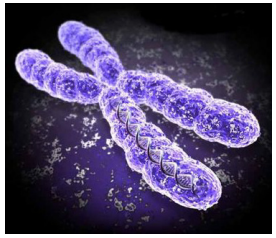
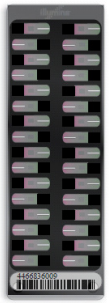
Impact of imputing markers from a low density chip on the reliability of genomic breeding values in Holstein populations





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Study of the Illumina 3K chip

EuroGenomics collaboration

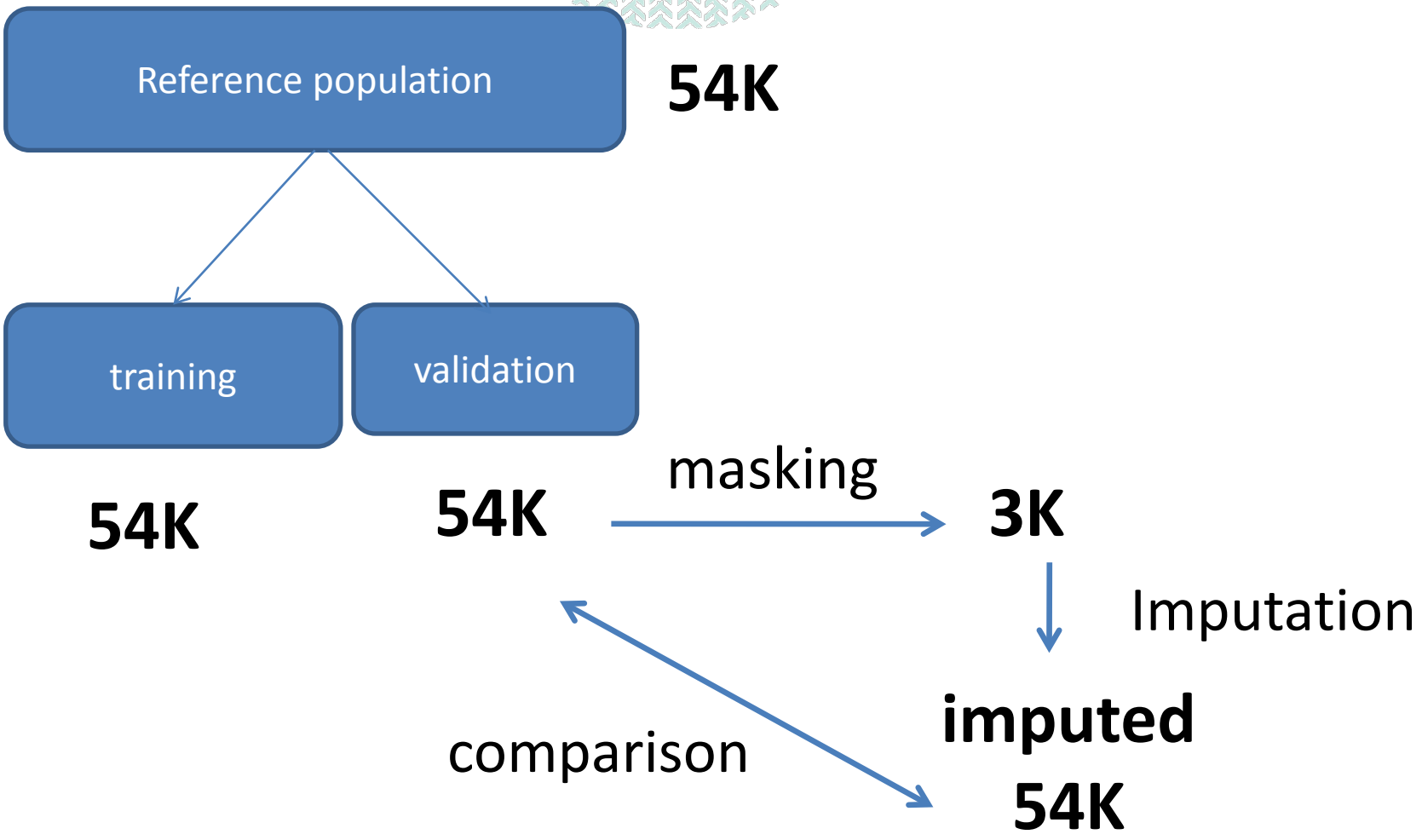
Objectives :

- ✓ Measure imputation error rate *Zhang and Druet , 2010*
- ✓ Study impact on GEBV reliability *Weigel et al, 2010*
- ✓ Study influence of reference population size

Previous studies →3K custom in silico chip

Our study → commercially available 3K chip

Data


Reference population
54K
training
validation
54K
54K
masking
3K
Imputation
imputed
54K
comparison

Data

Number of animals and number of markers used

***Including bulls with partially reconstructed genotypes**

	National		EuroGenomics		No. of Markers	
	Training	Validation	Training	Validation	Training	Validation
Nordic	3,058	1086	10,880	1,086	38,545	2,285
France	3,071/ 3,505*	966	12,078/ 13,947 *	966	43,582	2,635

Imputation Method

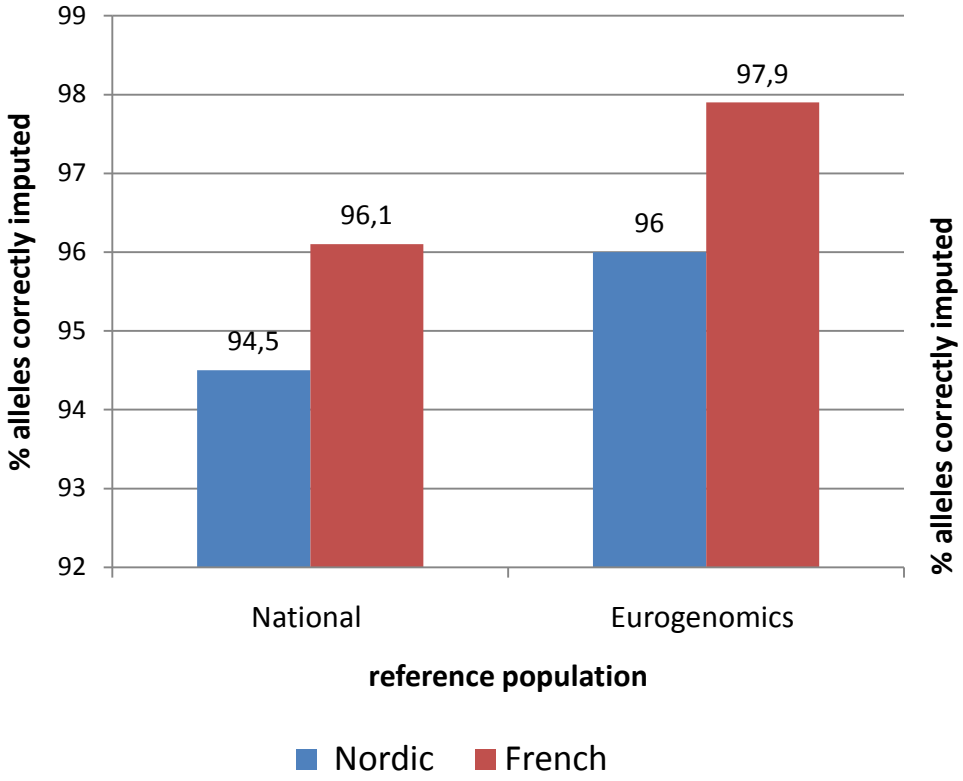
- Combination of the DAGPHASE 1.1 and Beagle 2.1.3 software

Druet et Georges, 2010 *Browning and Browning, 2007*
PHASEBOOK package

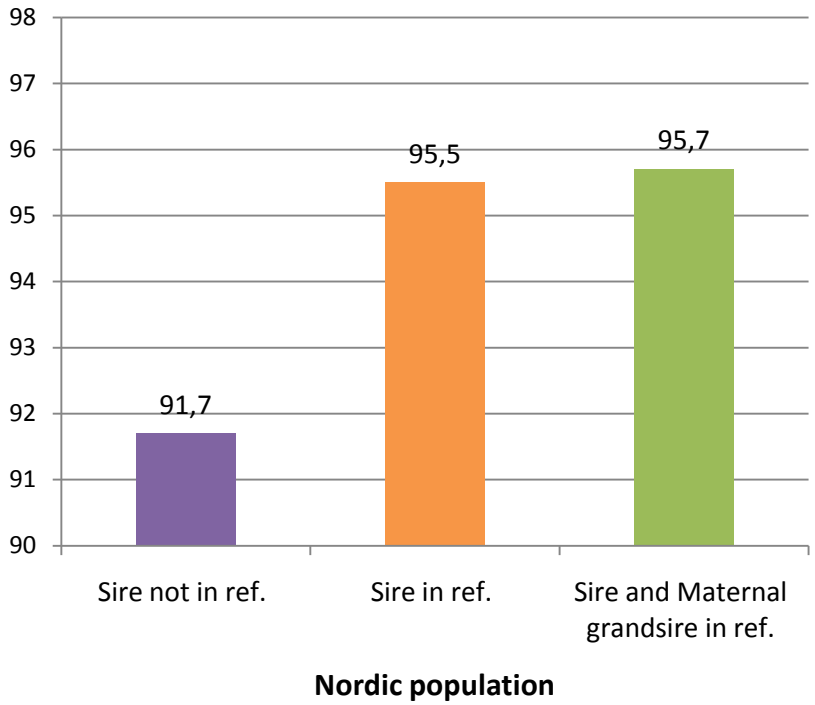
- Combines :
  - ❖ Pedigree based family information (segregation rules)
  - ❖ Population Linkage Disequilibrium

Results

Imputation accuracy



Influence of genotyped ancestors



France: more 3K markers, more genotyped ancestors

Data for genomic evaluation

Traits studied :

- protein yield (h^2=0.3-0.39)
- somatic cell count (SCC, h^2=0.15)
- fertility (Non Return Rate or Conception rate, h^2=0.02)
- udder depth (h^2=0.36-0.37)

Genomic evaluation model

Nordic:

- GBLUP $y = 1\mu + Zg + e$ *VanRaden, 2008*

French:

- GMAS, QTL-BLUP combines LDLA and EN

$$y = 1\mu + Zu + \sum_{i=1}^{nQTL} (h_{i1} + h_{i2}) + e$$

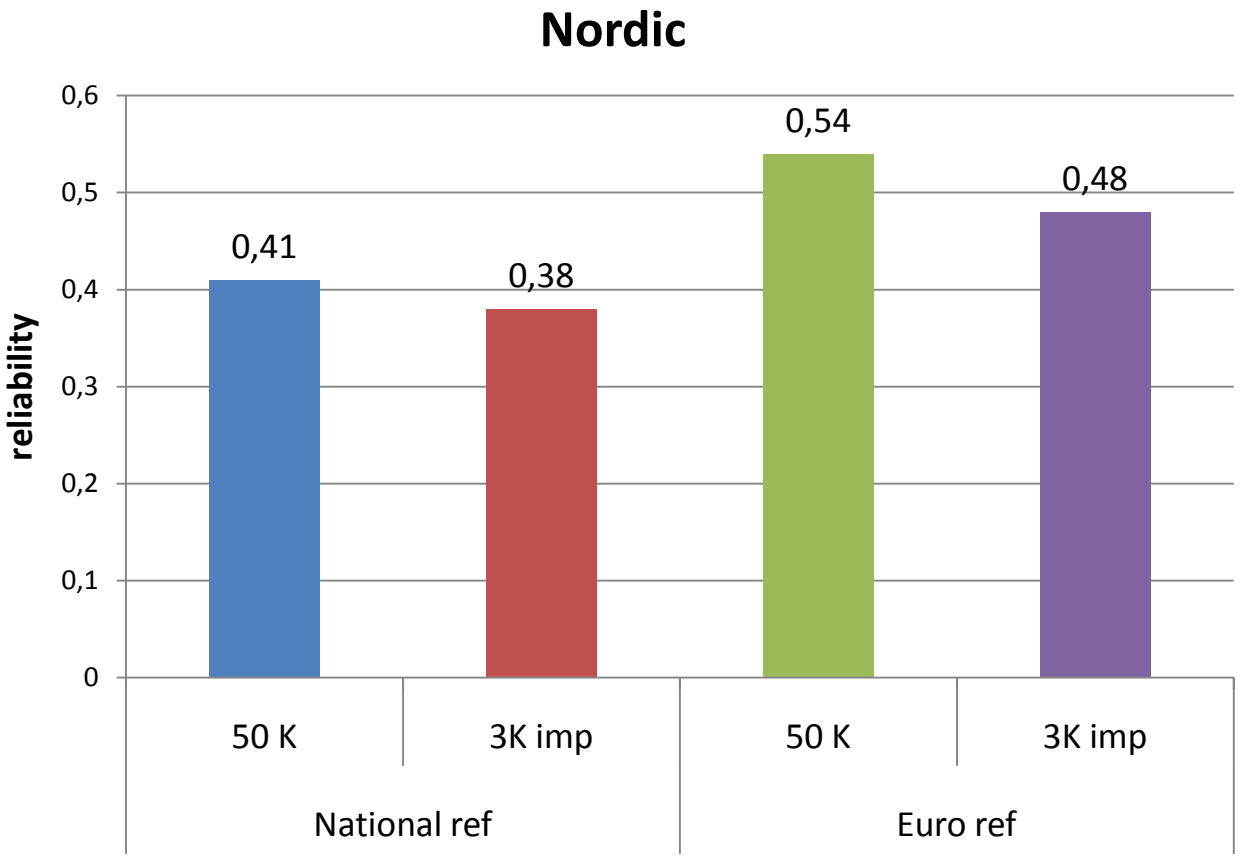
haplotypes

Boichard et al., WCGALP 2010

u: polygenic effect based on pedigree

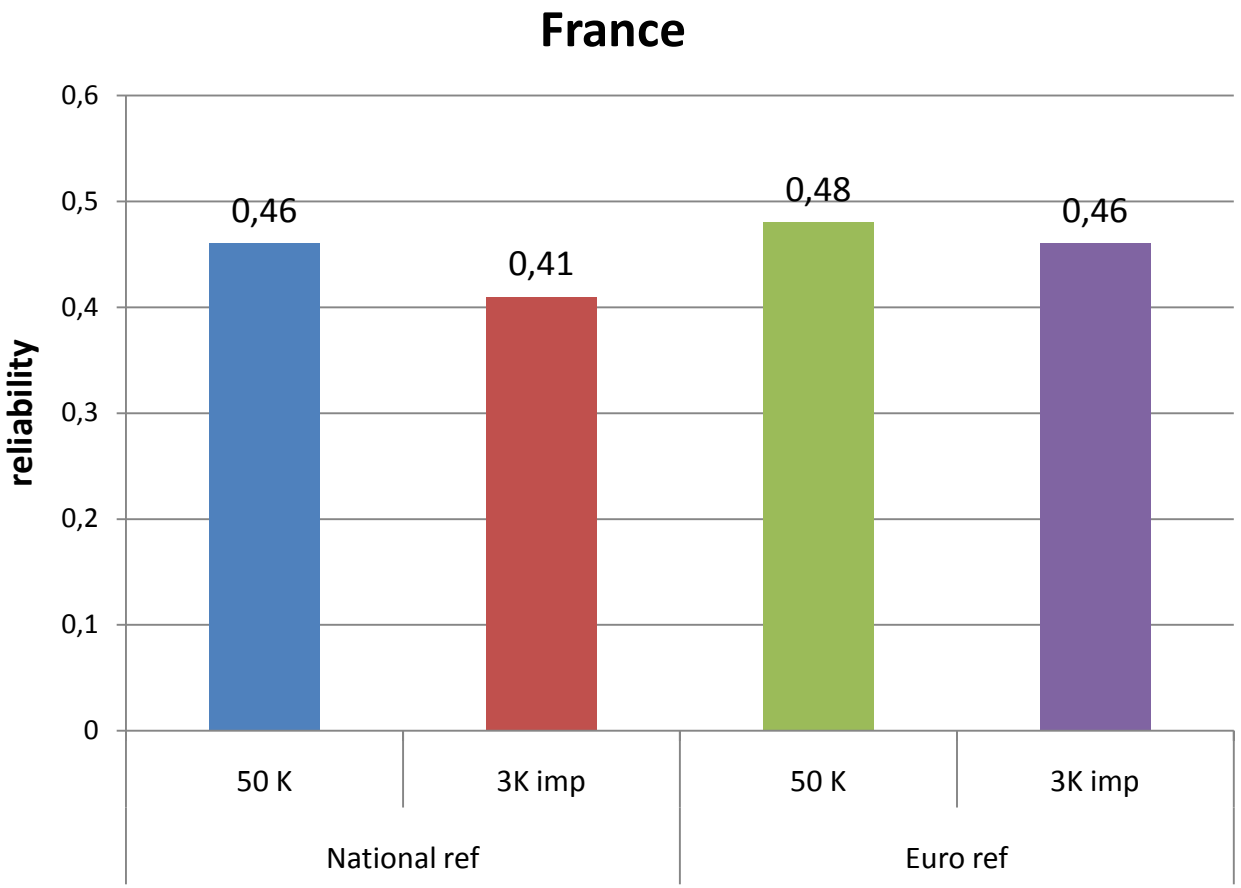
LDLA : Linkage Disequilibrium Linkage Anaysis
EN : Elastic Net

Results – Reliability of DGV



Reliability = squared correlation (DGV, deregressed proofs) for validation population
Mean over the 4 traits

Results – Reliability of GEBV



Reliability = squared correlation (GEBV, DYD) for validation population
Mean over the 4 traits

Conclusion - discussion

- Imputation accuracy = 2.5-5% = close to litterature
  - ✓ Commercially available 3K chip contains less markers after editing
  - ✓ Bigger reference population size
  - ✓ Beagle and DAGphase: efficient imputation softwares

- Reliability of GEBV:
  - ✓ Reliability of GEBV based on imputed genotypes slightly lower
  - ✓ Correlations (GEBV-50K, GEBV-3Kimp) are high (0.91-0.97)

➢ Low density chip imputed to 50 K:
  - ❖ Feasible alternative for pre-selection of young animals
  - ❖ Attractive tool for a large screening of the female population

If you want some more details

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Effect of imputing markers from a low-density chip on the reliability of genomic breeding values in Holstein populations

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Merci ! Tack !

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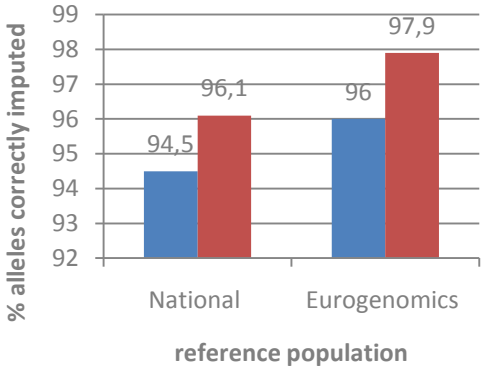
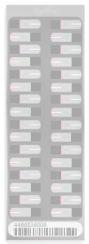
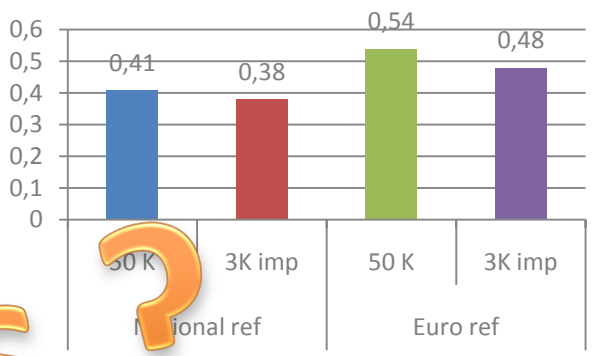


Nordic

French





questions ?

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