



Improving genomic predictions with inbreeding and non-additive effects using two hybrid admixed populations in maize

Morgane Roth, Aurélien Beugnot, Tristan Mary-Huard, Laurence Moreau, Alain Charcosset, Julie Fiévet

► To cite this version:

Morgane Roth, Aurélien Beugnot, Tristan Mary-Huard, Laurence Moreau, Alain Charcosset, et al.. Improving genomic predictions with inbreeding and non-additive effects using two hybrid admixed populations in maize. Eucarpia Biometrics, Sep 2022, Gif-sur-Yvette, France. 2022. hal-04132668

HAL Id: hal-04132668

<https://hal.science/hal-04132668>

Submitted on 20 Jun 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Improving genomic predictions with inbreeding and non-additive effects using two hybrid admixed populations in maize

Morgane Roth^{1,2*}, Aurélien Beugnot³, Tristan Mary-Huard^{3,4}, Laurence Moreau³, Alain Charcosset³, Julie B. Fiévet³

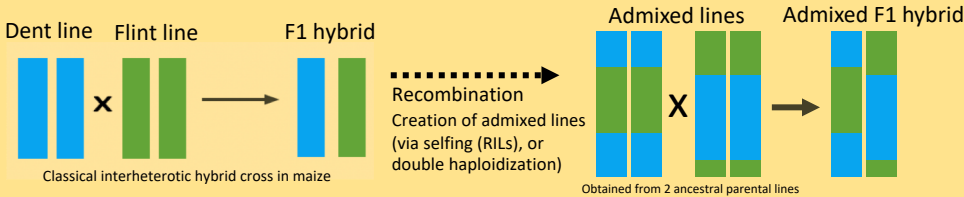
¹ Plant Breeding Research Division, Agroscope, Wädenswil, 8820 Zurich, Switzerland
² present address: INRAE, GAFL 1052, Allée des Chênes, 84143 Montfavet, France
³ Université Paris-Saclay, INRAE, CNRS, AgroParisTech, UMR GQE-Le Moulon, 91190 Gif-sur-Yvette, France
⁴ Université Paris-Saclay, INRAE, AgroParisTech, UMR MIA-Paris Paris, 75005 Paris, France
* contact: morgane.roth@inrae.fr



Background

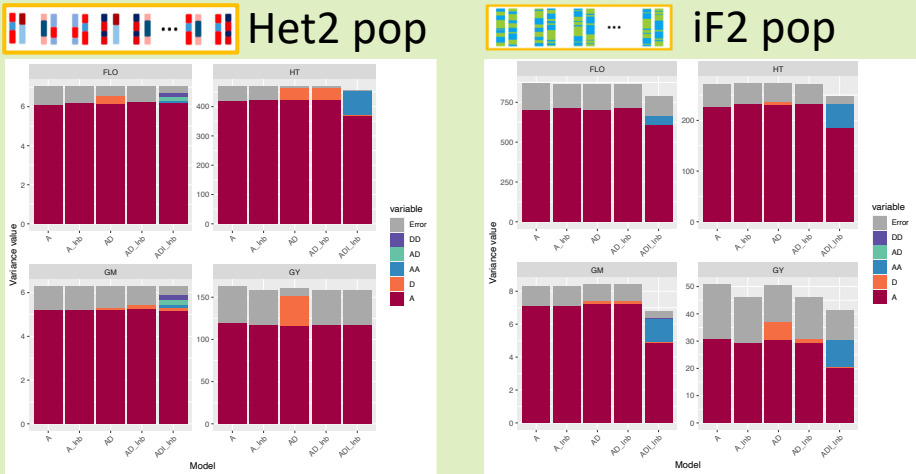
Why are non-additive effects relevant?

- Non-additive genetics effects are involved in complex traits and heterosis**
They include dominance, epistasis and contribute to inbreeding depression
- Predicting non-additive effects is useful, but challenging**
We should use the Natural and Orthogonal Interactions Approach (Vitezica et al. 2017) to alleviate the confounding between genetic effects
- Can we improve genomic predictions using orthogonal models and inbreeding parameters?**
Application to maize using admixed hybrid material



Result 1

Variance component analyses



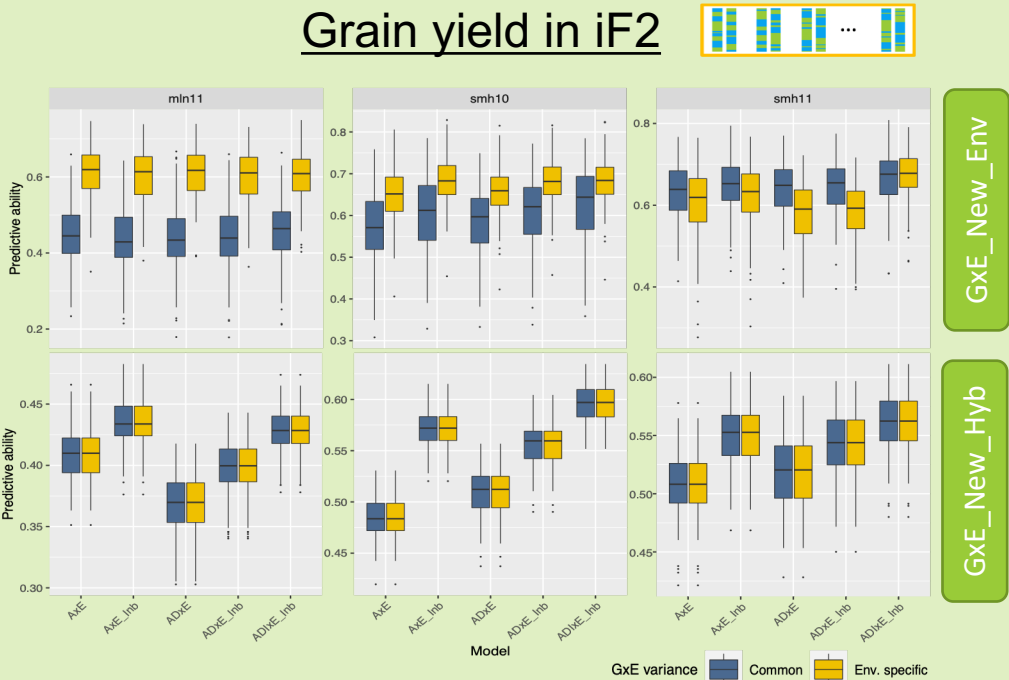
Analyses on adjusted means

- Stable total variance across the different models tested
- Including inbreeding reduces the variance associated with dominance effects
- Large epistatic effects for all traits, prevalence of additive by additive effect

Result 3

Prediction performance across environments

Grain yield in iF2



- In GxE_New_Env, the type of GxE modelling depends on correlation between environments and heritability
- Including non-additive effects efficient for predicting new hybrids in all environments (GxE_New_Hyb)
→ Gain of 0.02 to 0.11 in predictive ability for GY in iF2

Material and Methods

Two admixed hybrid maize populations



291 hybrids

Obtained from 321 admixed lines (admixture between 300 dent and 304 flint parental lines)

265 hybrids

obtained from 184 highly recombinant inbred lines (admixture between one dent and one flint parental lines)

→ Phenotyped for 4 traits (flowering date FLO, plant height HT, grain moisture GM and grain yield GY) at 3 to 5 sites for iF2 and Het2 respectively

Modeling non-additive effects

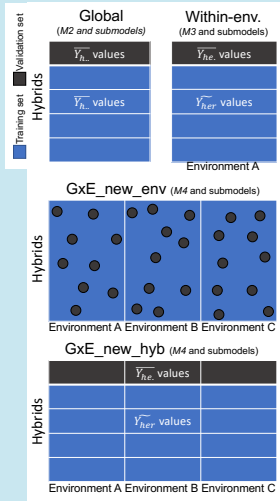
Most complete model for adjusted-means

$$\begin{aligned} \bar{Y}_{h..} &= \mu + \beta Inb_h + A_h + D_h + AA_h + AD_h + DD_h + \varepsilon_h \\ A &\sim N(0, \sigma_A^2 K_A), D \sim N(0, \sigma_D^2 K_D), \varepsilon \sim N(0, \sigma_\varepsilon^2 I) \\ AA &\sim N(0, \sigma_{AA}^2 K_{AA}), AD \sim N(0, \sigma_{AD}^2 K_{AD}), DD \sim N(0, \sigma_{DD}^2 K_{DD}) \\ A &\perp D \perp AA \perp AD \perp DD \perp \varepsilon \end{aligned}$$

Inb_h : percentage of homozygosity ; β : associated regression coefficient ; A_h and D_h : additive and dominant random effects associated to hybrid h ; AA_h , AD_h and DD_h : random effects modeling epistasis, accounting for additive by additive, additive by dominant and dominant by dominant effects, respectively; ε_h : random error ; $\sigma_A^2 \dots \sigma_{DD}^2$: variance terms associated to genetic effects ; $K_A \dots K_{DD}$: kinship matrices corresponding to each genetic effect, after Vitezica et al. 2017.

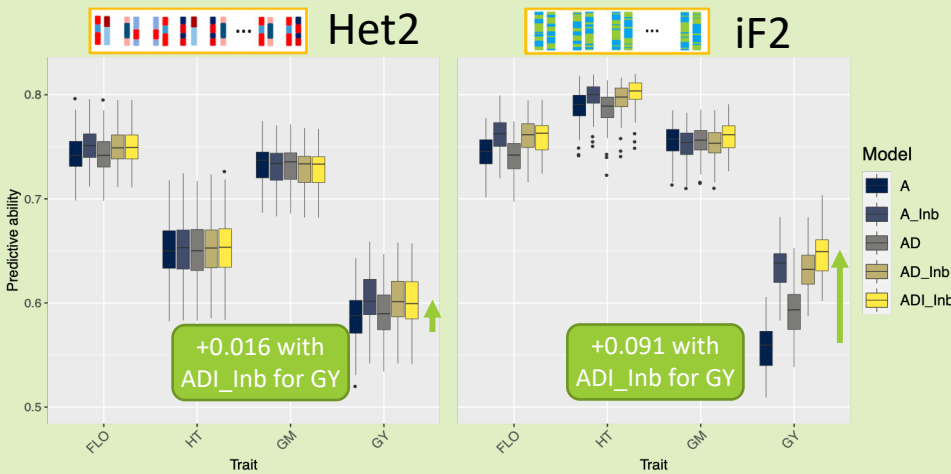
5 different sub-models considered

Effects	Inbreeding	A	D	AA	AD	DD	Residual
A		X					X
A_Inb	X	X					X
AD		X	X				X
AD_Inb	X	X	X				X
ADI_Inb	X	X	X	X	X	X	X



Result 2

Prediction performance - Adjusted means



- Overall more accurate predictions with inbreeding in the model
- Gains in accuracy strongest in iF2 population, especially for yield

Outlook

Practical use for maize breeding

Improved predictions of complex traits with A_Inb and ADI_Inb models

Facilitating the use of admixed plant material in breeding

More diversified genetic resources, less genetic drift

Useful references:
Roth, M., Beugnot, A., Mary-Huard, T., Moreau, L., Charcosset, A., and Fiévet, J.B. (2022). Improving genomic predictions with inbreeding and nonadditive effects in two admixed maize hybrid populations in single and multienvironment contexts. *Genetics* 220: iyac018.
Varona, L., Legarra, A., Toro, M.A., and Vitezica, Z.G. (2022). Genomic Prediction Methods Accounting for Nonadditive Genetic Effects. In *Genomic Prediction of Complex Traits, Methods in Molecular Biology*, Vol 2467, N. Ahmadi, and J. Bartholomé, eds. (New York), pp. 219–243.
Vitezica, Z.G., Legarra, A., Toro, M.A., and Varona, L. (2017). Orthogonal estimates of variances for additive, dominance, and epistatic effects in populations. *Genetics* 206, 1297–1307.