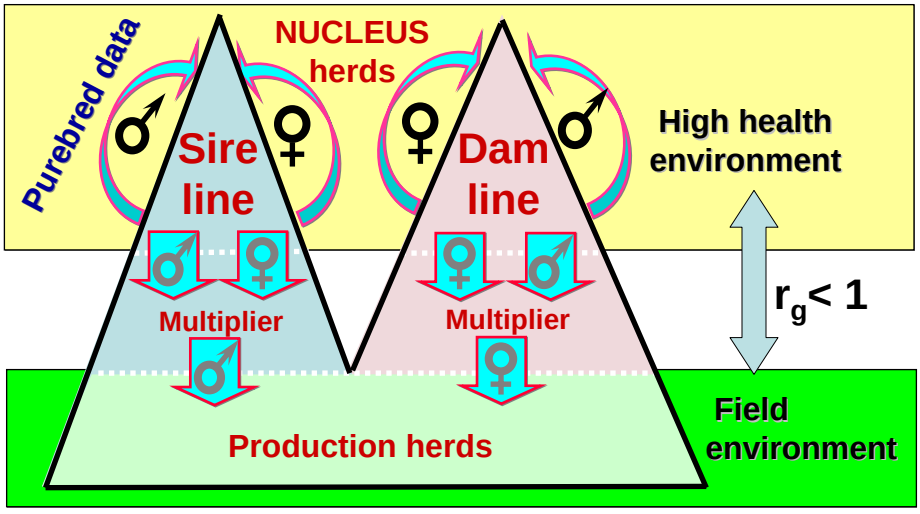
Day 10 Outline

- Impact of recent vs. historic LD on genomic predictions
- Development of low-density SNP panels
- Response to Genomic Selection
- **Genomic Selection for Commercial Crossbred Performance**
  - **Potential Benefits**
  - **Statistical Implementation**
- Open Discussion

Course Evaluation

Current Pyramid Selection Programs

Limitations: - limited selection for performance in the field
- no selection for traits not recorded in nucleus
- disease traits

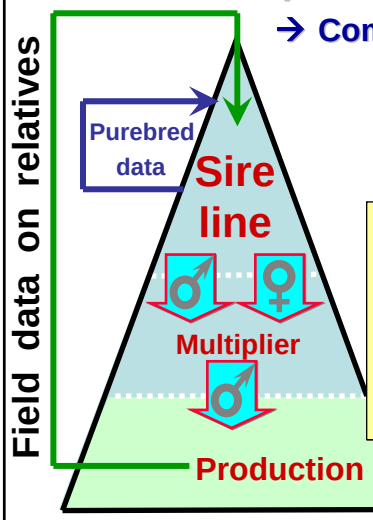


Selection for Performance in Field

'Traditional' Breeding Solution:

Collect phenotypes on relatives in field

→ **Combined Crossbred-Purebred Selection**



→ ↑ ΔG_{field}
→ ↑ ΔF
Bijma & van Arendonk, '98

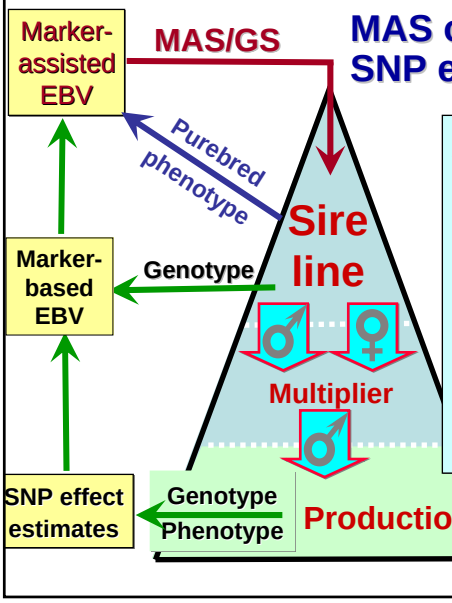
Requirements/limitations:

- Costly logistics - Pedigree-based phenotyping in field
- Longer generation intervals
- Higher rates of inbreeding
  - family data vs. own phenotype

Selection for Performance in Field

Molecular Genetic Solution:

MAS or Genomic selection with SNP effects estimated in field



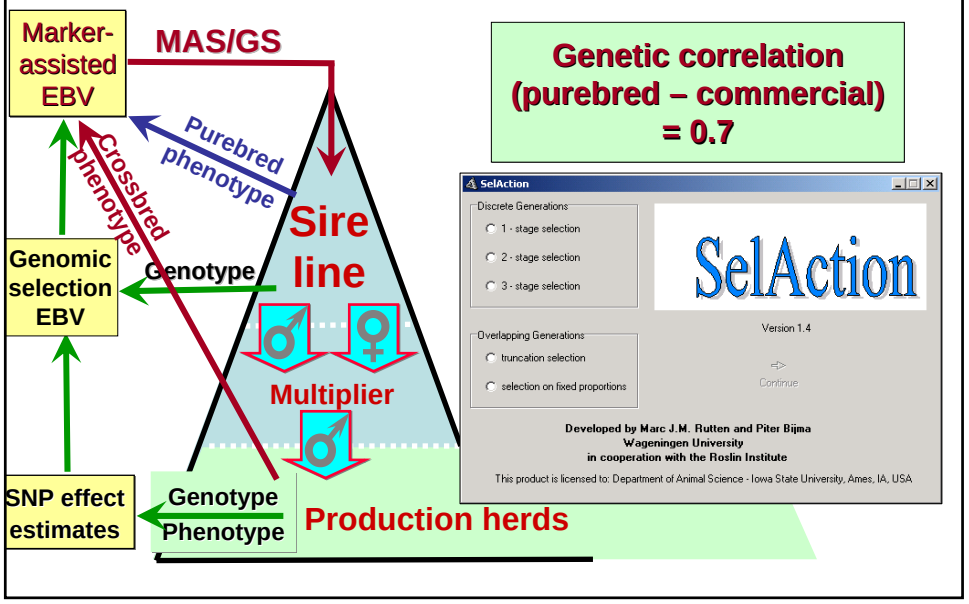
Advantages:

- Does not require pedigree-based phenotypes
- Opportunities to reduce generation intervals
- Opportunities to select for traits not observed in nucleus

Genomic Selection for Field Performance

Potential benefits

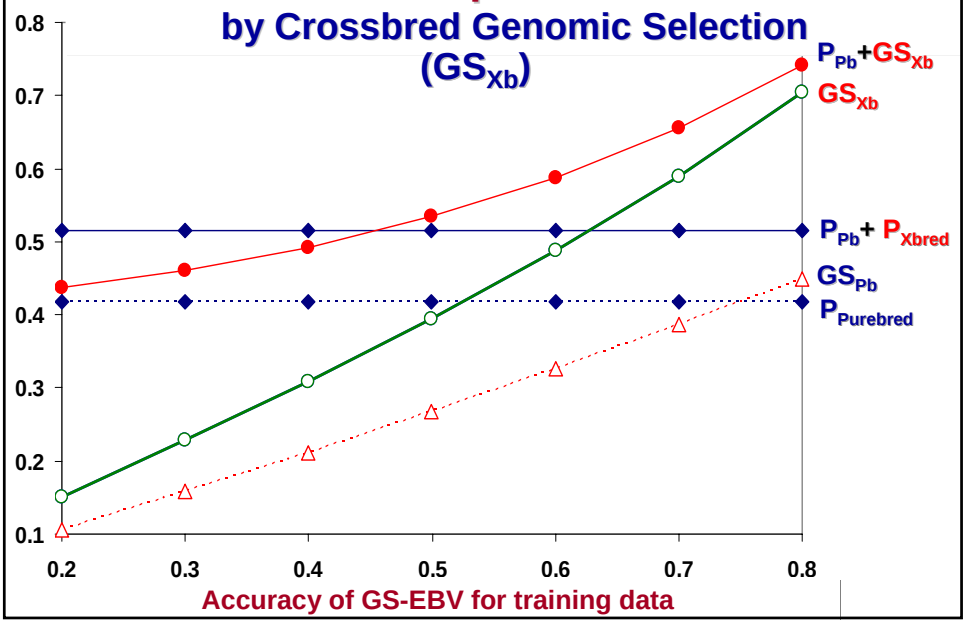
(Dekkers 2007 JAS)



Accuracy of selection for field performance

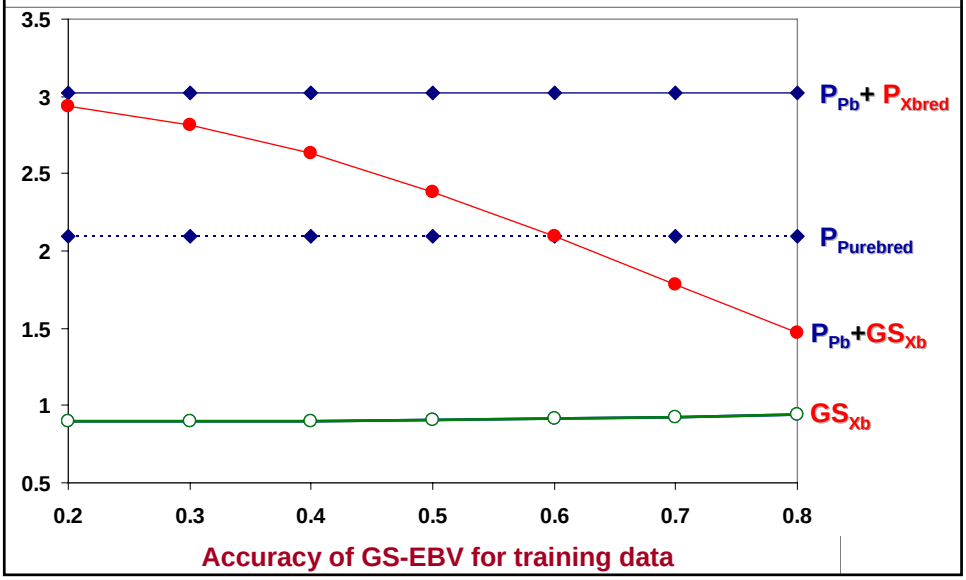
by Crossbred Genomic Selection (GS_{Xb})

Dekkers JAS, 2007



Impact on Inbreeding
Crossbred Genomic Selection (GS_{Xb})

Dekkers
JAS, 2007



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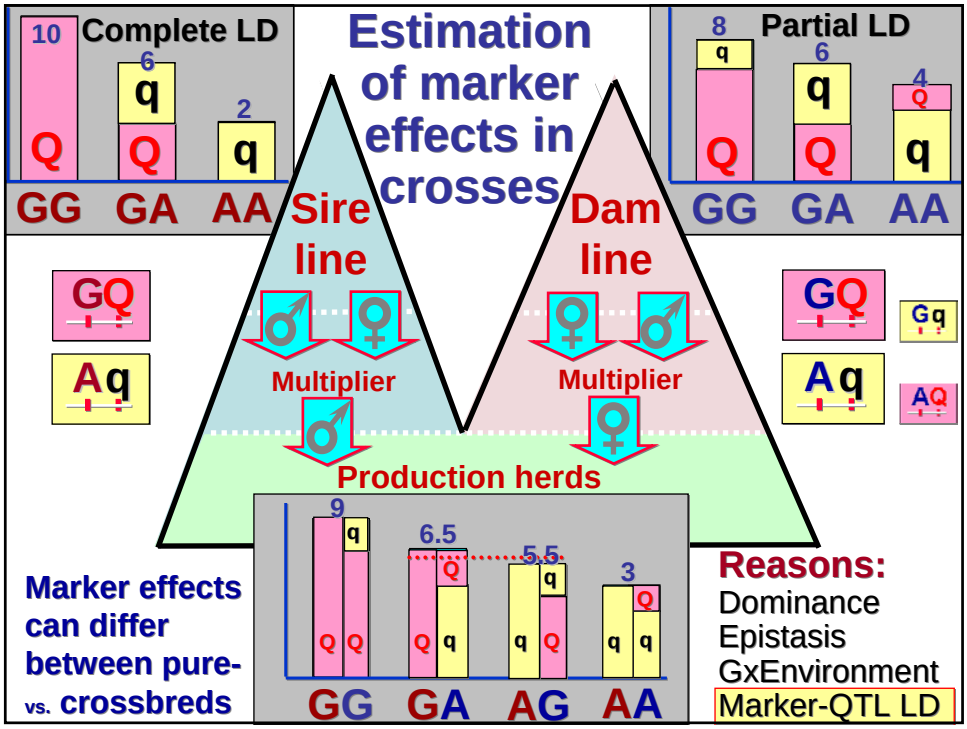
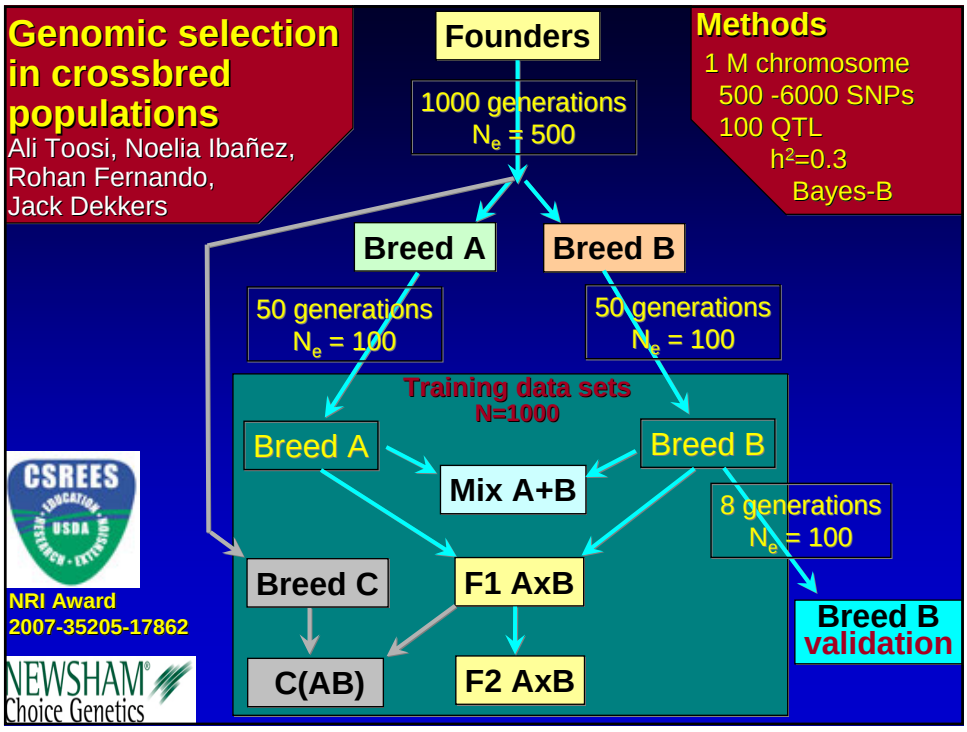
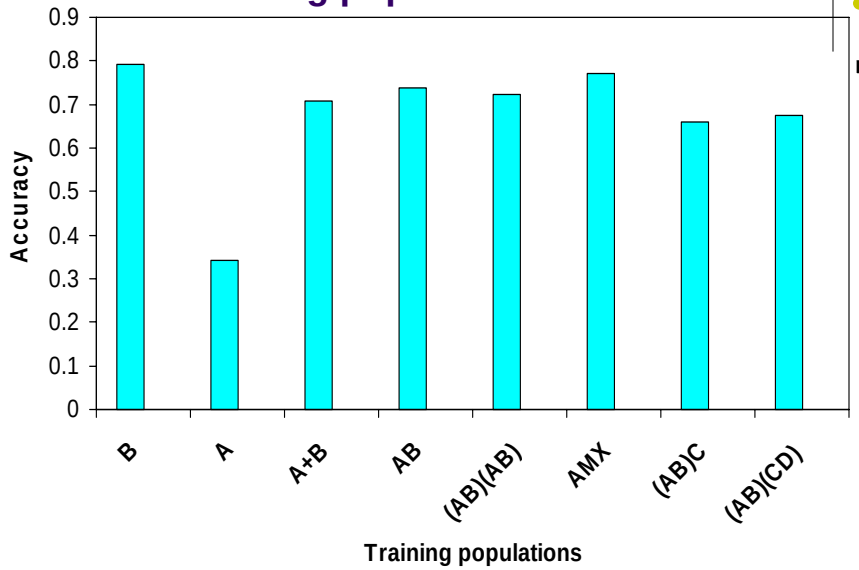

Estimation of marker effects in crosses
Complete LD
Partial LD
Sire line
Dam line
Multiplier
Multiplier
Production herds
GG GA AA
GG GA AA
GG GA AG AA
Marker effects can differ between pure- vs. crossbreds
Reasons:
Dominance
Epistasis
GxEnvironment
Marker-QTL LD


Genomic selection in crossbred populations
Ali Toosi, Noelia Ibañez, Rohan Fernando, Jack Dekkers
Methods
1 M chromosome
500 -6000 SNPs
100 QTL
h²=0.3
Bayes-B
Founders
1000 generations
Ne = 500
Breed A
Breed B
50 generations
Ne = 100
50 generations
Ne = 100
Training data sets
N=1000
Breed A
Breed B
Mix A+B
8 generations
Ne = 100
Breed C
F1 AxB
C(AB)
F2 AxB
Breed B validation
NRI Award
2007-35205-17862

Accuracy of GS based on admixed training populations



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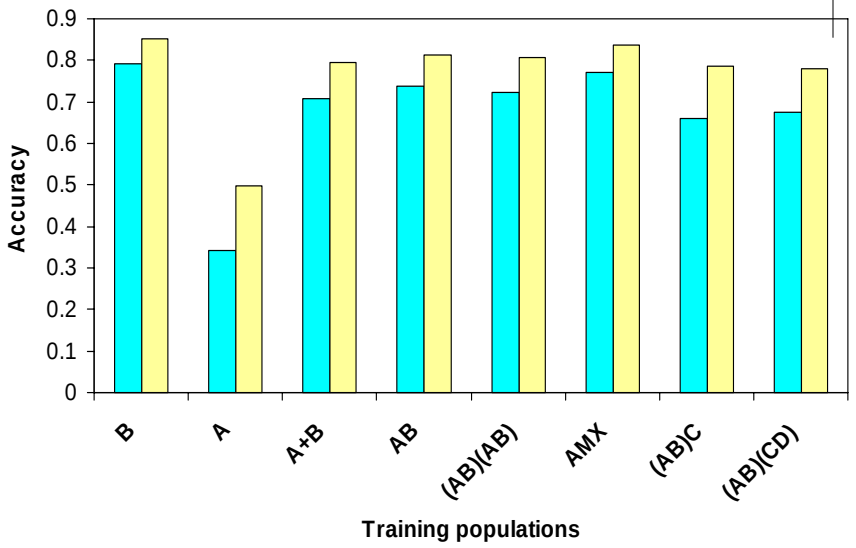
Accuracy of GS based on admixed training populations



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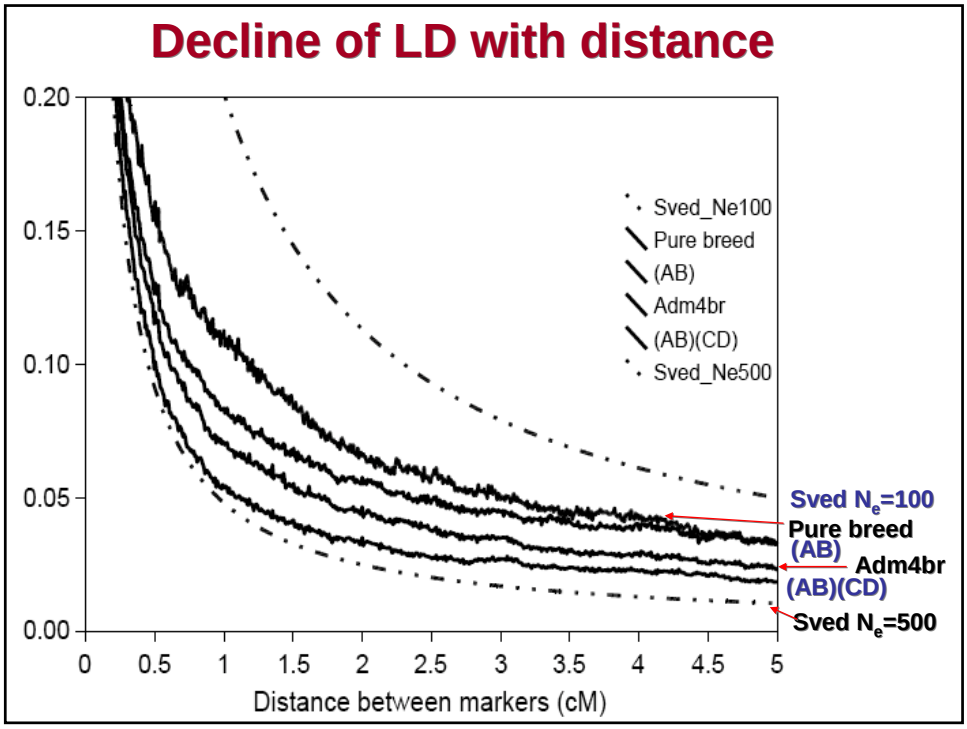
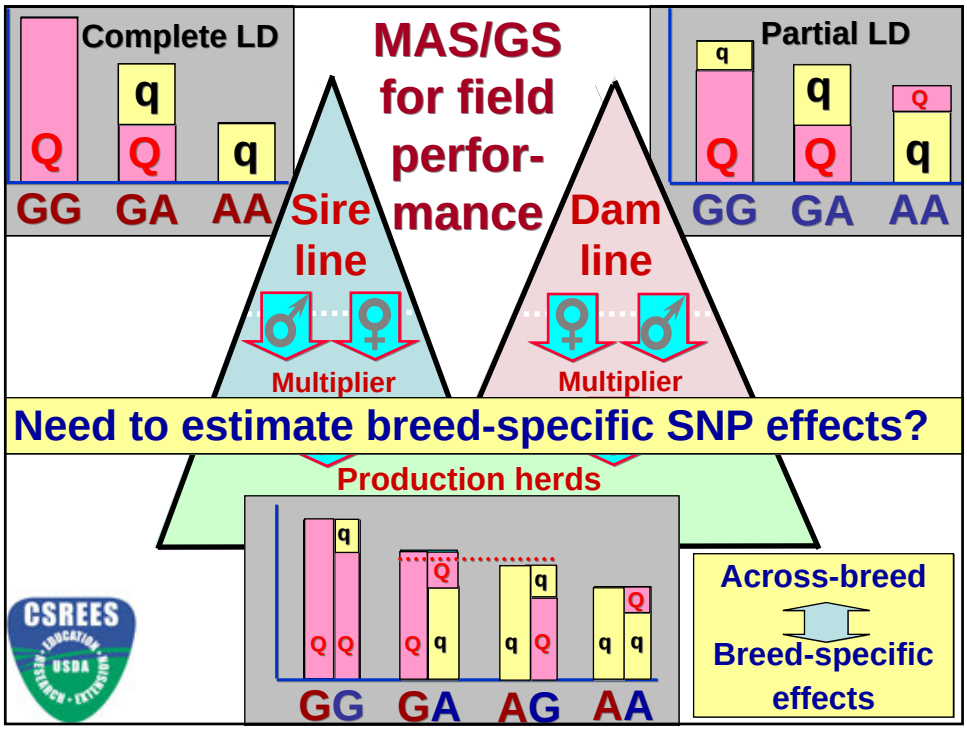
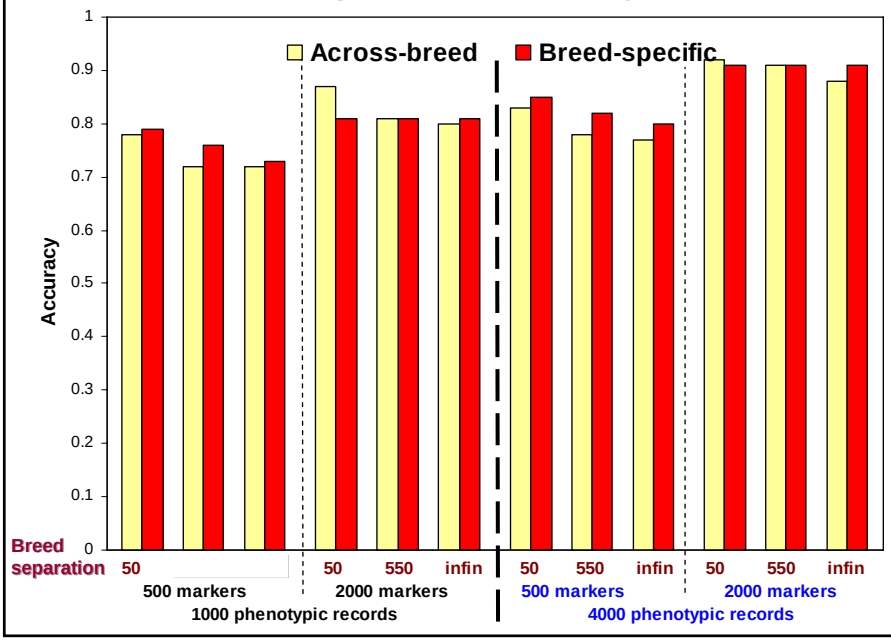

Decline of LD with distance
0.20
0.15
0.10
0.05
0.00
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
Distance between markers (cM)
Sved_Ne100
Pure breed
(AB)
Adm4br
(AB)(CD)
Sved_Ne500
Sved Ne=100
Pure breed
(AB)
Adm4br
(AB)(CD)
Sved Ne=500


Complete LD
Q
q
Q
q
GG
GA
AA
MAS/GS for field perfor-mance
Partial LD
q
Q
q
Q
q
GG
GA
AA
Sire line
Dam line
Multiplier
Multiplier
Need to estimate breed-specific SNP effects?
Production herds
q
Q
q
Q
q
Q
q
Q
q
GG
GA
AG
AA
CSREES
USDA
Across-breed
Breed-specific effects

Noelia Ibanez-Escriche, Rohan Fernando, Ali Toosi, Jack Dekkers

GSE Open Access, January 2009

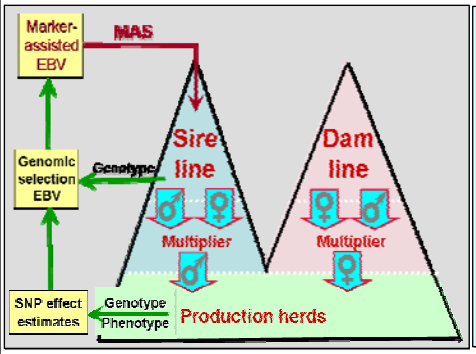


Summary / Conclusions

HD SNP genotyping offers unique opportunities for direct genetic improvement of field performance

by removing limitations on when, where, and on whom phenotypes are recorded

i.e. record on the animals that matter for production



- **Genomic selection of pure-breds for field performance of crossbreds**
- **With opportunities to**
  - reduce generation intervals
  - reduce inbreeding
  - select for combining ability
- **Detect QTL for animal health**
- **Select for animal health**

Simulation results look very promising

Empirical results are becoming available