Application of single-step genomic evaluation for crossbred performance

Tao Xiang
Aarhus University,Denmark
AgroParisTech, France

Bjarne Nielsen, Guosheng Su, Andres Legarra, Ole F Christensen

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Background

- **Reference:** *Christensen, O. F et al.* (2014). Genomic evaluation of both purebred and crossbred performances. *Genetics Selection Evolution*, 46(1), 23.

$$\mathbf{y}_A = \mathbf{X}_A\boldsymbol{\beta}_A + \mathbf{Z}_A\mathbf{a}_A + \mathbf{e}_A$$

$$\mathbf{y}_B = \mathbf{X}_B\boldsymbol{\beta}_B + \mathbf{Z}_B\mathbf{a}_B + \mathbf{e}_B$$

$$\mathbf{y}_{AB} = \mathbf{X}_{AB}\boldsymbol{\beta}_{AB} + \mathbf{c}_{AB} + \mathbf{e}_{AB}$$

$$\mathbf{c}_{AB} = 0.5(\mathrm{Z}_{AB,A}\mathbf{c}_A + \mathbf{Z}_{AB,B}\mathbf{c}_B) + \mathbf{MS}_{AB}$$

$$\mathrm{Var}\begin{bmatrix}\boldsymbol{a}_A\\ \boldsymbol{c}_A\end{bmatrix} = \begin{bmatrix}\sigma^2_{a_A} & \sigma_{a_A,c_A}\\ \sigma_{c_A,a_A} & \sigma^2_{c_A}\end{bmatrix}\otimes \boldsymbol{A}_A$$

Background

$$\mathbf{c}_{\mathrm{AB}} = \mathbf{c}_{\mathrm{AB}}^{(\mathrm{A})} + \mathbf{c}_{\mathrm{AB}}^{(\mathrm{B})}$$

$$\mathbf{y}_{\mathrm{AB}} = \mathbf{X}_{\mathrm{AB}}\boldsymbol{\beta}_{\mathrm{AB}} + \mathbf{c}_{\mathrm{AB}}^{(\mathrm{A})} + \mathbf{c}_{\mathrm{AB}}^{(\mathrm{B})} + \mathbf{e}_{\mathrm{AB}}$$

$$\mathrm{Var}\begin{bmatrix} \boldsymbol{c}_{A} \\ \boldsymbol{c}_{AB}^{(A)} \end{bmatrix} = \mathbf{A}^{(A)}\,\sigma_{c_A}^2$$

$$\mathrm{Var}\begin{bmatrix} \mathbf{a}_{\mathrm{A}} \\ * \\ \mathbf{c}_{\mathrm{A}} \\ \mathbf{c}_{\mathrm{AB}}^{(\mathrm{A})} \end{bmatrix} = \begin{bmatrix} \sigma_{a_A}^2 & \sigma_{a_A,c_A} \\ \sigma_{c_A,a_A} & \sigma_{c_A}^2 \end{bmatrix} \otimes \mathbf{A}^{(\mathrm{A})}$$

How to construct $\boldsymbol{A}^{(A)}$ and $\boldsymbol{A}^{(B)}$?

Background

Pedigree-based breed A specific

partial relationship matrix

$$\mathrm{A}^{(\mathrm{A})} = \begin{bmatrix} \mathbf{A}_{\mathrm{A}} & \mathbf{A}^{(\mathrm{A})}_{\mathrm{A,AB}} \\ \mathbf{A}^{(\mathrm{A})}_{\mathrm{AB,A}} & \mathbf{A}^{(\mathrm{A})}_{\mathrm{AB,AB}} \end{bmatrix}$$

Marker-based breed A specific

partial relationship matrix

$$G^{(A)} = \begin{pmatrix} G^{(A)}_{A,A} & G^{(A)}_{A,AB} \\ G^{(A)}_{AB,A} & G^{(A)}_{AB,AB} \end{pmatrix}$$

Assumption: known alleles origin

- $\mathbf{G}^{(A)}$ **is adjusted, compatible with** $\mathbf{A}^{(A)}$

- Inverse scale of combined breed A partial relationship

$$\left(H^{(A)}\right)^{-1} = \begin{pmatrix} \left(G^{(A)}_{\omega}\right)^{-1} - \left(A^{(A)}_{11}\right)^{-1} & 0 \\ 0 & 0 \end{pmatrix} + \left(A^{(A)}\right)^{-1}$$

Materials & Methods

- **Phenotypic data**
  - Trait: TNB at the first parity of sows (h^2 is around 0.1)
  - Records: 293,339 Landrace (LL); 180,112 Yorkshire(YY);
    10,974 crossbreds (LY)
  - Purebreds farrowed 2003~2013; Crossbreds farrowed 2010-2013

- **Pedigree**
  - Traced back to year 1994 by DMU Trace (Madsen, 2010)
  - 332,929 LL & 210,554 YY

Materials & Methods

- **Models:**
  - Purebreds: $y = hys + month + hybrid + b_1 * age + b_2 * age^2 + \underline{a} + \underline{sb} + \underline{e}$

    $a \sim N(0, \mathbf{H}_{(L)}\sigma^2_{a_L})$ or $a \sim N(0, \mathbf{H}_{(Y)}\sigma^2_{a_Y})$, depending on LL and YY;
    $sb \sim N(0, \mathbf{I}\sigma^2_{sb})$; $e \sim N(0, \mathbf{I}\sigma^2_{e})$

  - Crossbreds: $y = hys + month + b1 * age + b2 * age^2 + \underline{c^{(L)}} + \underline{c^{(Y)}} + \underline{e}$

    $c^{(L)} \sim N(0, \mathbf{H}_{(L)}\sigma^2_{c_L})$, $c^{(Y)} \sim N(0, \mathbf{H}_{(Y)}\sigma^2_{c_Y})$, $e \sim N(0, \mathbf{I}\sigma^2_{e})$

Materials & Methods

- **Genotypes**
  - ➢41,009 SNPs (60K) genotyped in 7,723 LL & 7,785 YY

  - ➢7,940 SNPs (8K) genotyped in 5,203 LY
    $\xrightarrow{\text{Imputation}}$ 41,009 genotyped crossbred SNPs

- **Crossbred alleles tracing**
  - ➢ Two phased imputed crossbred alleles segmented to segments
  - ➢ LL and YY segmented to small segments same length, position
  - ➢ Crossbred phased segment should match to purebred segments
  - ➢ Proportions of matched segment counted in LL and YY separately

  - ➢ Known which phased LY allele originated from LL or YY

Materials & Methods

- **Scenarios (SC):**

Scenarios	Genotypes	Phenotypes	Targets
Nogen_SC	NO, pedigree only	All phenotypic records	• VC estimation • Model reliabilites for crossbred performance in purebred boars
Genpure_SC	7723LL, 7785YY		
Genall_SC	7723LL, 7785YY, 5203LY		

- $r^2 = \sum_{i=1}^{n}(1 - \mathrm{SEP}_{\mathrm{i}}^2/\sigma_{\mathrm{c}}^2)/n$

Results & Discussion

- **Genetic correlation between purebred and crossbred performance**

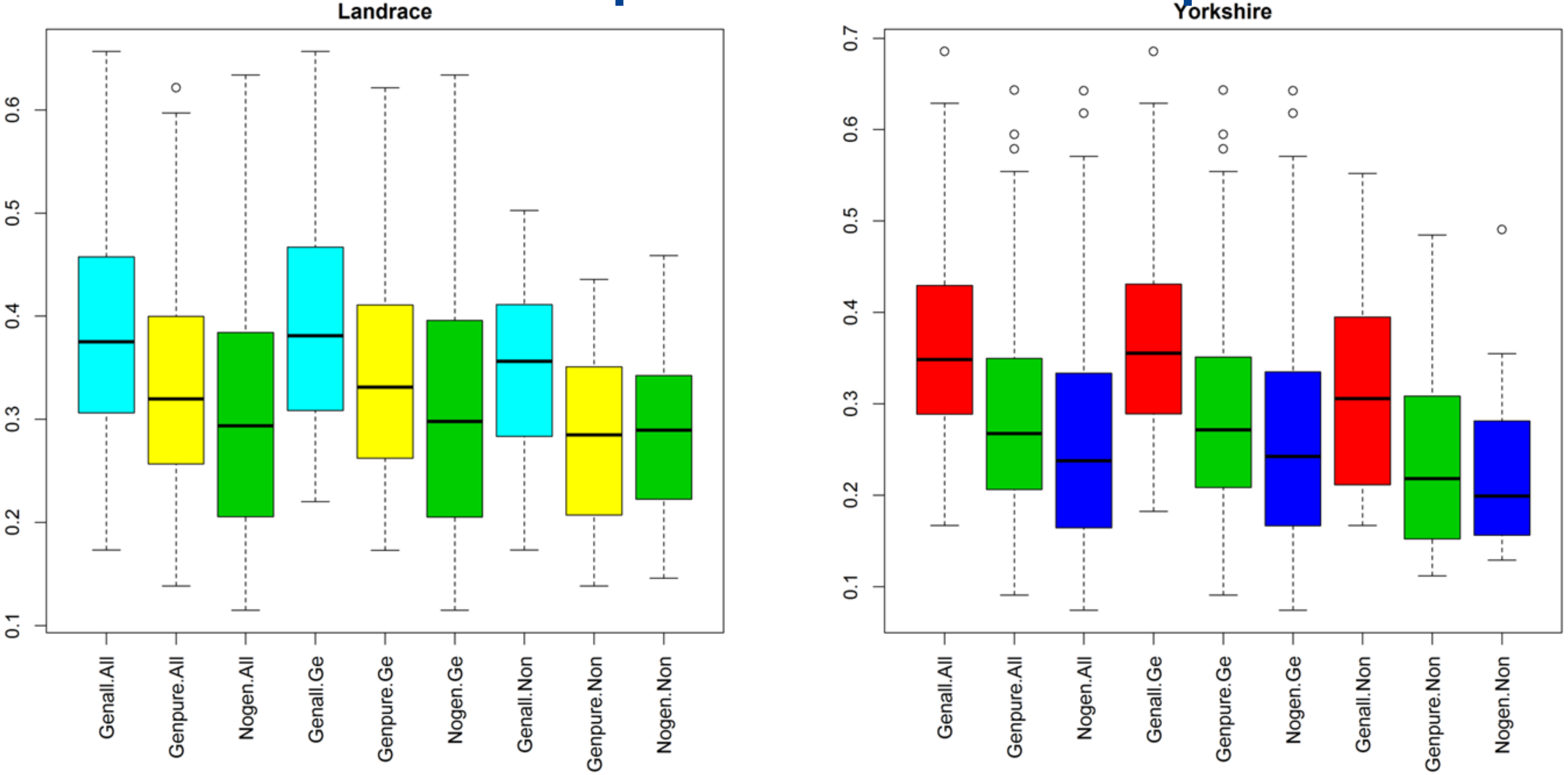
	Nogen_SC	Genpure_SC	Genall_SC
Landrace	0,700 (0,119)	0,736 (0,114)	0,785 (0,090)
Yorkshire	0,570 (0,129)	0,591 (0,124)	0,676 (0,100)

❖ **Confirm the existence of a moderate correlation.**

❖ **Crossbred genomic information reduce standard errors.**

Results & Discussion

- **Model reliabilities for purebred boars for cp.**



❖ **R^2 generally low, increases with genomic info included**

❖ **Non-genotyped animals benefit from genomic info on genotyped animals, especially crossbred info**

Conclusions

- **New single-step model is applicable for genetic evaluation for crossbred performance**
- **Model with marker information perform better than pedigree based model**
- **Crossbred genomic information is as essential as purebred genotypes**
- **Confirm moderate, positive genetic correlation between purebred and crossbred performance in TNB**

Thank you for your attention!