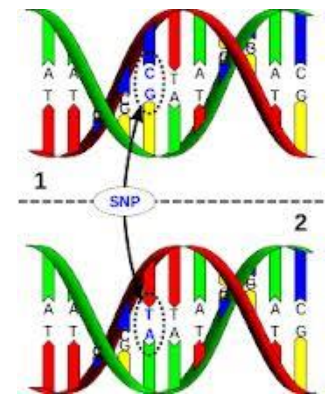
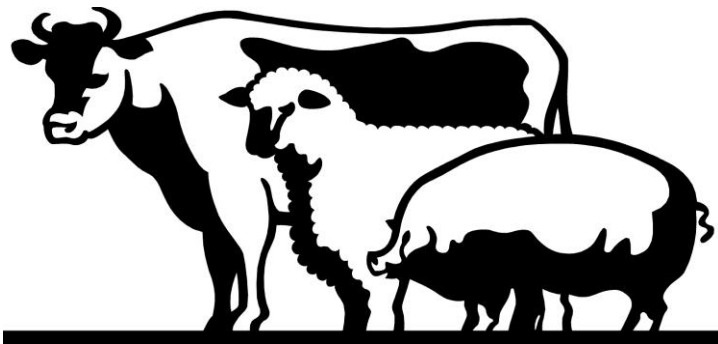


# Genomic information and inbreeding

AABSC



# Inbreeding- revision

- Mating of relatives
- Consequences
  - Many are bad, but not all.....
- Management – restricting mating of relatives
  - Optimal contribution selection
- How does Genomics change this?
  - *If performing truncation selection....*
  - *If performing optimal contribution selection...*

# Truncation selection

- TBLUP or Pedigree BLUP

Vs

- Genomic breeding value (GBLUP)
- Variation in BV among selection candidates

$$V_a = \frac{1}{4} \text{ sire} + \frac{1}{4} \text{ dam} + \frac{1}{2} \text{ MS}$$

# What information is used in BVs

- $$V_a = \frac{1}{4} \text{ sire} + \frac{1}{4} \text{ dam} + \frac{1}{2} \text{ MS}$$

Across family

Within Family

Table 2- The proportion of variation in breeding value explained by between family (Sire and Dam) and within family (MS) information.

<i>LIC</i>					<i>ADHIS</i>				
BV	Sire	Dam	MS+e	Prop. of PT	BV	Sire	Dam	MS+e	Prop. of PT
PA EBV	0.56	0.44	0.001	0.001	PA EBV	0.44	0.52	0.04	0.05
GEBV	0.43	0.26	0.31	0.56	GEBV	0.33	0.37	0.30	0.36
PT	0.21	0.31	0.48	1.0	PT	0.16	0.32	0.52	1.0

# Correlation of breeding values and co-selection of relatives

Breeding value type	Half sib correlation	Full Sib correlation	Accuracy
PA EBV	0.55	1.0	0.45
GEBV	0.50	0.85	0.57
TBV	0.26	0.53	1.0

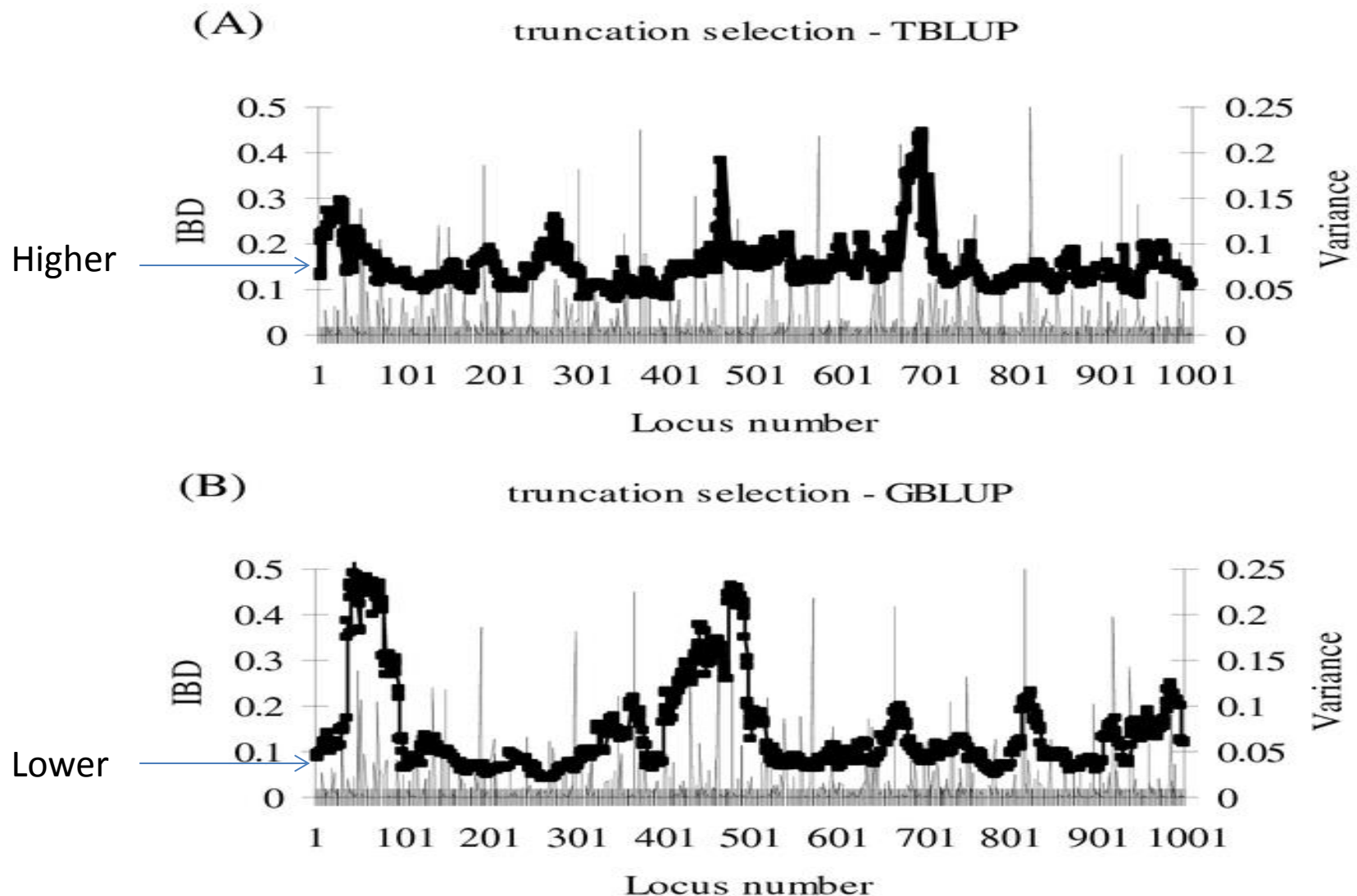
## Full Sibs

- share the same Parent average BV ( $\frac{1}{2}$  sire  $\frac{1}{2}$  dam)
- no longer the case with genomics

## Half Sibs

- Share different PA breeding values
- Small advantage of using G to restrict inbreeding

# Sonesson et al 2013



---- Selecting 100 sires and 100 dams from 3000 cand. ---- After 10 generations

# Truncation selection on breeding values estimated using TBLUP or GBLUP

Genetic gain

Inbreeding

Breeding value  
estimation

$\Delta G$  (se)

$\Delta F_{\text{ped}}$  (se)

$\Delta F_{\text{IBD}}$  (se)

TBLUP

2.49 (0.035)

0.0156 (0.0001)

0.0235 (0.0009)

GBLUP

2.77 (0.026)

0.0053 (0.0002)

0.0209 (0.0005)

# Genomics and Optimal contributions

- Measures of genetic merit ( $\bar{g}$ )
  - Pedigree vs genomic  
*Pedigree based BLUP --- Genomic BLUP*
- Measures of inbreeding
  - Pedigree vs genomic (A or G)  
*NRM (Pedigree) --- GRM (genomic)*

$$\mathbf{Max} = \mathbf{c}_t' \bar{\mathbf{g}}_t - \lambda \mathbf{c}_t' \mathbf{A}_t \mathbf{c}_t$$



# Measuring inbreeding

- Pedigree
  - The probability that animals share alleles IBD.
- Genomics
  - GRM (IBS) *or what is shared*.
  - others

# Genomic Inbreeding estimates

- Estimates of the number of homozygotes
  - Sharing of markers (IBS)
  - Long runs of homozygotes (more IBD)
- Genomic relationships (IBS)
  - Various methods
  - Choice of allele frequencies

# Example GRM

- $Z = M - 2(\pi - 0.5)$
- $ZZ' / 2 * \sum \pi_i(q_i)$  (more weighting to rare alleles)
- Choice of allele frequencies
  - Forni 2012
  - Sets base population
  - Although this is relative and is more important when combining data (Single step)

# management

- Optimal contribution
- Pedigree or genomic
  - Pedigree – expected based on IBD prob.
  - Genomic observed (although an estimate)

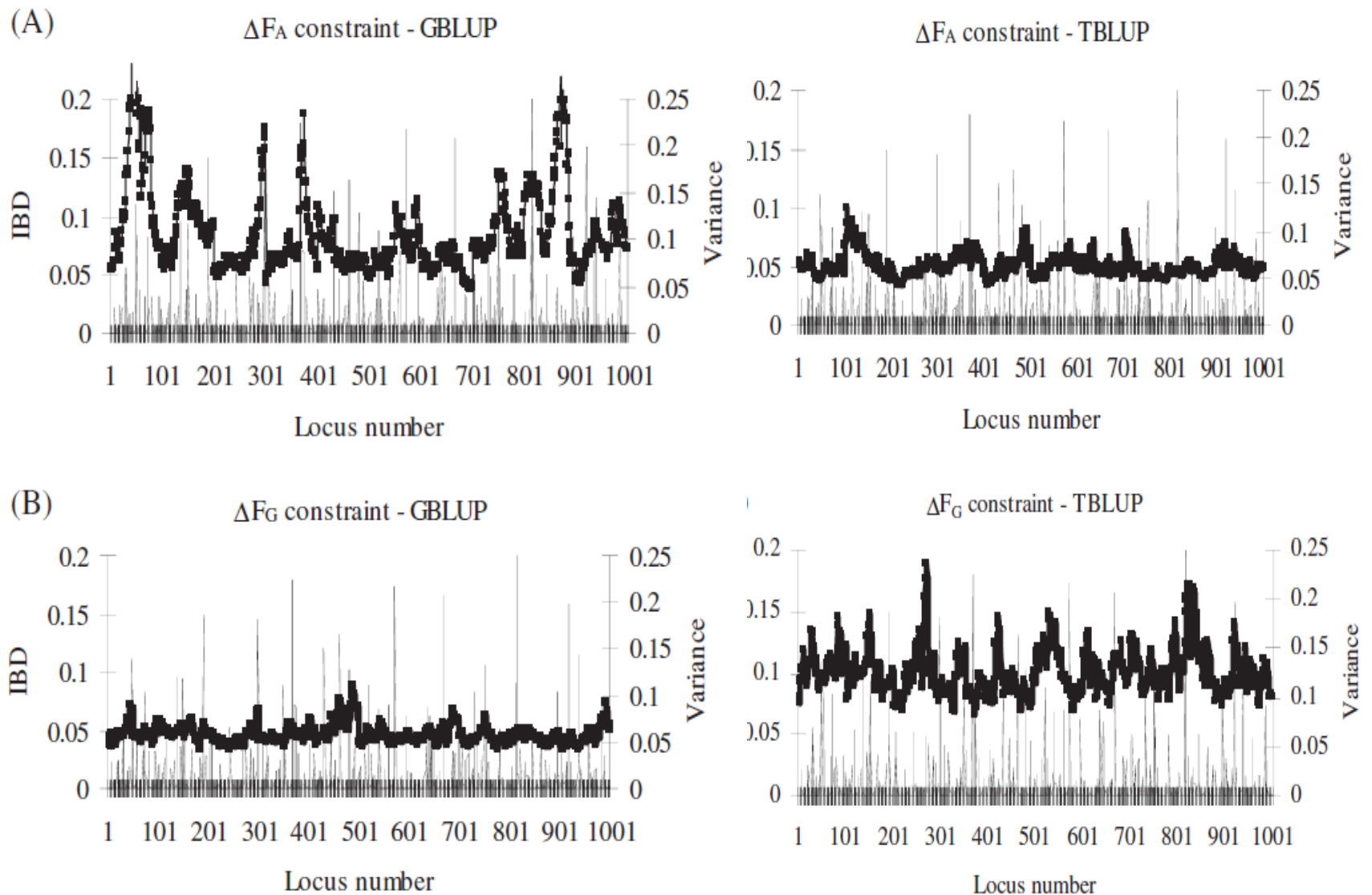
**Table 2 Optimum contribution selection on breeding values estimated using TBLUP or GBLUP**

Ntest	$\Delta F_d$	$\Delta G$ (se)	$\Delta F_{ped}$ (se)	$\Delta F_{IBD}$ (se)
<b><math>\Delta F_A</math> constraint – GBLUP</b>				
3000	0.005	3.08 (0.035)	0.0050 (0.0001)	0.0211 (0.0004)
6000	0.005	3.10 (0.035)	0.0048 (0.0001)	0.0226 (0.0004)
6000	0.010	3.31 (0.037)	0.0098 (0.0003)	0.0422 (0.0008)
<b><math>\Delta F_G</math> constraint – GBLUP</b>				
3000	0.005	1.91 (0.026)	0.0041 (0.0001)	0.0051 (0.0001)
6000	0.005	1.95 (0.024)	0.0039 (0.0001)	0.0053 (0.0001)
6000	0.010	2.41 (0.028)	0.0071 (0.0002)	0.0102 (0.0002)
<b><math>\Delta F_A</math> constraint – TBLUP</b>				
3000	0.005	2.26 (0.003)	0.0050 (0.0001)	0.0068 (0.0001)
6000	0.005	2.50 (0.003)	0.0049 (0.0001)	0.0074 (0.0001)
6000	0.010	2.63 (0.003)	0.0102 (0.0002)	0.0151 (0.0003)
<b><math>\Delta F_G</math> constraint – TBLUP</b>				
3000	0.005	1.41 (0.041)	0.0193 (0.0004)	0.0121 (0.0002)
6000	0.005	1.44 (0.039)	0.0185 (0.0004)	0.0122 (0.0002)
6000	0.010	1.48 (0.046)	0.0300 (0.0008)	0.0183 (0.0003)

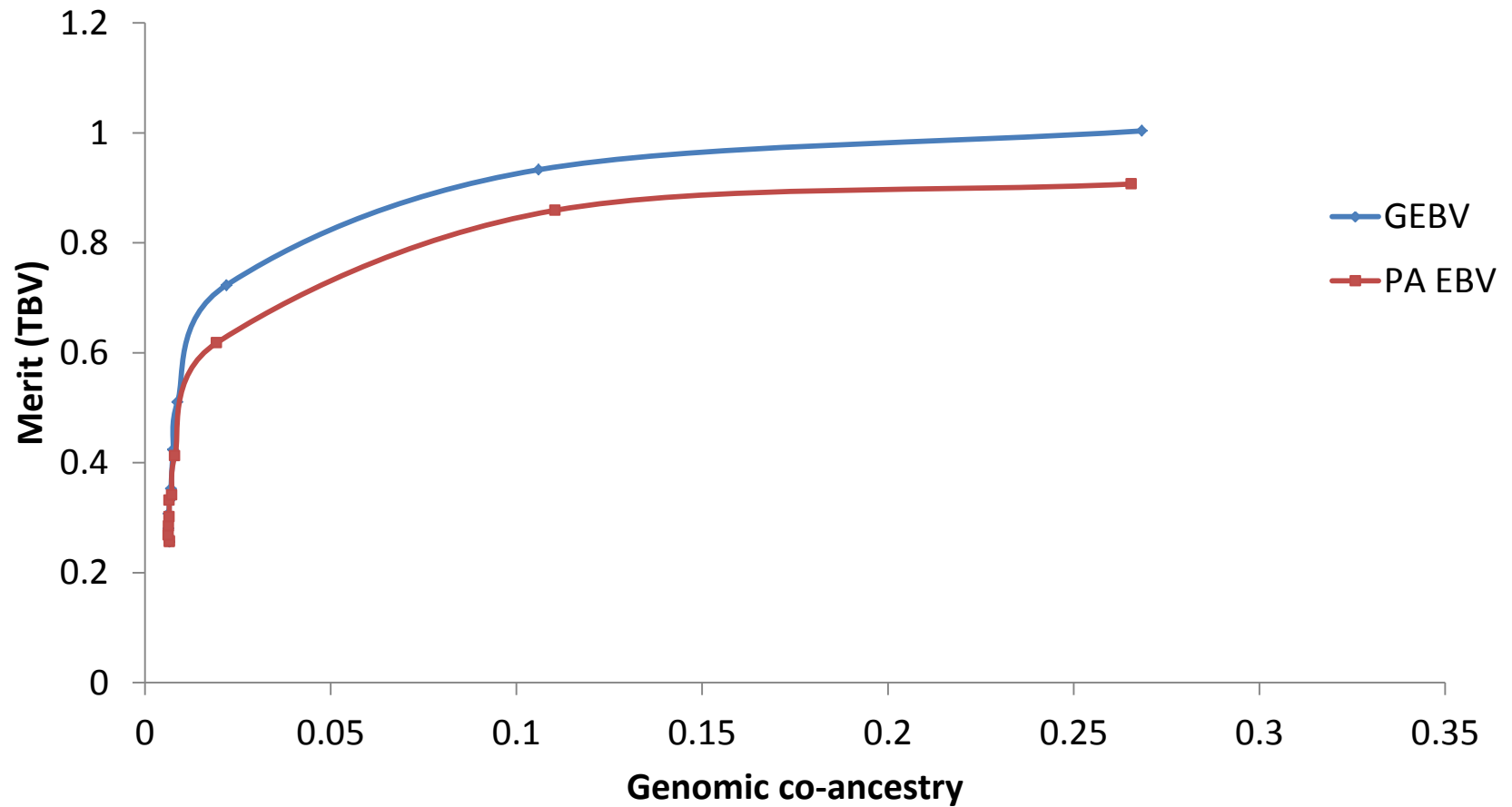
Genetic gain ( $\Delta G$ ), rate of inbreeding based on pedigree ( $\Delta F_{ped}$ ) and on genomic IBD ( $\Delta F_{IBD}$ ) relationship matrices at generation *G10* when the constraint on relationship was either pedigree-based ( $\Delta F_A$ ) or marker-based ( $\Delta F_G$ ) with TBLUP or GBLUP breeding value estimates<sup>a</sup>.

<sup>a</sup>Ntest = number of test sibs;  $\Delta F_d$  = desired rates of inbreeding; number of selection candidates = 3000.

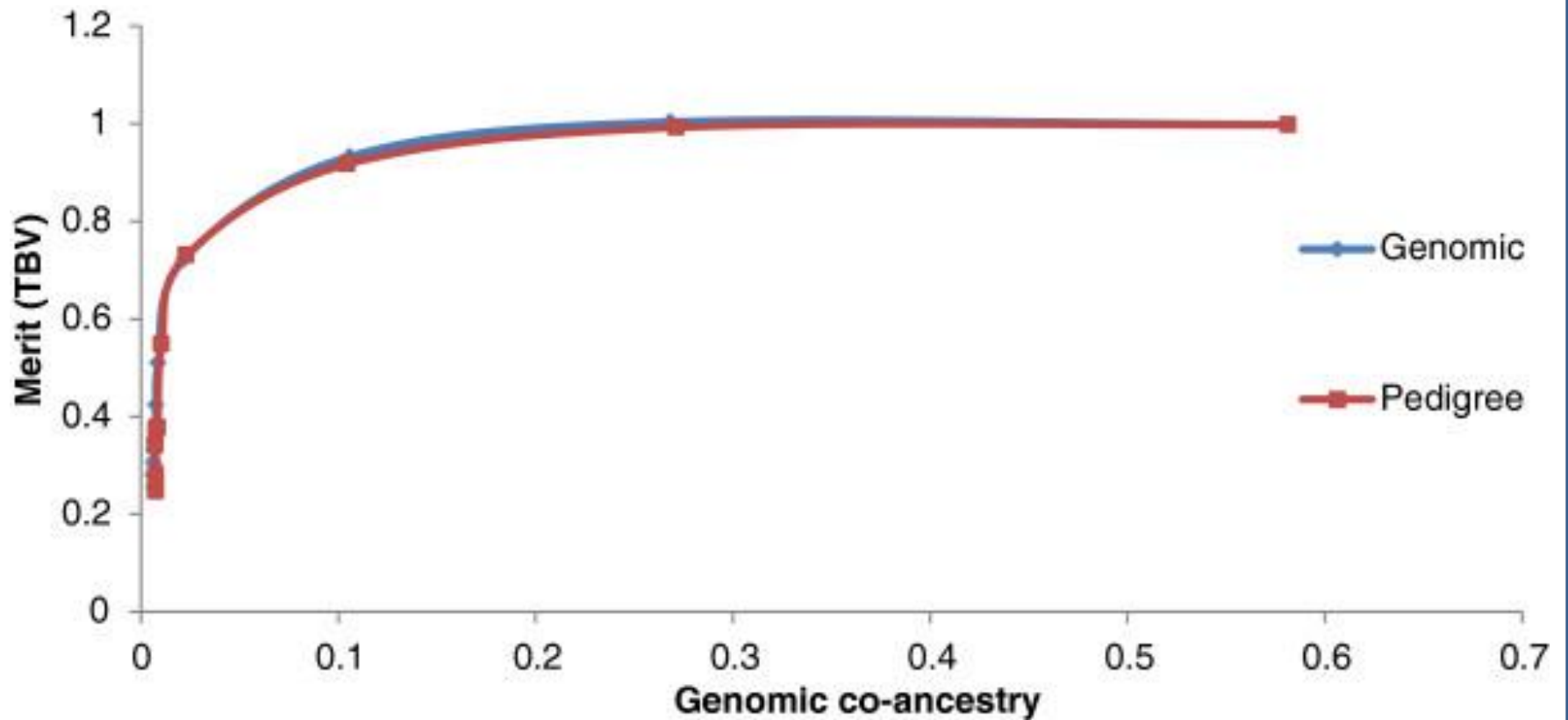
## IBD profiles with OC selection



# Entire frontier

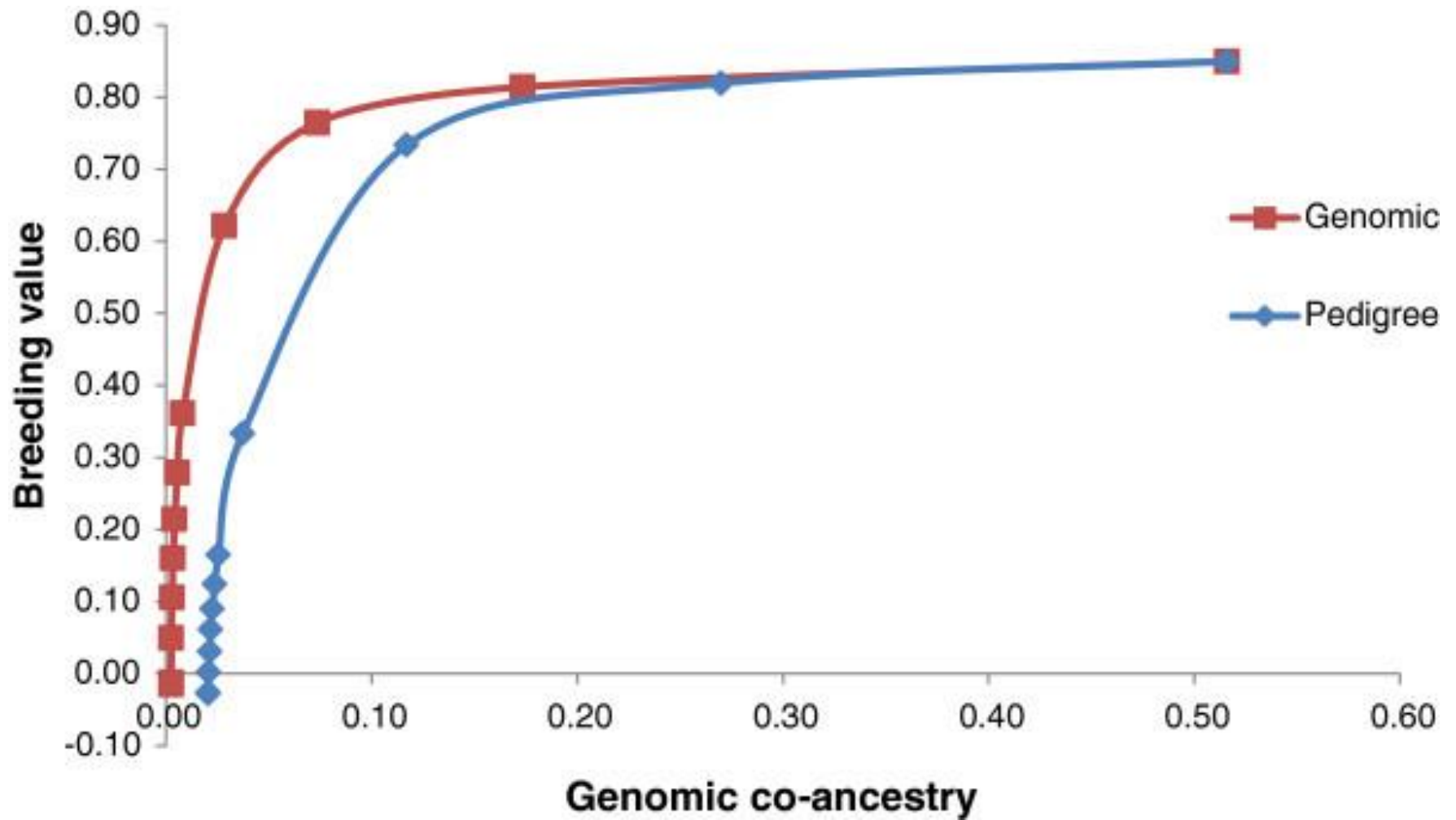


# Half sibs





# Full sibs



# Genomic information helps to manage inbreeding

- In two ways:
- 1. Using genomic relationships helps to restrict genomic inbreeding.
- 2. GEBV's utilize more Mendelian sampling variance.