



Benefits from marker assisted selection under an infinitesimal model

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Molecular genetic information

➤ **large amount available**

➤ **potential uses**

- **increase response in selection programmes**
- **maintain genetic variability in conservation programmes**

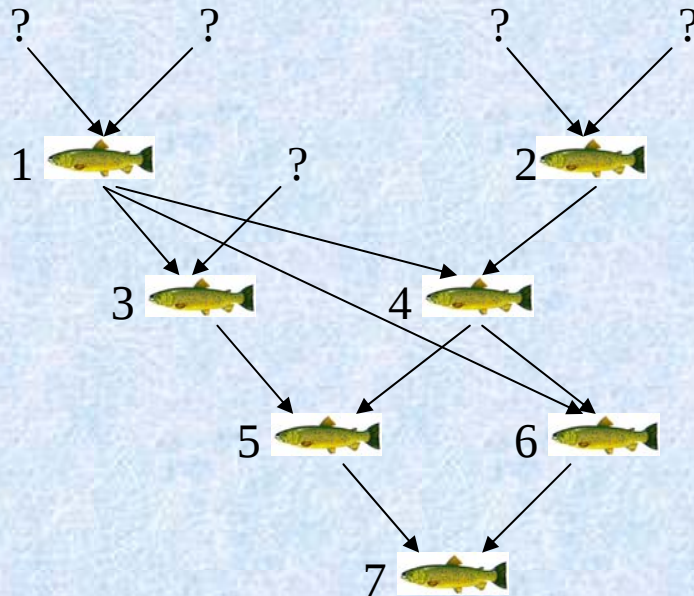
➤ **little known about how best to use it**

BLUP

Performance
Genetic relationships

more accurate than phenotype

Relationship matrix (A)



	1	2	3	4	5	6	7
1	1	0	0.5	0.5	0.5		
2							
3							
4							
5							
6							
7							

Matrix A in BLUP

- **Normally computed only from pedigree (A_p)**
 - gives only expectations
 - ignore variation around expected values
- **Use markers (+ pedigree) to compute A_{pm}**
 - increase accuracy and response

Difference with previous MAS studies

➤ Previous

- mixed inheritance model: QTL of large effect + polygenes**
- markers used to better estimate effect of QTL**

➤ Here

- infinitesimal model: polygenes**
- markers used to better estimate genetic relationships**

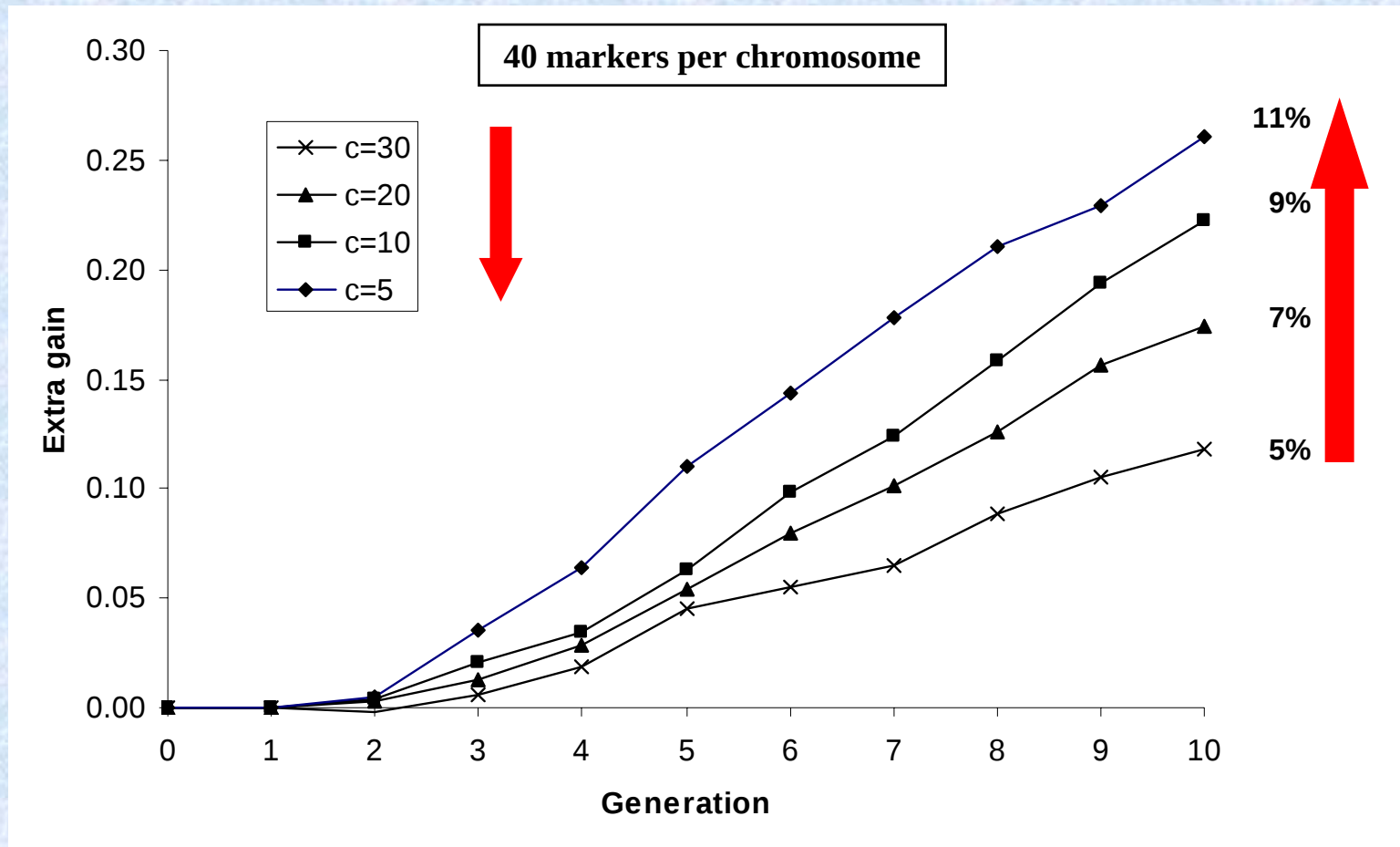
Model

- ✓ c pairs of chromosomes of 1 Morgan each
($c = 5, 10, 20, 30$)
- ✓ 2000 biallelic loci of small effects
- ✓ m markers with 10 alleles each
($m = 1, 2, 5, 10, 20, 40$)
- ✓ selected individuals
 - those with highest estimated breeding values
 - proportion selected: 1/10

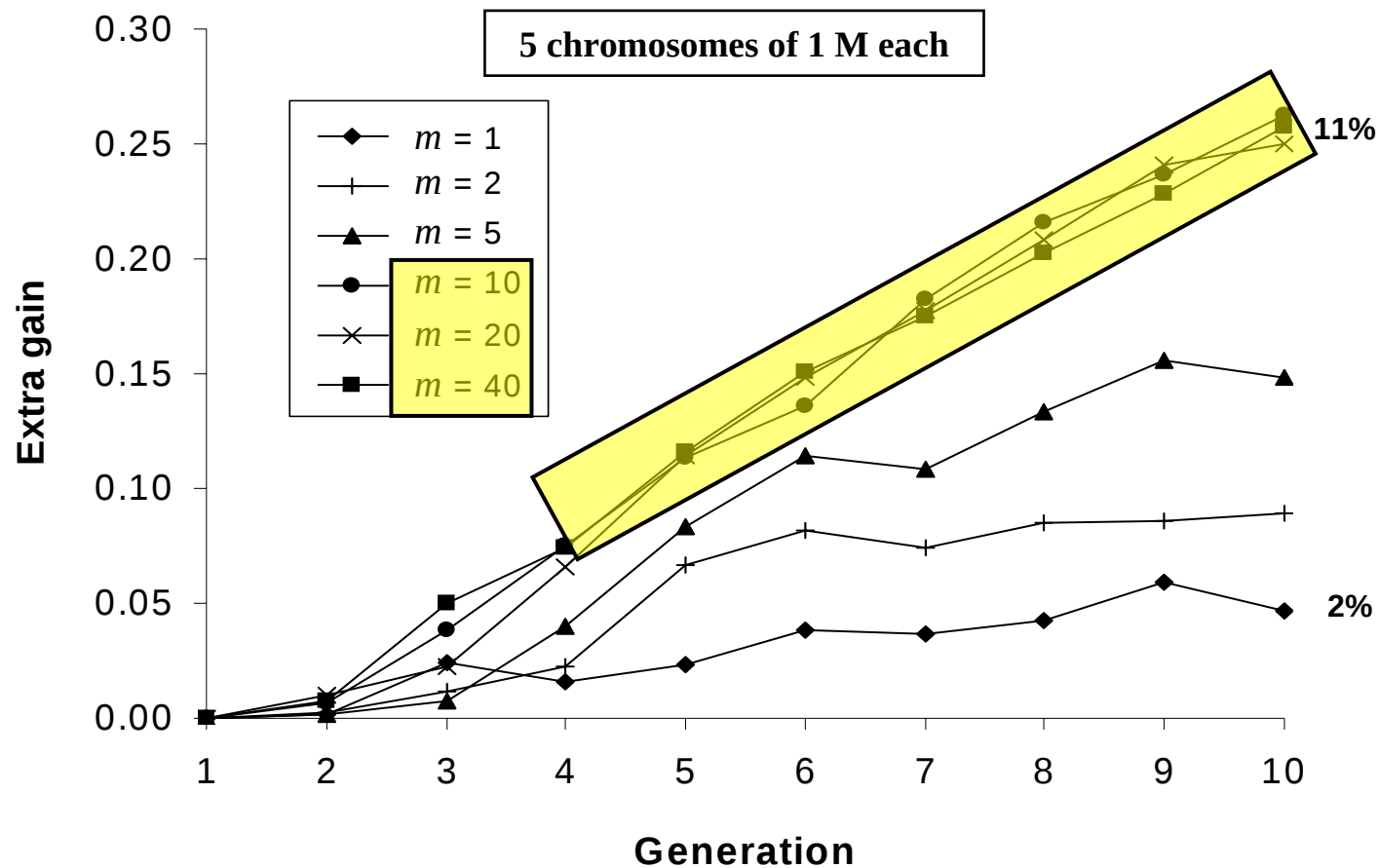
Schemes compared

- **Standard BLUP ($BLUP_s$)**
 - Relationship matrix computed from pedigree information (A_p)
- **Marker BLUP ($BLUP_m$)**
 - Relationship matrix computed from pedigree and marker information (A_{pm})

Effect of Genome Length on Benefit of $BLUP_m$



Effect of number of markers on benefit of BLUP_m



Conclusions

- **Extra responses (5 – 11%) obtained**
 - even for large genomes
 - due to increased accuracy
 - for small genomes: magnitude similar as extra responses from BLUP vs. phenotypic
- **Most benefit - 1 marker every 10cM**