Impacts of Genotype-by-Environment Interaction on across-Environment Genomic Evaluation and Joint Selection of Bulls

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BACKGROUND

 $P = G + E + G \times E$



(J. C. Bowman, 1972)

Reranking
$$\Rightarrow r_g < 1$$





M & M



2 environments both select for MY with $r_{g_{(MY_1,MY_2)}}$ less than 1





M & M

□ 3 solutions (generation 6-20)

AG-J (Basic solution)



Across-environment Genomic evaluation & Joint selection of bulls (Coop, GS)

 $W \\ \text{ithin-environment} \ G \\ \text{enomic evaluation} \\$

& Within-environment selection of bulls (Non-coop, GS)

A cross-environment T raditional evaluation

& **J**oint selection of bulls (Coop, non GS)





M & M

□ Individual evaluation

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

 y_i : vector of observations of *i*th trait, *i*=1, 2

 β_i : vector of herd-year-season fixed effects in *i*th environment

a_i: vector of additive genetic effects of *i*th trait

 \mathbf{e}_i : vector of residual effects of *i* th trait

 X_i and Z_i : incidence matrices connecting β_i and a_i to y_i , respectively.

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

 \Box Linkage disequilibrium (LP) matrix of additive genetic relationships among pedigree individuals (BLUP),

unified genetic relationship matrix of all genotyped and

2,000 QTL, 40,000 markers tomly distributed among 30 tomly distributed among 30

(randomly distributed among 30 chromosomes of 100 cM each)

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Danish Red Dairy Cattle (incl. 6,581 animals with 43,621 markers) otyped



□ Stochastic simulation (50 replicates)

ADAM

Program to simulate selective-breeding schemes for animals and plants

Developers

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(*∆F based on 6000 IBD loci)

D Proportion of foreign sires in AG-J



 $- \bullet r_g = 0.8$ $- \Delta r_g = 0.825 + r_g = 0.85$ $- \star r_g = 0.875 + r_g = 0.9$ $- \bullet Y = 0.02$

(* Equal Population Sizes: select 50 or 1000 9 / generation 6-20)



- Proportion of foreign sires in AG-J
 - ▶ 0 ~ 42.6%
 - > Higher r_g , weaker GxE, more foreigners
 - > $r_a < 0.85 \sim 0.875$, coop diverged $r_g > 0.85 \sim 0.875$, long-term coop
 - " split-point " r_g : 0.85~0.875



 \rightarrow $r_{a} = 0.825 \rightarrow$ $r_{a} = 0.85 \rightarrow$ $r_{a} = 0.875 \rightarrow$ $r_{a} = 0.9$ r_a =0.8 _0_





\square Illustration for "*split – point* " r_g : **0.85~0.875** in AG-J



Fig. Distributions of male GEBVs for a randomly selected replicate in AG-J & EPS. (h²=0.3)





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D Understand "*split – point* " r_g : **0.85~0.875** in AG-J











 \square Absolute $\Delta G/\Delta F$ in AG-J

> Higher r_g , higher ΔG

 \succ "turning-point " r_g : 0.85~ 0.875





D Understand "*turning* – *point* " r_g : **0.85~0.875** in AG-J

(E1, h²=0.3)

	r _g	Sex	Generation										
r_i^2			20	19	18	17	16	15	14	13	12	11	10
	0.8	ð	1500	50	50	50	50	50	50	50	50	49	50
		우		1000	679	534	457	405	363	339	332	314	308
stor i	0.005	ð	1500	50	50	50	50	50	50	49	50	50	48
	0.825	Ŷ		1000	683	536	456	408	360	331	301	292	290
÷	0.95	ð	1500	50	50	50	50	50	50	49	50	50	50
	0.85	<u></u>		1000	694	551	456	401	370	344	325	315	307
	0.875	ð	1500	50	54	59	64	74	72	78	76	69	65
		<u>٩</u>		1000	707	580	503	475	463	454	456	446	444
	0.9	\$	1500 -	50	54	55	55	57	59	59	62	59	59
		<u></u>		1000	692	543	481	450	421	425	424	423	42.6 N PA



 r_i : long-term genetic contribution of ancestor α : constant departure from H-W proportion

(Bijma P et al., 2000)



D Understand "*turning* – *point* r_g " = "split – point r_g " : 0.85~0.875 in AG-J







- \blacksquare Relative * $\Delta G/\Delta F$ in AG-J
 - r∆G >1: coop beneficial for genetic gain
 - r∆F <1: coop beneficial for controling inbreeding



(* Relative to WG-W situation)



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D Proportion of foreign sires in AG-J



(* Unequal Population Sizes: E1 select 50 & 400 P /generation₆₋₂₀ E2 select 50 & 1600 P /generation₆₋₂₀)

 Δ r_a = 0.825 + r_a = 0.85 - r_a = 0.875 - r_a = 0.9

Generation



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Generation

—o— r_a =0.8

Y=0.02



Fig. Distributions of male GEBVs for a randomly selected replicate in AG-J & UPS. (h²=0.3)





 \blacksquare Absolute $\Delta G/\Delta F$ in AG-J

\blacktriangleright Δ G increased as r_g increased,	r _g =0.8	0.
E1 (small), larger increment: preference for coop	r _g =0.825	0.
E2 (big), larger ∆G: self-advantage	r _g =0.85	0.
	r_0975	\cap







D Relative $\Delta G/\Delta F$ in AG-J

- > Coop beneficial to $\Delta G/\Delta F$
- > E1 (small), larger increment: preference for coop

	٢٨	ΔG	٢z	ΔF
	E1	E2	E1	E2
r _g =0.8	1.33	1.02	0.78	0.96
r _g =0.825	1.36	1.02	0.96	0.97
r _g =0.85	1.43	1.03	1.00	0.95
r _g =0.875	1.46	1.03	1.08	0.94
r _g =0.9	1.52	1.04	1.04	0.97





CONCLUSIONS

opportunity of accounting for $G \times E$

- > For EPS, $r_g < 0.8$, little possibility in coop; $r_g < 0.85 \sim 0.875$, short-term coop; $r_g > 0.85 \sim 0.875$, long-term coop possible
- \succ For UPS, smaller environment more inclined to coop; long-term coop allowed at lower r_g
- > Coop in favor of genetic gain and controlling inbreeding
- > More opportunities of utilizing $G \times E$ in the era of GS



REFERENCE

- 1. Falconer DS: The Problem of Environment and Selection. Am Nat 1952,86(830):293–298.
- 2. Montaldo HH: Genotype by environment interactions in livestock breeding programs: A review. Interciencia 2001,26(6):229-235.
- Hugo H M, Alejandra Pelcastre-Cruz, Héctor Castillo-Juárez, Héctor Castillo-Juárez, Castillo-Juárez H: Genotype × environment interaction for fertility and milk yield traits in Canadian, Mexican and US Holstein cattle. Spanish Journal of Agricultural Research 2017,15(2):1-9.
- 4. Falconer DS, Mackary TFC: **19.Correlated characters** in **Introduction to quantitative genetics**. 4th ed. Longman Group; 1996.
- 5. Banos G, Smith C: Selecting bulls across countries to maximize genetic improvement in dairy cattle. J Anim Breed Genet 1991,108:174-181.
- 6. Mulder HA, Bijma P: **Benefits of cooperation between breeding programs in the presence of genotype by** environment interaction. J Dairy Sci 2006,89(5):1727-1739.







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Thanks for listening & questions



(http://www.nordicebv.info/)



