

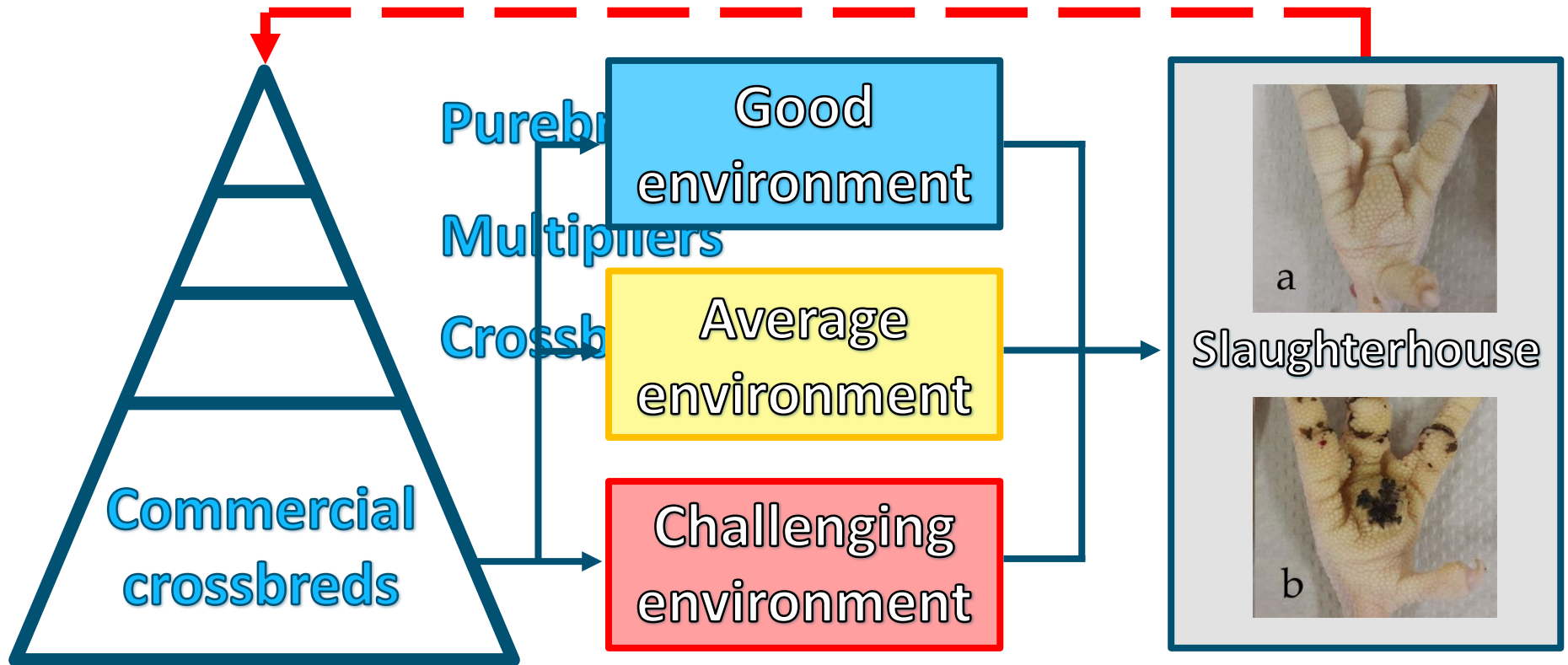
Potential of DNA pooling for the inclusion of commercial slaughterhouse data in genetic improvement.

'An old method with a new application.'

EAAP 2019 – **Michael Aldridge**, Britt de Klerk, Yvette de Haas, Karel de Greef, Jovana Marjanovic



The opportunity.



The problem.



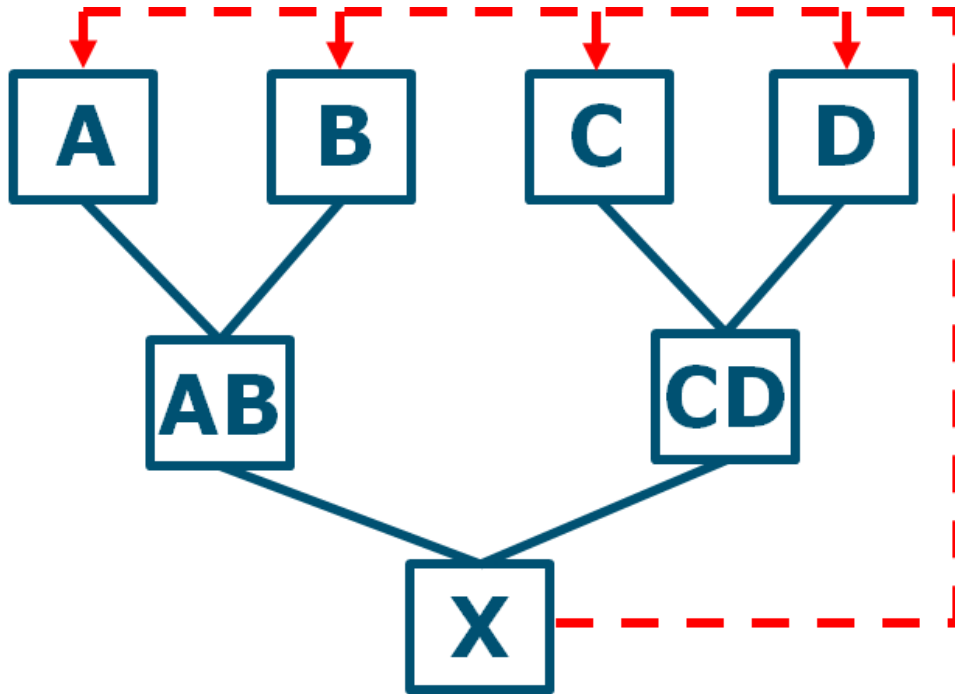
DNA pooling.



Bell *et al.* *Genet Sel Evol* (2017),
49:28

G Matrix

DNA pooling.



Using QMSim

Normal distribution

Heritability 0.3

Segregating SNPs 50,000

QTL 2,000

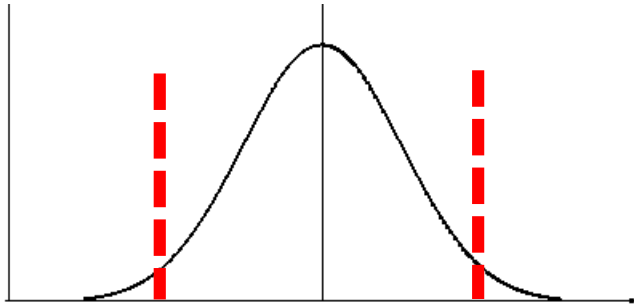
Historic population with bottleneck

Intensive selection BLUP

Divergent purelines

50,000 X-bred individuals

Simulation.



High pools

Low pools

Individual 1	0110002010110110
Individual 2	1000111022200000
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.	
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Individual 49	1001010001001022
Individual 50	0001110001002021

25 Individuals selected from 10%
Two methods for pooled genotypes

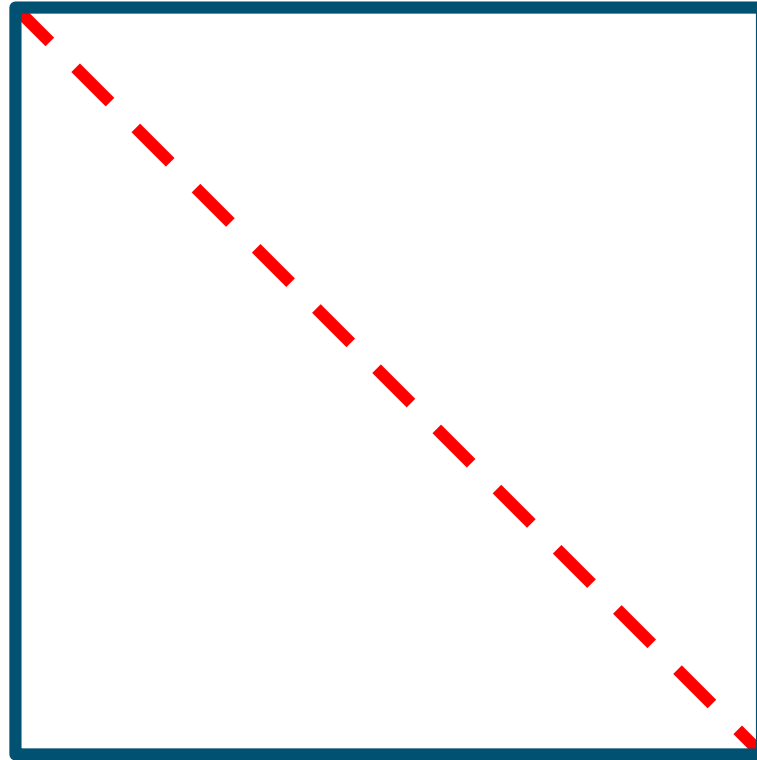
10 Individuals selected from 25
 High pool 25 1000111022200000

5 Individuals selected from 10
 Low pool 25 0001110001002022

X20

High and low pools for 25, 10, and 5

Self relationships were lower than 1.



Genomic relationships between pools.

	High 25	High 10	High 5	Low 25	Low 10	Low 5
High 25	0.31					
High 10	0.16	0.38				
High 5	0.12	0.21	0.44			
Low 25	0.06			0.31		
Low 10		0.04		0.16	0.39	
Low 5			0.02	0.11	0.21	0.45

Relationships between individuals and pools.

Low pool

Pool size = 25

High pool

GR with individual ≈ 0.06

Accuracy = 0%

Relationships between individuals and pools.

Low pool

Pool size = 10

High pool

GR with individual ≈ 0.12

Accuracy = 95%

Pool 25 ≈ 0.06 0% accuracy

Pool 10 ≈ 0.15 95% accuracy

Relationships between individuals and pools.

Low pool

Pool size = 5

High pool

GR with individual ≈ 0.20

Accuracy = 100%

Pool 25 ≈ 0.06 0% accuracy

Pool 10 ≈ 0.15 95% accuracy

Footpad lesions proof of concept.

Validation of simulation

Are the expected allele frequencies observed?

What is the maximum pool size?

Estimate SNP effects

First with simulated data

Then with commercial flocks

Conclusion.

- Adding commercial slaughterhouse data to breeding decisions is difficult.
- DNA pooling is a promising method.
- Further proof of concepts are needed.

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