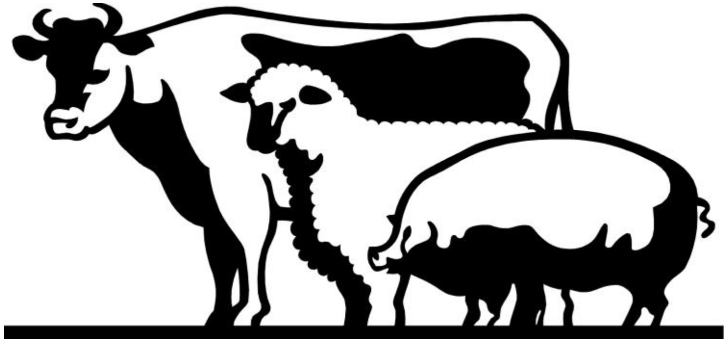
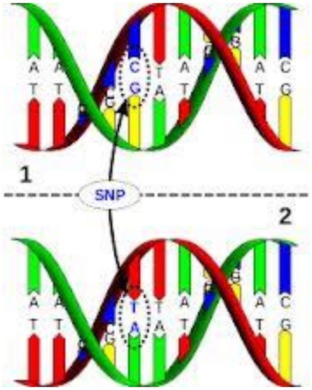
Genomic information and inbreeding

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

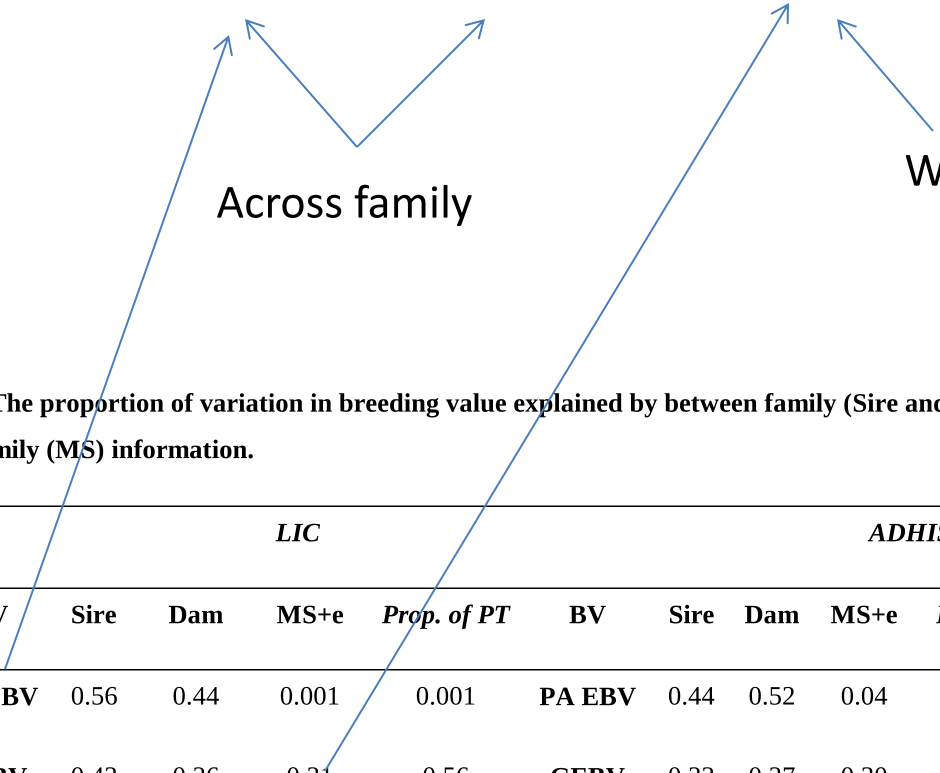
- Genomic breeding value (GBLUP)

- Variation in BV among selection candidates

Va = ¼ sire + ¼ dam + ½ MS

What information is used in BVs

- Va= ¼ sire + ¼ dam + ½ 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.

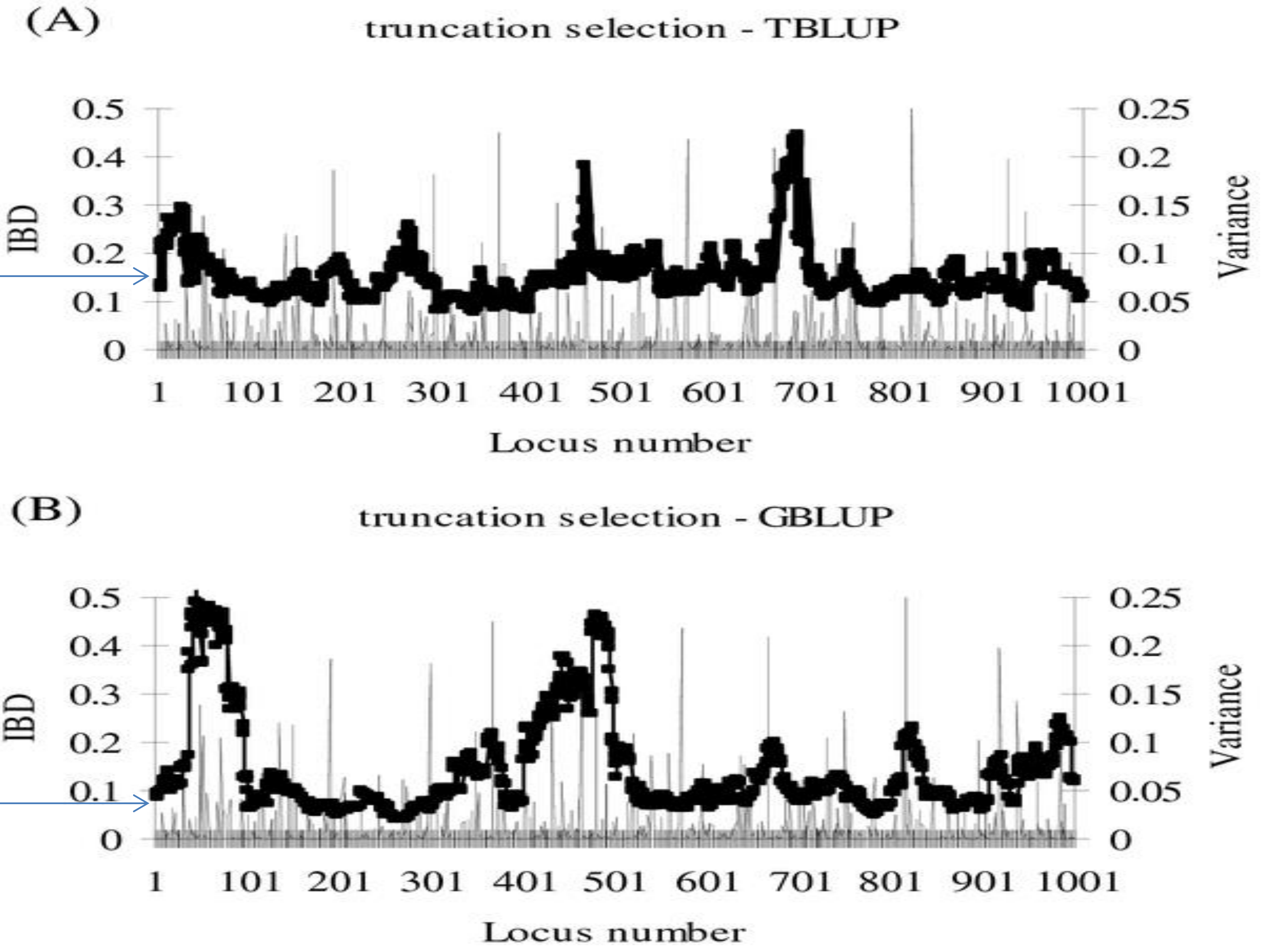
	LIC					*ADHIS*			
BV	**Sire**	**Dam**	**MS+e**	***Prop. of PT***	**BV**	**Sire**	**Dam**	**MS+e**	***Prop. of PT***
PA EBV	0.56	0.44	0.001	0.001	**PA EBV**	0.44	0.52	0.04	0.05
GEBV	0.43	0.26	0.31	0.56	**GEBV**	0.33	0.37	0.30	0.36
PT	0.21	0.31	0.48	1.0	**PT**	0.16	0.32	0.52	1.0

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 (½ sire ½ 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



Higher

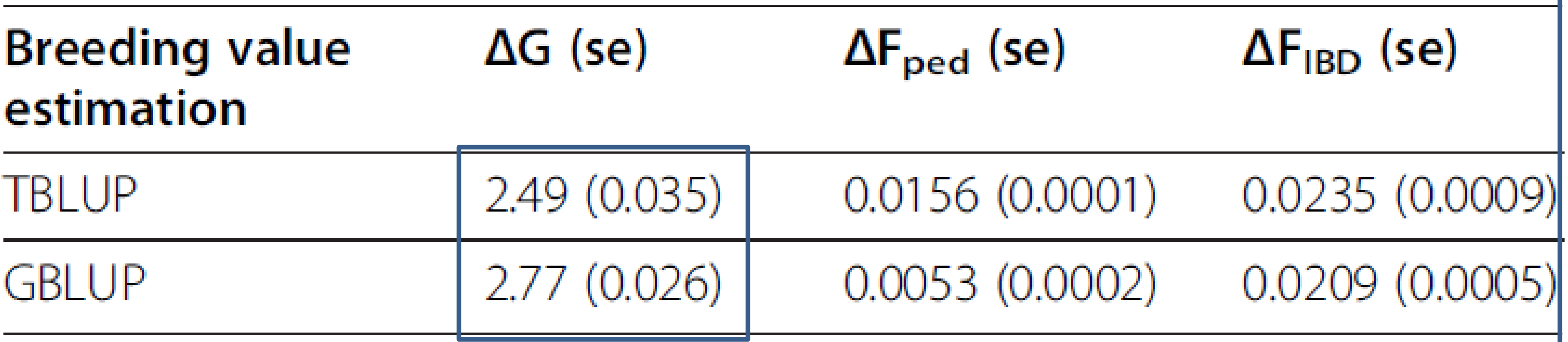
Lower

---- 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	**ΔG (se)**	**ΔF_{ped} (se)**	**ΔF_{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)

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

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(qi) (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)

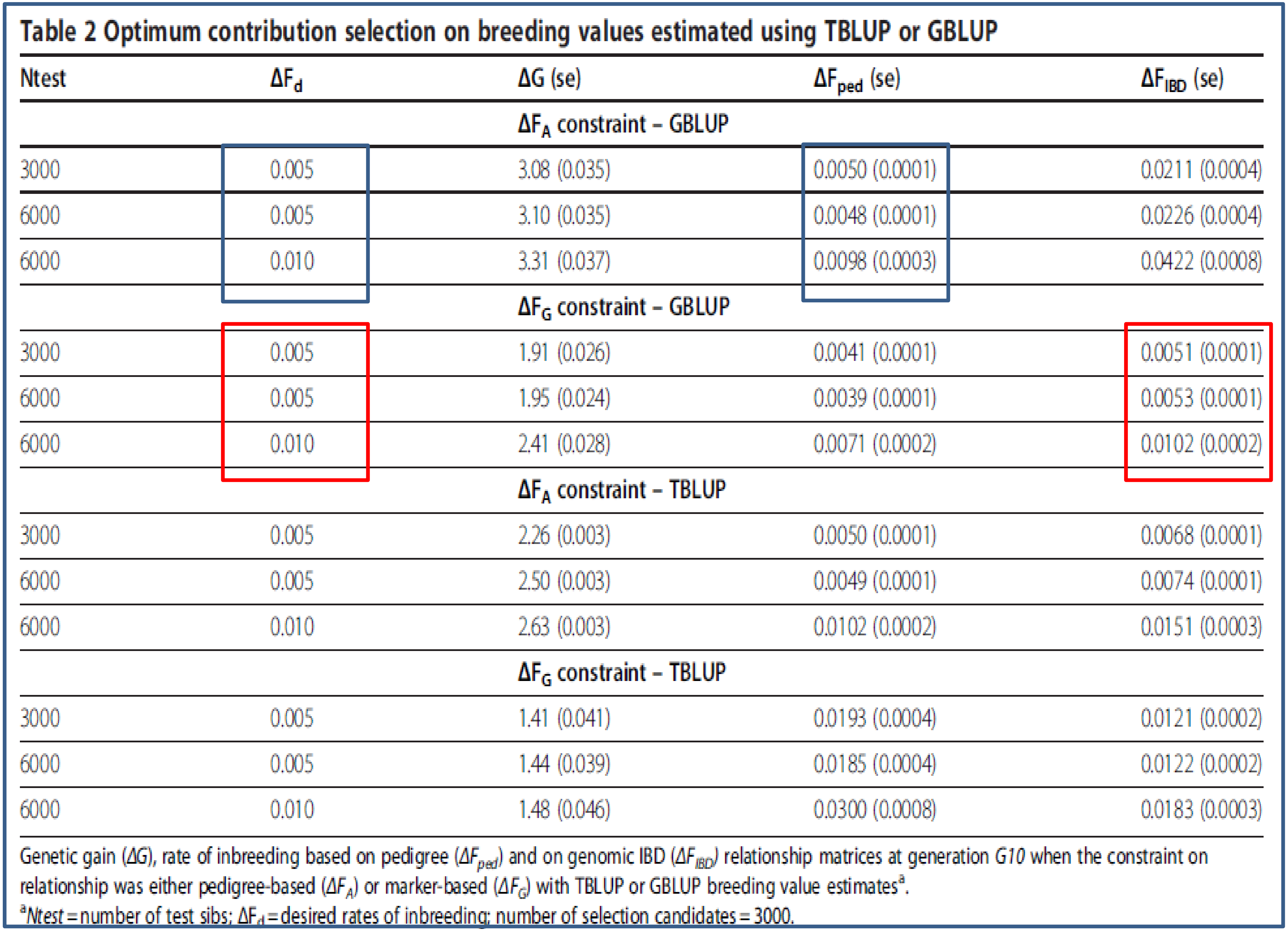


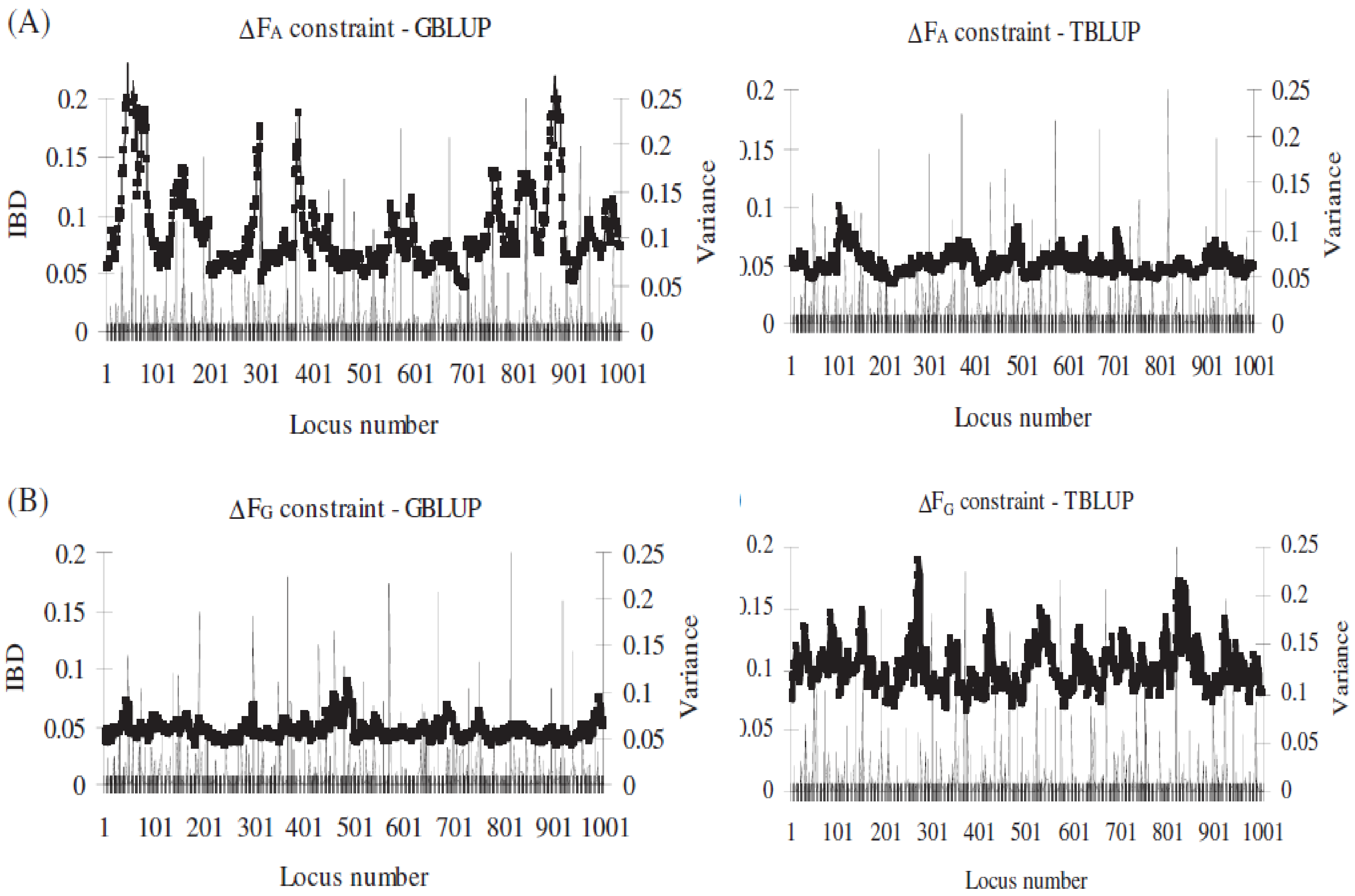
Table 2 Optimum contribution selection on breeding values estimated using TBLUP or GBLUP

Ntest	ΔF_d	ΔG (se)	ΔF_{ped} (se)	ΔF_{IBD} (se)
		ΔF_A constraint – GBLUP		
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)
		ΔF_G constraint – GBLUP		
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)
		ΔF_A constraint – TBLUP		
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)
		ΔF_G constraint – TBLUP		
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)

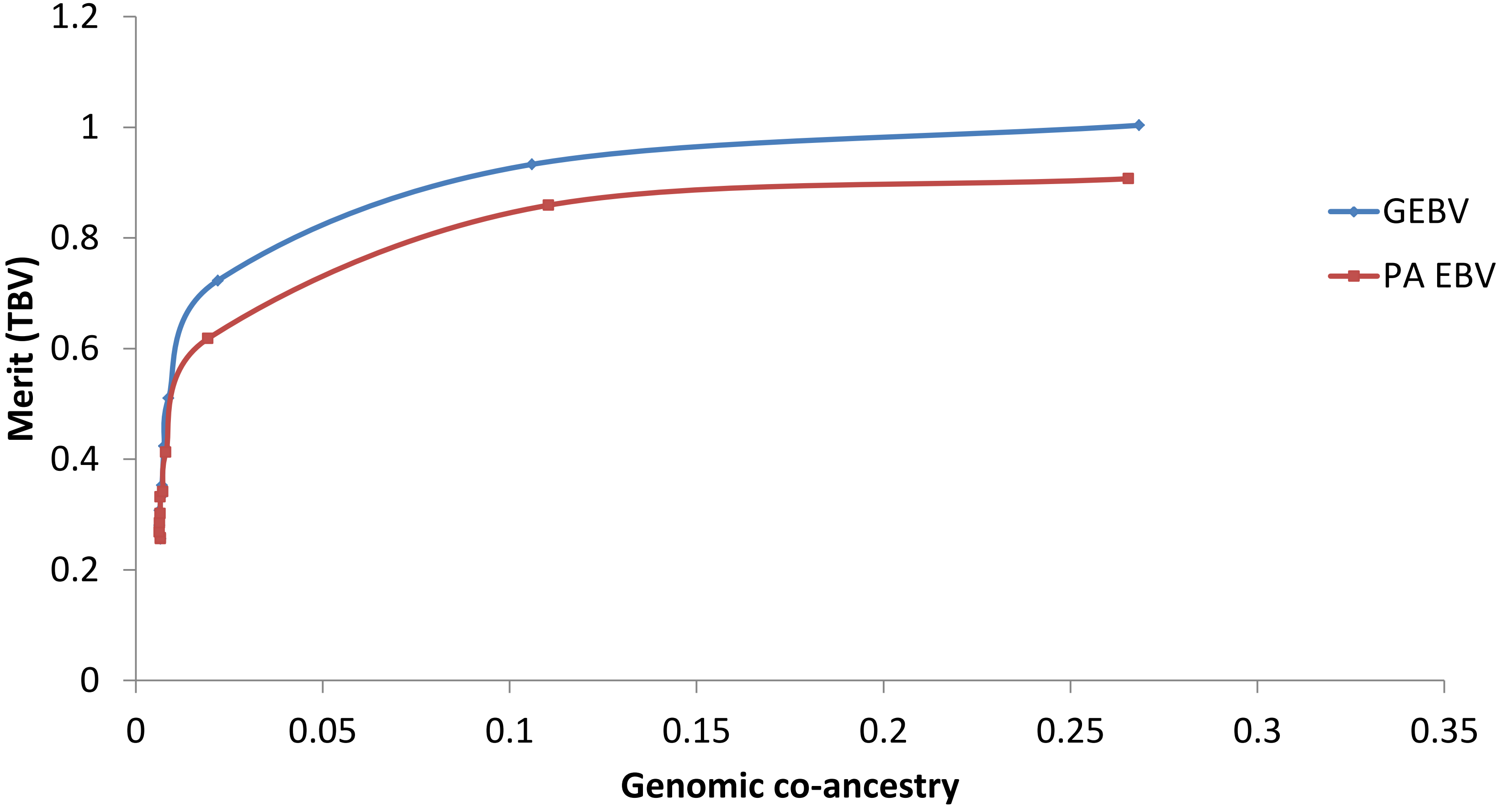
Genetic gain (ΔG), rate of inbreeding based on pedigree (ΔF_{ped}) and on genomic IBD (ΔF_{IBD}) relationship matrices at generation *G10* when the constraint on relationship was either pedigree-based (ΔF_A) or marker-based (ΔF_G) with TBLUP or GBLUP breeding value estimates[a].

[a] *Ntest* = number of test sibs; ΔF_d = desired rates of inbreeding; number of selection candidates = 3000.

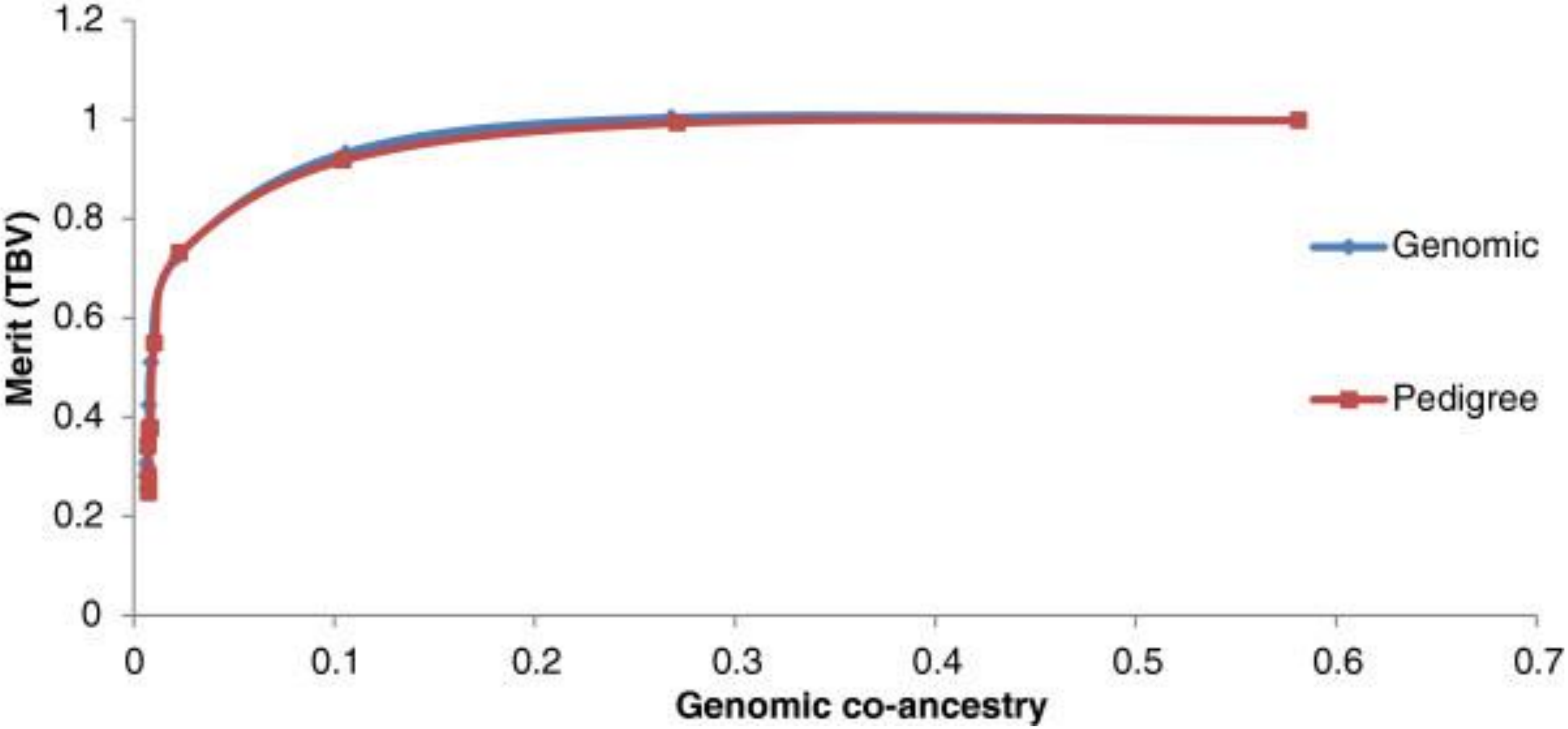
IBD profiles with OC selection



Entire frontier

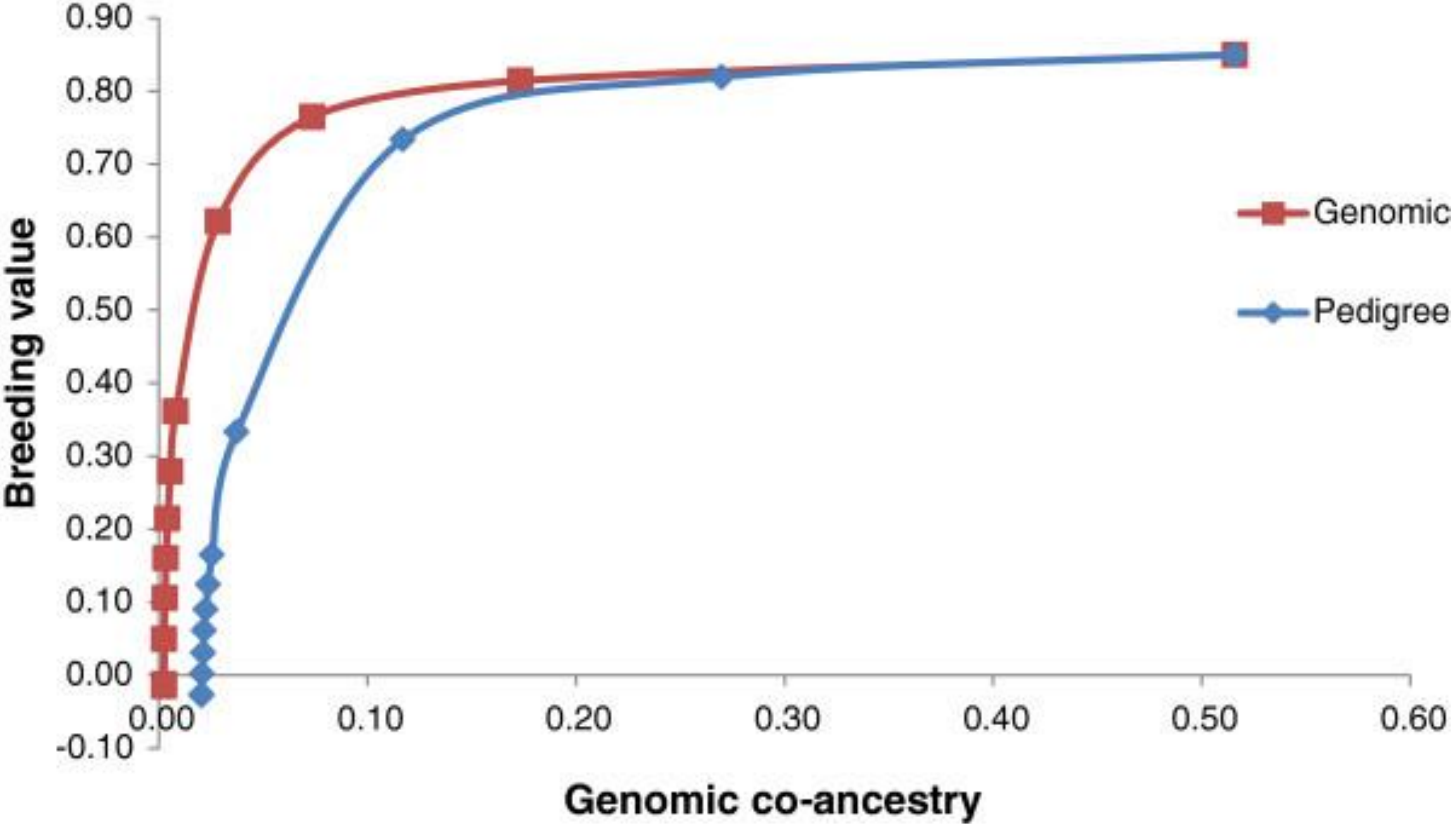


Half sibs



1.2
1
0.8
0.6
0.4
0.2
0
Merit (TBV)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
Genomic co-ancestry
Genomic
Pedigree

Full sibs



Breeding value
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
-0.10
0.00
0.10
0.20
0.30
0.40
0.50
0.60
Genomic co-ancestry
Genomic
Pedigree

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.