

# Use of phenotypes from multi-trait national evaluations in genomic evaluations

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# What are multi-trait evaluations?

- Take into account correlations between traits
- Increase the accuracy of Estimated Breeding Values (EBV)
- This model is implemented in total merit index in France
- A byproduct of multi-trait evaluations is an improved EBV
  - Correlated traits are used as predictors
  - Higher reliability
  - Especially relevant for functional traits



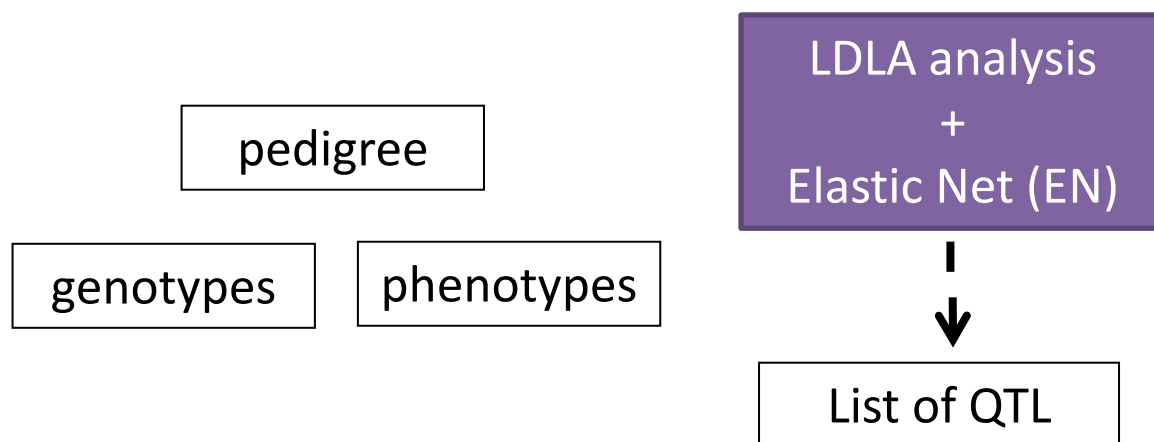
# Aim of the study

- Find an « easy » way to improve genomic evaluations of functional traits
- Genomic evaluations require accurate phenotypes
  - In dairy cattle : Daughter Yield Deviation (DYD) are often used
  - Mean performance of daughters corrected for fixed effect
  - Based on a single trait model
- Problem with low heritability traits
  - Need a large number of daughters
  - Deregressed Proofs from multi-trait evaluation (mt-DP) can also be used to mimic phenotypic data



# French approach for genomic evaluation

## 1. QTL detection : combination of LDLA analysis and Elastic Net

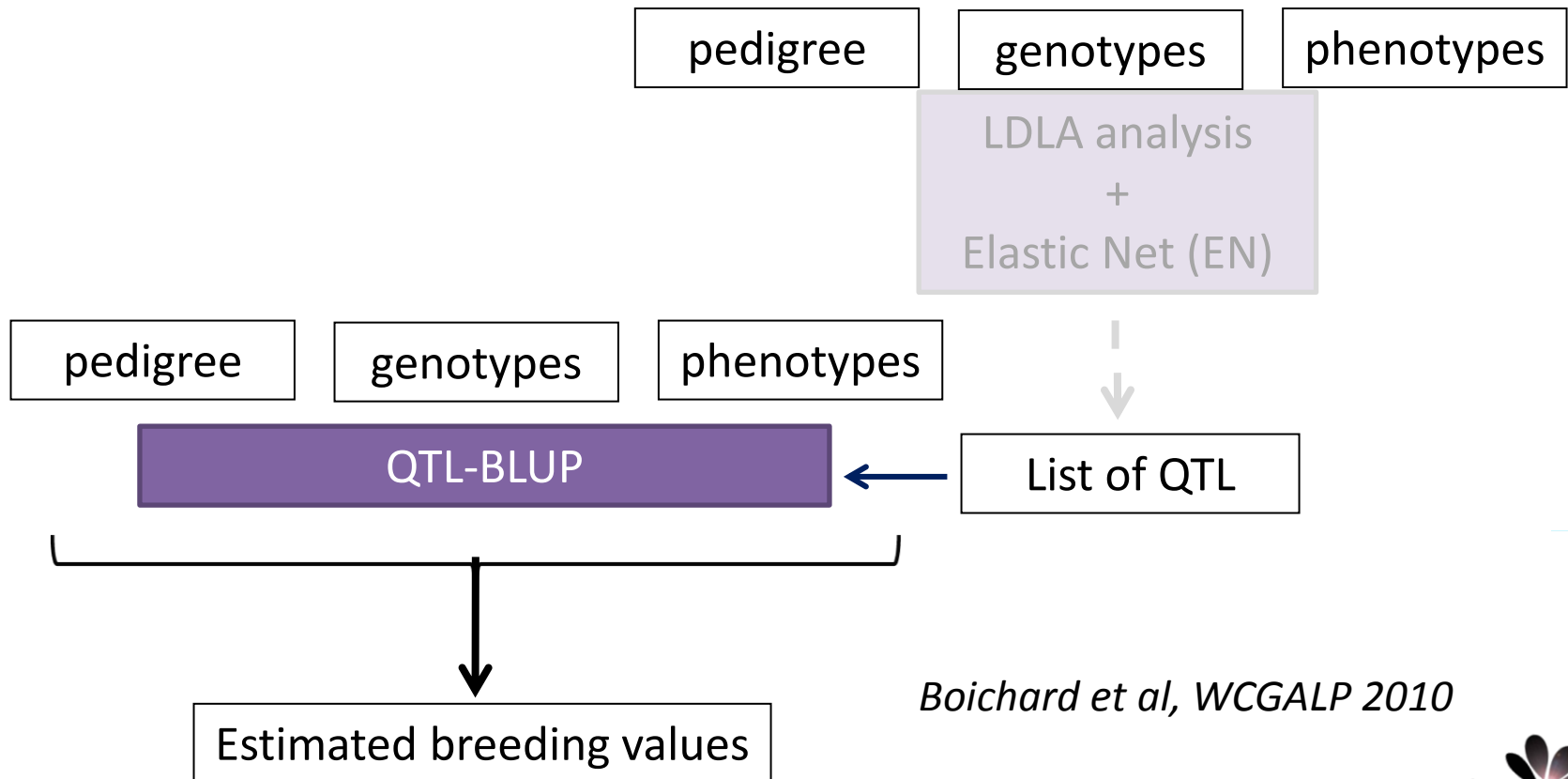


*Boichard et al, WCGALP 2010*



# French approach for genomic evaluations

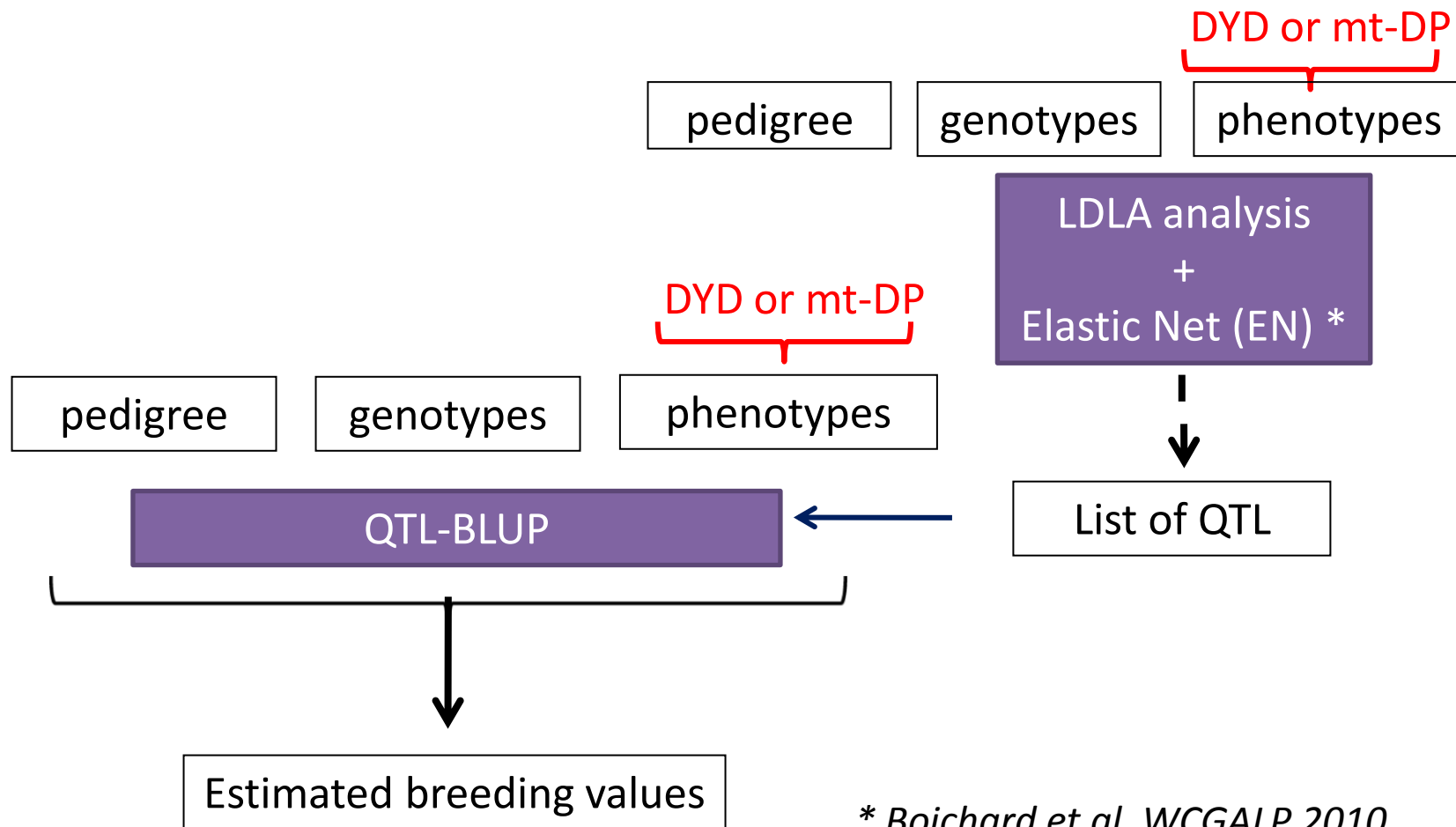
1. QTL detection : combination of LDLA analysis and Elastic Net
2. QTL-BLUP (MA-BLUP): use haplotypes to estimate QTL effect



*Boichard et al, WCGALP 2010*



# French approach for genomic evaluations



\* Boichard et al, WCGALP 2010



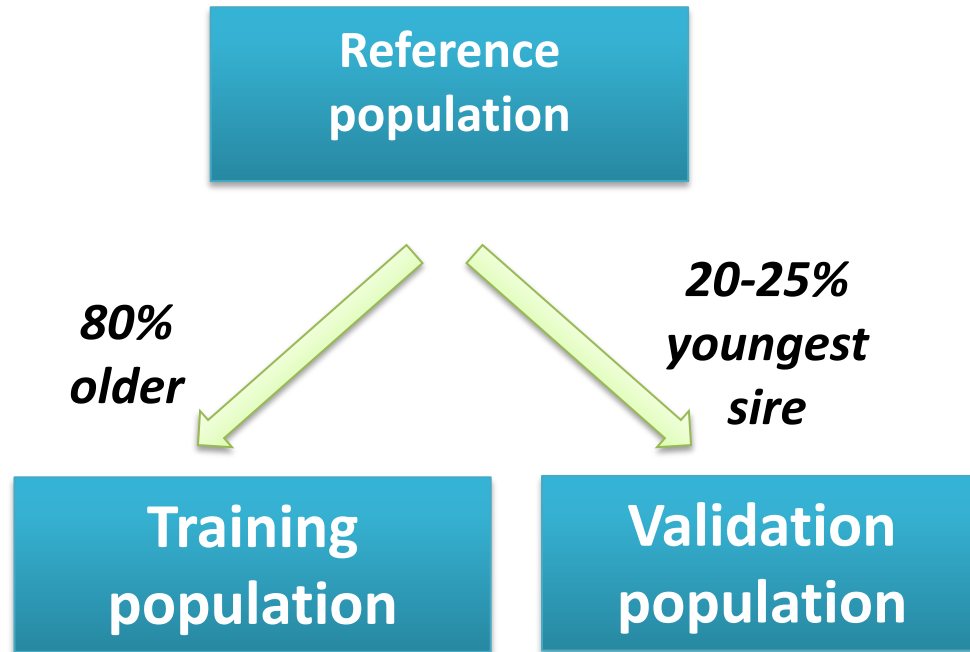
# Three methods for genomic evaluations

	Input for QTL detection		Input for QTL-BLUP	
	DYD	multi-trait DP	DYD	multi-trait DP
<b>GEN single trait (st)</b>	<b>X</b>		<b>X</b>	
<b>GEN multi-trait (mt)</b>		<b>X</b>		<b>X</b>
<b>GEN mix</b>		<b>X</b>	<b>X</b>	

- Methods were compared on a validation population



# Validation study



Remove phenotypes for validation population bulls  
Study correlations between EBV and DYD





# About the data

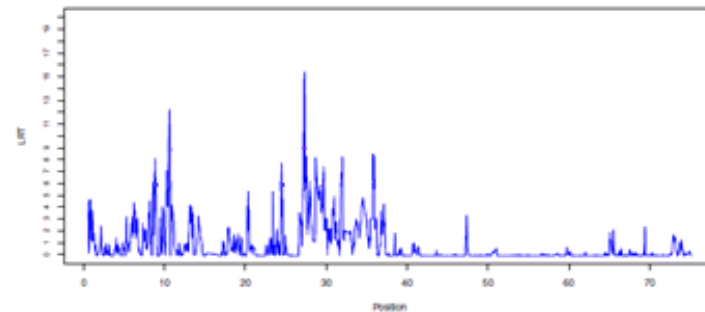
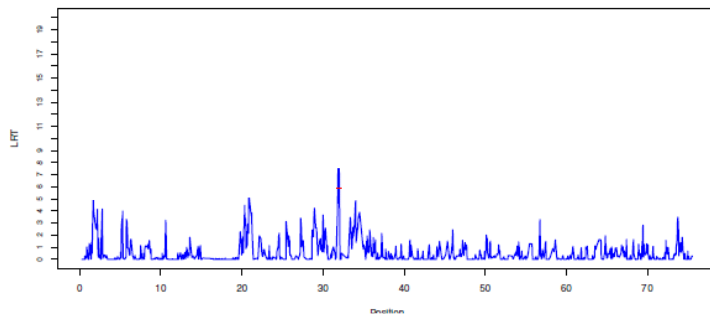
- Traits :
  - Somatic Cell Count (SCC)  $h^2 = 0.15$
  - Conception rate for cow (CR)  $h^2 = 0.02$
  - Longevity (LGF)  $h^2 \approx 0.12$
- Two breeds:
  - 16,632 (13,734 Training + 2,898 Validation) Holstein bulls
  - 2,111 (1,842 Training + 269 Validation) Montbéliarde bulls
- Genotyped on the Illumina commercial chip BovineSNP50<sup>®</sup>.



# Gain of power for QTL detection

## Example on Montbéliarde breed . Conception Rate

- LDLA analysis when phenotypes used come from
  - Single trait model
  - Multi trait model



- Number of QTL detected after LDLA analysis and EN

Phenotype used	Single-trait	Multi-trait
Nb of QTL	322	462



# Gain of accuracy in genomic evaluation

- Correlations between EBV and DYD

Montbéliarde

Holstein

Corr	SCC	CR	LGF
POL*DYD	0.56	0.38	0.11
GENst*DYD	0.56	0.41	0.25

Corr	SCC	CR	LGF
POL* DYD	0.49	0.37	0.30
GENst*DYD	0.67	0.50	0.35

GENst : QTL detection and QTL-BLUP on DYD



# Gain of accuracy in genomic evaluation

- Correlations between EBV and DYD

Montbéliarde

Holstein

Corr	SCC	CR	LGF
POL*DYD	0.56	0.38	0.11
GENst*DYD	0.56	0.41	0.25
GENmt*DYD	<u>0.72</u>	<u>0.48</u>	<u>0.51</u>

Corr	SCC	CR	LGF
POL* DYD	0.49	0.37	0.30
GENst*DYD	<u>0.67</u>	<u>0.50</u>	0.35
GENmt*DYD	0.64	0.38	<u>0.48</u>

GENa : QTL detection and QTL-BLUP on DYD

GENb : QTL detection and QTL-BLUP on DP from multi-trait evaluations



# Gain of accuracy in genomic evaluation

- Correlations between EBV and DYD

Montbéliarde

Corr	SCC	CR	LGF
POL*DYD	0.56	0.38	0.11
GENst*DYD	0.56	0.41	0.25
GENmt*DYD	<u>0.72</u>	<u>0.48</u>	<u>0.51</u>
GENmix*DYD	0.67	0.46	0.35

Holstein

Corr	SCC	CR	LGF
POL*DYD	0.49	0.37	0.30
GENst*DYD	0.67	0.50	0.35
GENmt*DYD	0.64	0.38	<u>0.48</u>
GENmix*DYD	<u>0.70</u>	<u>0.51</u>	0.45

GENst : QTL detection and MA BLUP on DYD

GENmt : QTL detection and QTL-BLUP on DP from multi-trait evaluations

GENmix: QTL detection on DP from multi-trait evaluations QTL-BLUP on DYD



# Conclusion

- Using more accurate phenotypes improve the efficiency of genomic evaluations particularly in smaller breeds
- Keep in mind that we want to improve direct traits
  - Not their predictors
- Method using both DYD and multi-trait DP is a good compromise to increase accuracy
- This strategy is now implemented in national French genomic evaluations.



# Acknowledgements

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