



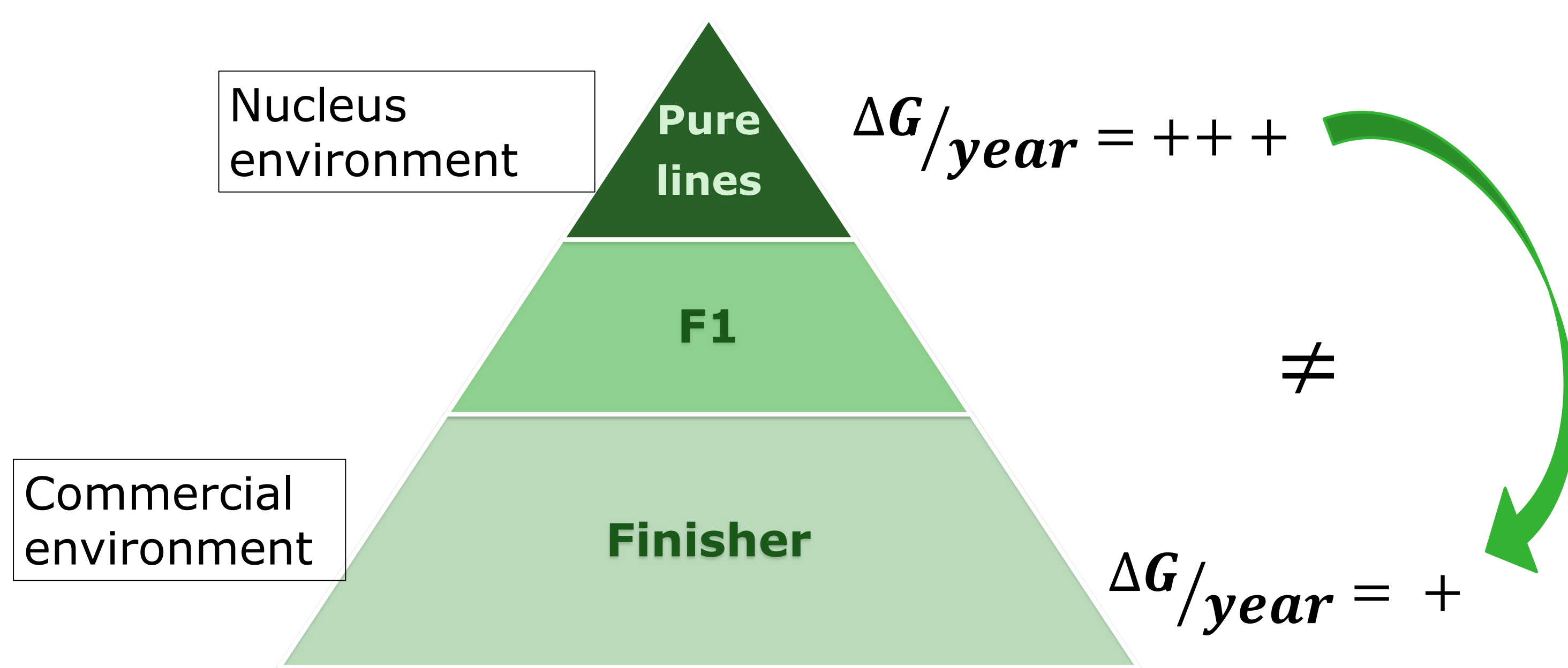
Using breed-origin-of-alleles (BOA) in genomic prediction

Mario P. L. Calus, Claudia A. Sevillano, Pascal Duenk, Yvonne C. J. Wientjes, Piter Bijma, Jeremie Vandenplas

Conclusions: Breed-origin-of-alleles (BOA) of crossbred animals can be:

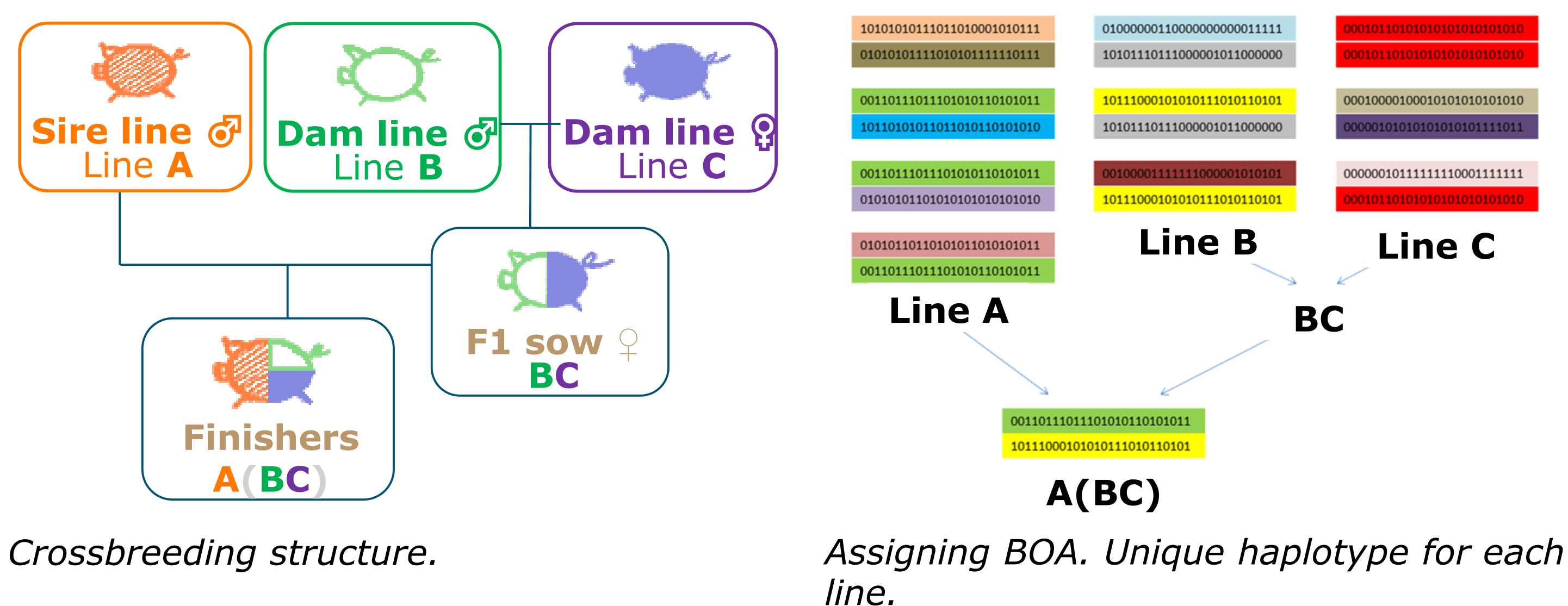
- Empirically accurately derived without need for pedigree information
- BOA-GBLUP provides limited improvement compared to GBLUP (in pigs and broilers)

Why do we need to use crossbred information?



Step 1: Deriving BOA - Approach

Aim: Trace back the **breed-origin-of-alleles (BOA)** and construct a BOA based genomic relationship matrix to predict genomic breeding values from crossbred animal information.



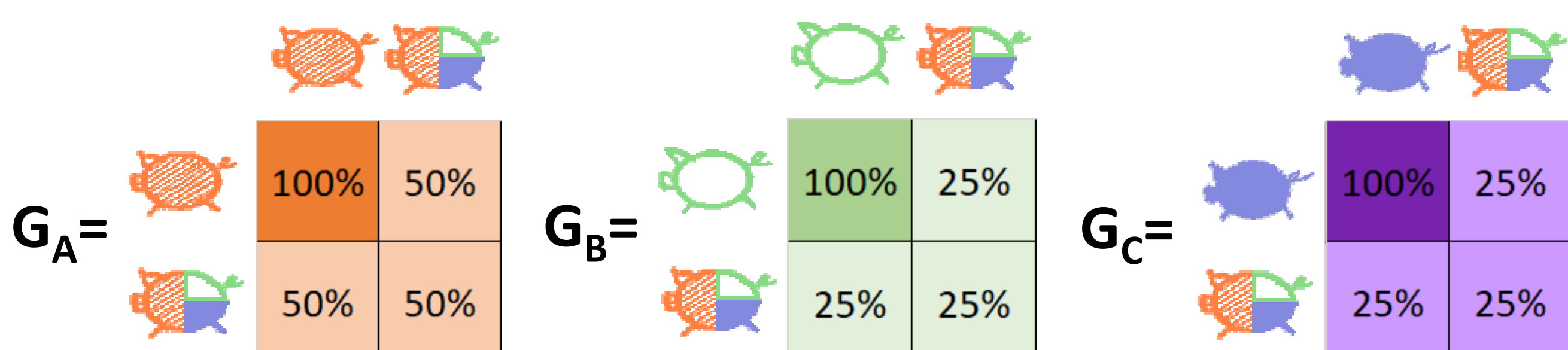
Step 1: deriving BOA – Empirical results

Line (expectation BOA %)					Reference
Species	Sire A (50%)	Dam B (25%)	Dam C (25%)	Total (100%)	
Simulated ¹				92.4-96.4	Vandenplas et al., 2016, Genet. Sel. Evol. 48:61.
Pigs	49.6	23.0	22.7	95.2	Sevillano et al., 2016, Genet. Sel. Evol. 48:55.
Broilers	49.5	20.3	22.1	91.9	Calus et al., 2019, Poult. Sci. 98:6270-6280.

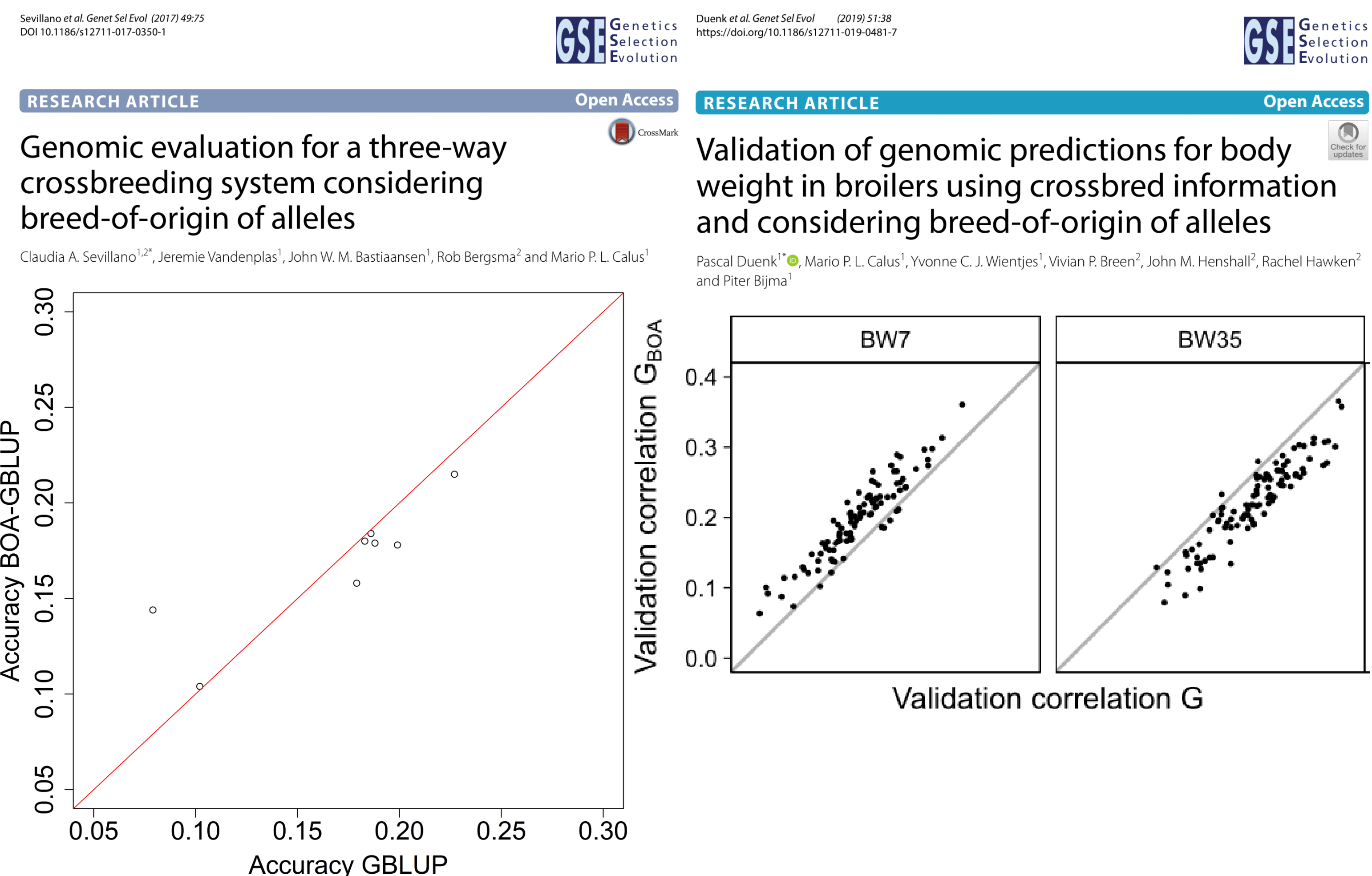
¹Range of correctly assigned BOA across closely (lowest %), distantly, and unrelated (highest %) breeds.

Step 2: GBLUP considering BOA (BOA-GBLUP)

- One (partial) **G** matrix for each breed (**G_A**, **G_B**, **G_C**).
- No relationships between breeds.
- Expected diagonal value = breed proportion.



Step 2: BOA-GBLUP – Empirical results (compared to GBLUP)



Step 2: Understanding BOA-GBLUP – the MC4R gene

Sevillano et al. BMC Genomics (2018) 19:740
<https://doi.org/10.1186/s12864-018-5126-7>

RESEARCH ARTICLE Open Access

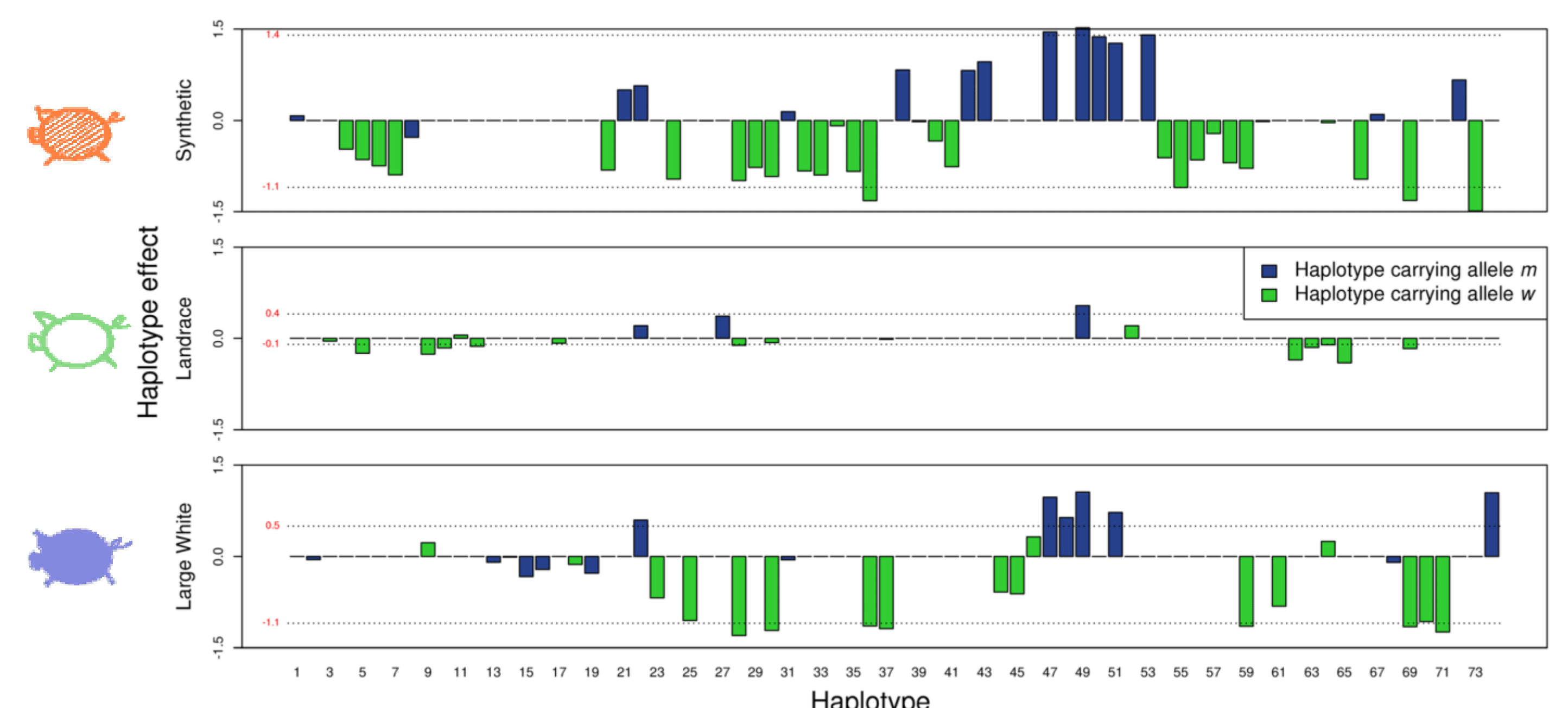
Effects of alleles in crossbred pigs estimated for genomic prediction depend on their breed-of-origin

Claudia A Sevillano^{1,2*}, Jan ten Napel¹, Simone E F Guimarães³, Fabyano F Silva³ and Mario P L Calus¹

Estimated effect of the causal mutation on average daily gain

BOA	p (m)	q (w)	α (g/d)	variance
Synthetic boar	0.81	0.19	-22.6	157.2
Landrace	0.12	0.88	-14.6	42.6
Large White	0.44	0.56	-21.7	232.1

Estimated effect of MC4R haplotypes based on 50k SNP panel



Estimated effects are:

- Very similar for the mutation, regardless of its frequency
- Reduced for SNP (haplotypes), with lower frequency of the mutation

