

# Impact of rare SNP variants on the genomic evaluation for conception rate

Tomasz Suchocki, A. Żarnecki, M. Jakimowicz and J. Szyda



**To verify whether including rare variants in genomic selection model allows to capture a considerable part of the missing heritability underlying cow conception rate (CR) under selection in dairy cattle.**



**Trait = cow conception rate ( $h^2=0.028$ )**

**33,534 HF reference bulls**

**46,216 SNP with  $MAF > 0.01$  (ORIG)**

**54,378 SNP without MAF selection (RARE)**

**23,448 HF candidate bulls**

**43,392 HF candidate cows**



$$\mathbf{y} = \mu + \mathbf{Z}_1 \mathbf{g} + \mathbf{Z}_2 \mathbf{a} + \boldsymbol{\varepsilon},$$

- $\mathbf{y}$  - deregressed EBV for CR
- $\mu$  - general mean
- $\mathbf{g}$  - additive SNP effect  $\left( \mathbf{g} \sim N\left(0, I \frac{\hat{\sigma}_a^2}{N_{\text{snp}}}\right) \right)$
- $\mathbf{Z}_1 \in \{-1, 0, 1\}$
- $\mathbf{a}$  - additive polygenic effects  $\left( \mathbf{a} \sim N(0, A \hat{\sigma}_{a^*}^2) \right)$
- $\boldsymbol{\varepsilon}$  - residuals  $\left( \boldsymbol{\varepsilon} \sim N(0, D \hat{\sigma}_\varepsilon^2) \right)$



Model 1:

$$\mathbf{y} = \beta_0 + \beta_1 \cdot \mathbf{G}_r + \boldsymbol{\varepsilon},$$

- $\mathbf{y}$  - deregressed EBV for CR
- $\mathbf{G}_r$  - GEBV for CR for truncated data set

Model 2:

$$\mathbf{y} = \beta_0 + \beta_1 \cdot \mathbf{PI}_r + \boldsymbol{\varepsilon},$$

- $\mathbf{PI}_r$  - pedigree index for CR for truncated data set

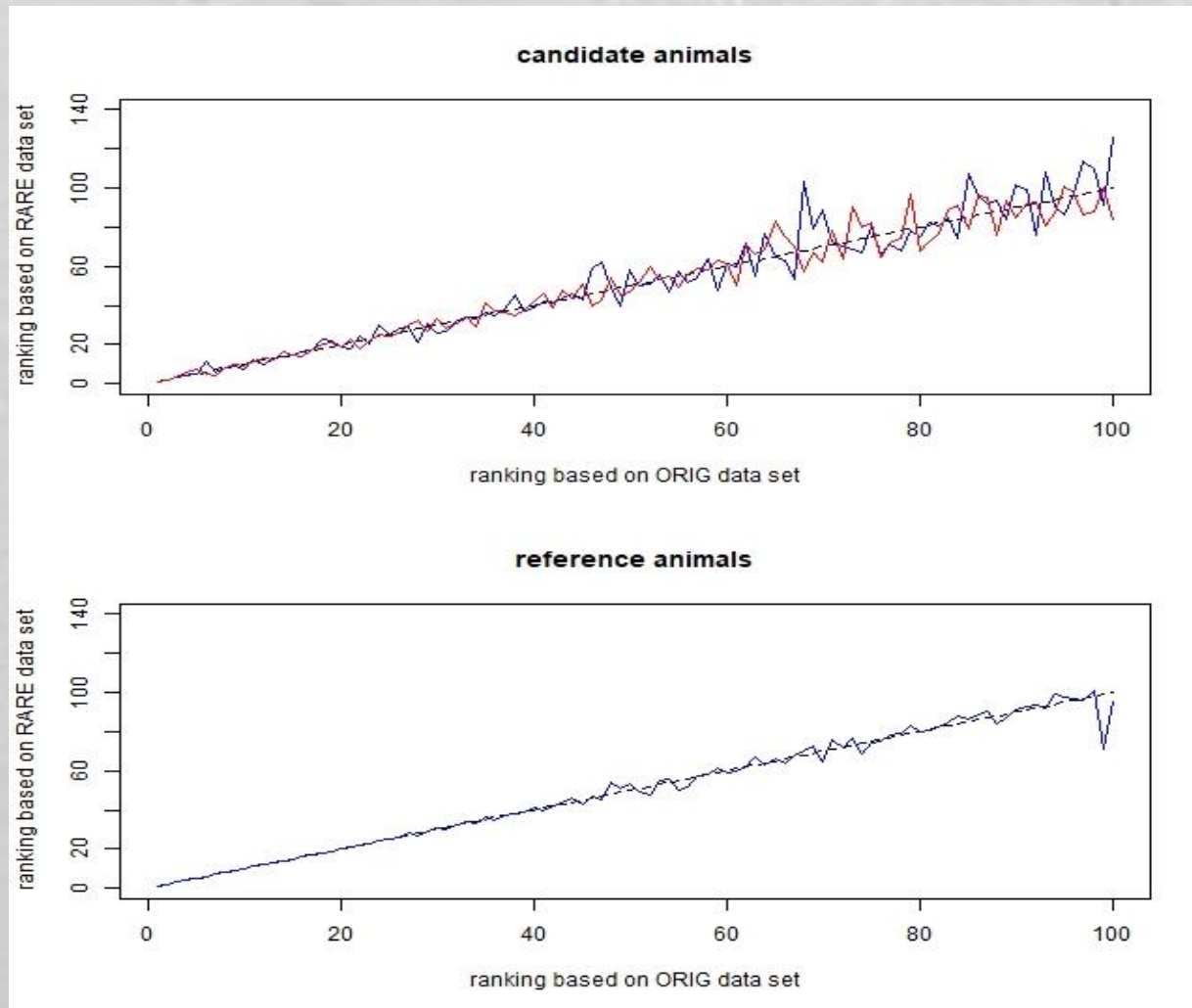


- Time of estimation SNP effects for ORIG data set = 8,252 seconds
- Time of estimation SNP effects for RARE data set = 1,0563 seconds (increasing of 28%)

Data set	$\hat{\beta}_1$	$SE(\hat{\beta}_1)$	$R^2_{\text{model1}}$	$R^2_{\text{model2}}$	$ \hat{\beta}_1 - E(\beta_1) $	t	Result of Interbull test
RARE	1.131	0.028	20.1	2.4	0.131	4.671	passed
ORIG	1.081	0.027	20.4	2.4	0.081	3.038	passed

Summary statistics of the Interbull genetic trend validation test based on the RARE and ORIG data set.





Re-ranking for CC1 of the 100 top candidate animals (blue = bulls, red = cows) and the 100 top reference bulls based on the RARE data set as compared to the ORIG data set.



## Using rare variants in evaluation

- more time consuming
- could have a stronger impact on selection, evaluation and reliability
- influence on ranking on top young bulls and cows

