
h^2	r_g	Genetic gain				Inbreeding rate			
		AG-AS		AP-AS		AG-AS		AP-AS	
0.1	0.8	0.4987	(0.023)	0.3079	(-0.008)	0.0100	(-0.145)	0.0130	(0.015)
	0.825	0.5141	(0.054)	0.3300	(0.064)	0.0096	(-0.179)	0.0132	(0.031)
	0.85	0.5331	(0.093)	0.3173	(0.023)	0.0093	(-0.205)	0.0129	(0.006)
	0.875	0.5454	(0.118)	0.3387	(0.092)	0.0097	(-0.171)	0.0138	(0.076)
	0.9	0.5818	(0.193)	0.3400	(0.096)	0.0106	(-0.094)	0.0124	(-0.034)
0.2	0.8	0.5983	(0.037)	0.3815	(0.025)	0.0097	(-0.04)	0.0115	(-0.068)
	0.825	0.5920	(0.026)	0.3768	(0.012)	0.0090	(-0.109)	0.0119	(-0.03)
	0.85	0.6171	(0.07)	0.3769	(0.012)	0.0086	(-0.149)	0.0116	(-0.059)
	0.875	0.6384	(0.107)	0.3860	(0.037)	0.0087	(-0.139)	0.0125	(0.018)
	0.9	0.6546	(0.135)	0.3954	(0.062)	0.0088	(-0.129)	0.0109	(-0.111)
0.3	0.8	0.6448	(0.012)	0.4236	(0.039)	0.0091	(-0.071)	0.0109	(-0.057)
	0.825	0.6522	(0.023)	0.4312	(0.057)	0.0082	(-0.163)	0.0118	(0.021)
	0.85	0.6632	(0.041)	0.4182	(0.026)	0.0082	(-0.163)	0.0102	(-0.116)
	0.875	0.6887	(0.081)	0.4224	(0.036)	0.0078	(-0.204)	0.0114	(-0.013)
	0.9	0.7047	(0.106)	0.4397	(0.078)	0.0081	(-0.173)	0.0097	(-0.154)
0.4	0.8	0.6945	(0.035)	0.4583	(0.038)	0.0085	(-0.086)	0.0101	(-0.026)
	0.825	0.6868	(0.024)	0.4583	(0.038)	0.0083	(-0.108)	0.0105	(0.02)
	0.85	0.7014	(0.046)	0.4622	(0.046)	0.0077	(-0.172)	0.0095	(-0.075)
	0.875	0.7199	(0.073)	0.4503	(0.02)	0.0074	(-0.204)	0.0107	(0.038)
	0.9	0.7542	(0.124)	0.4767	(0.079)	0.0076	(-0.183)	0.0095	(-0.077)
0.5	0.8	0.7228	(0.023)	0.4849	(0.007)	0.0086	(-0.044)	0.0093	(-0.111)
	0.825	0.7257	(0.027)	0.4736	(-0.017)	0.0081	(-0.1)	0.0104	(-0.003)
	0.85	0.7368	(0.043)	0.4835	(0.004)	0.0074	(-0.178)	0.0091	(-0.132)
	0.875	0.7622	(0.079)	0.4864	(0.01)	0.0068	(-0.244)	0.0098	(-0.063)
	0.9	0.7923	(0.121)	0.5080	(0.055)	0.0078	(-0.133)	0.0088	(-0.161)

9.7%

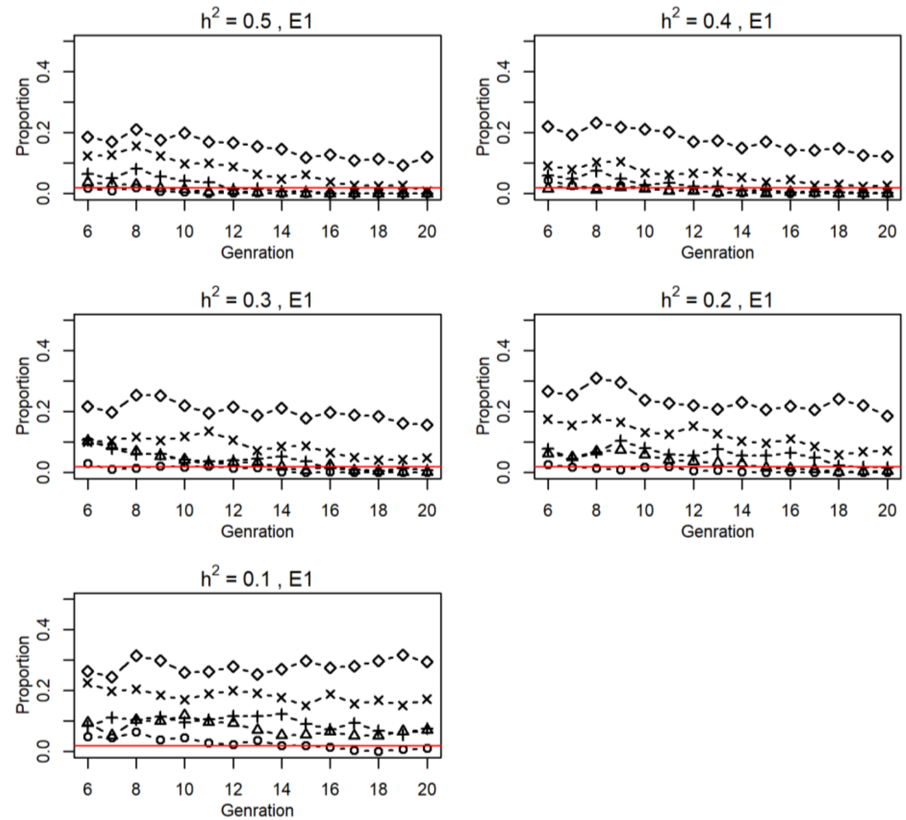
24.7%

Probability of long-term cooperation (equal sizes)

AG-AS: 0.85~0.875



AP-AS: ≥ 0.9



r_g =0.8 r_g =0.825 r_g =0.85 r_g =0.875 r_g =0.9

☐ G (unequal sizes; $h^2 = 0.3$)

	r_g	Genetic gain			
		AG-AS		AP-AS	
E1	**0.5**	0.4851	(0.039)	0.3359	(-0.019)
	0.6	0.4888	(0.047)	0.3337	(-0.025)
	0.7	0.5152	(0.104)	0.3510	(0.025)
	0.8	0.6223	(0.333)	0.3787	(0.107)
	0.9	0.7083	(0.517)	0.4175	(0.22)
E2	**0.5**	0.7266	(0)	0.4463	(-0.03)
	0.6	0.7319	(0.007)	0.4589	(-0.003)
	0.7	0.7329	(0.008)	0.4597	(-0.001)
	0.8	0.7439	(0.024)	0.4625	(0.005)
	0.9	0.7582	(0.043)	0.4579	(-0.005)

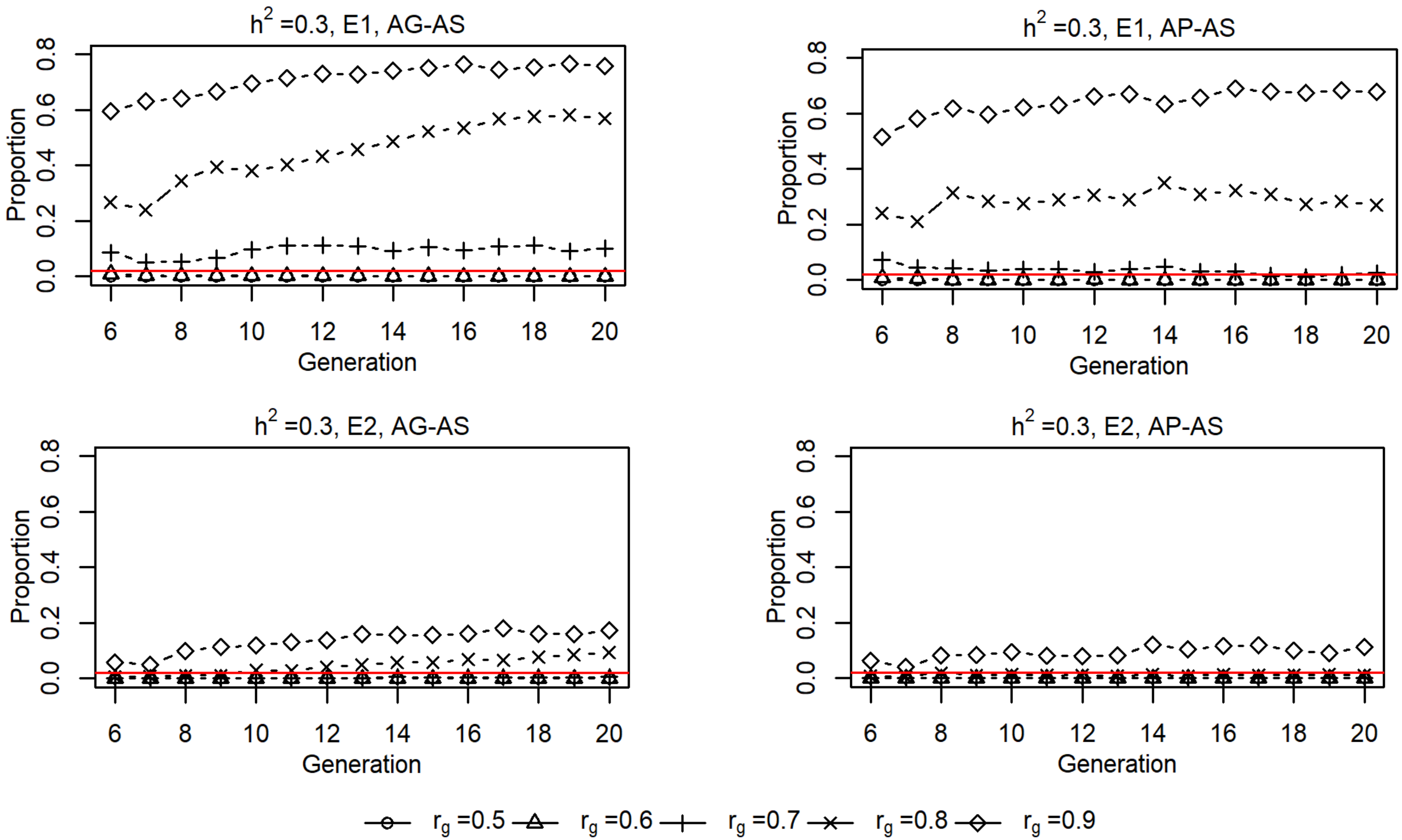
29.7%

4.8%

Probability of long-term cooperation (unequal sizes; $h^2 = 0.3$)

AG-AS: 0.6~0.7 (small)
0.7~0.8 (large)

AP-AS: 0.7~0.8 (small)
0.8~0.9 (large)



Take-home messages

- we recommend cooperative GS breeding programs within proper levels of G × E

- Cooperative GS breeding programs more benefitial to small populations while also beneficial but much less to large populations.

Thanks!