



IT-Solutions for
Animal Production

Prediction of expected variation in progeny groups and its application in mating programs

EAAP, 2013, Nantes, session 10:

How can farmer benefit from genomic information

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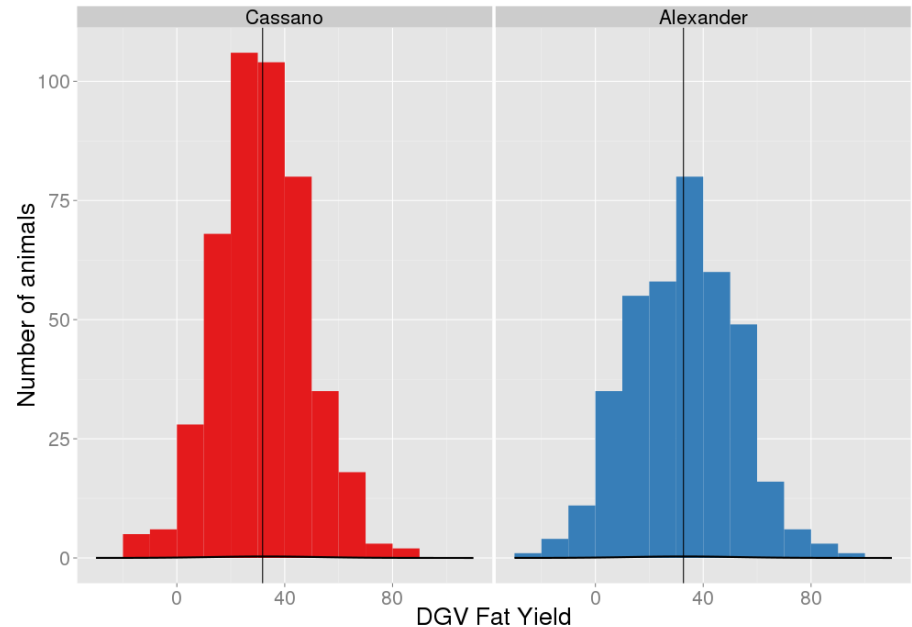
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Background

- Different variation of breeding values of sire progeny groups
- AI company: Sires showing high variation
 - Increased probability to find extreme positive candidates
- Production herds: Sires showing less variation
 - Uniform progeny groups are better to manage
- *Objective:* Predict the variability of future offspring groups using SNP data



Cassano:

- mean: 32 kg
- variation: 16.5 kg
- $p(>70\text{kg})$: 1.1%

Alexander:

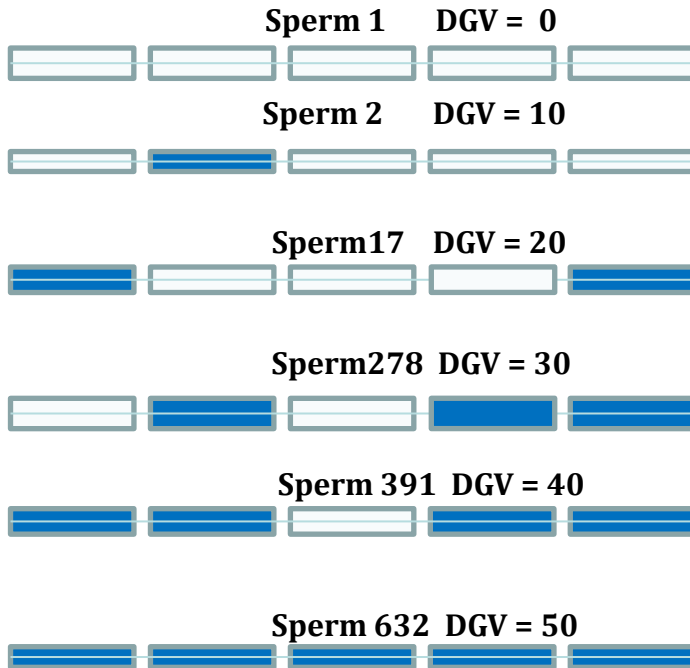
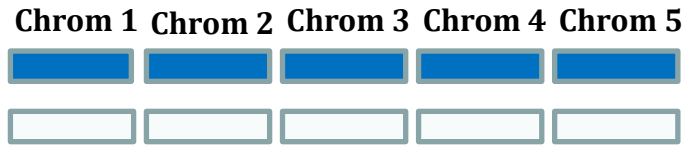
- mean: 33 kg
- variation: 19.5 kg
- $p(>70\text{kg})$: 2.8%



Background

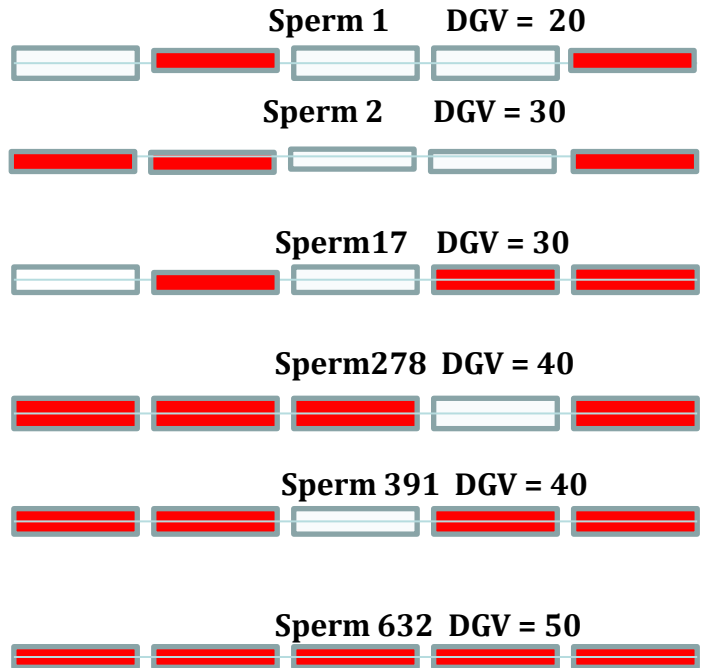
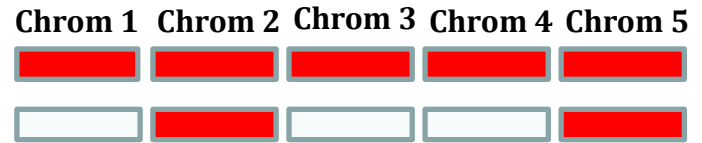
 Haplotype DGV +10
 Haplotype DGV = 0

Sire A: DGV +50



 Haplotype DGV +10
 Haplotype DGV = 0

Sire B: DGV +70

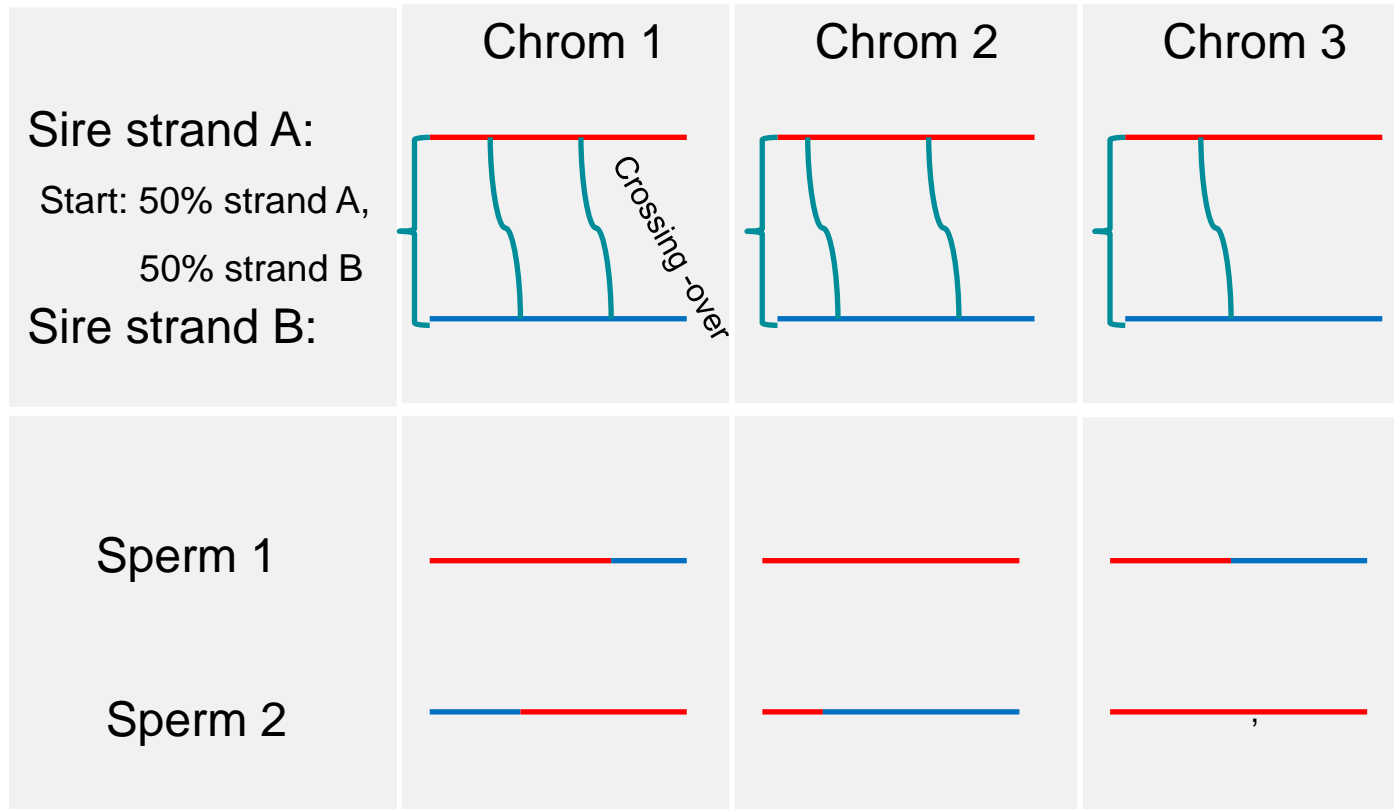


Mean & variation of sperms



Materials & Methods

Simulated mean and variation (n = 100.000)



→ Calculate sperm mean and sperm variation of 100.000 simulated sperms

Materials & Methods

- 58,035 Holstein animals (50K chip)
- Phasing via Beagle (v 3.3; Browning and Browning, 2010)
- Traits: Protein and fat yield

$$h_{ij} = \sum_{k=1}^n z_{kj} \alpha_k$$

$$\text{MGBV} = \frac{1}{N} \sum_{j=1}^N \sum_{i=1}^H h_{ij}$$

h_{ij} : i-th parental or maternal haplotype breeding value

z : indicator of marker k

α_k :k-th half SNP effect

n : number of SNP belonging to i-th haplotype

MGBV: mean gamete breeding value

N: number of repetitions of the simulation

H: number of haplotypes

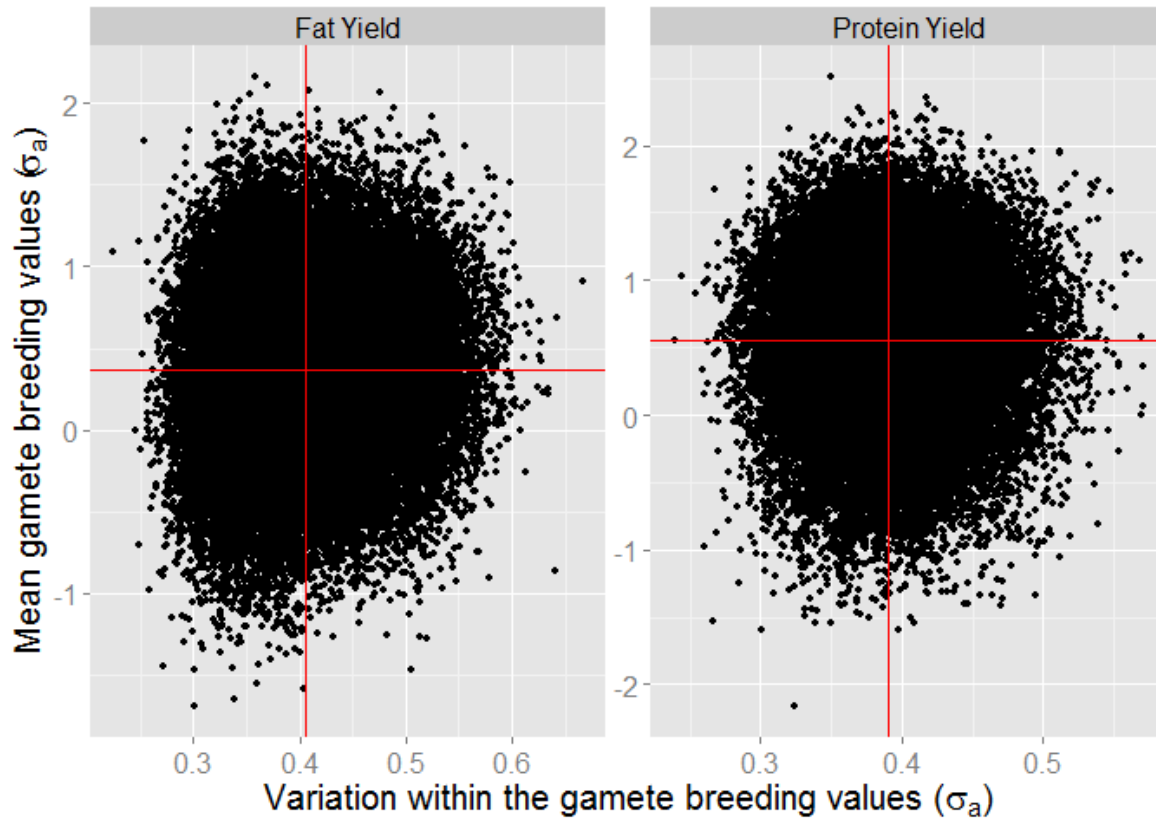
VGBV: Variation of the gamete breeding values

$$\text{VGBV} = \sqrt{\frac{1}{N-1} \left[\left(\sum_{j=1}^N \left(\sum_{i=1}^H h_{ij} \right)^2 \right) - \frac{1}{N} \left(\sum_{j=1}^N \sum_{i=1}^H h_{ij} \right)^2 \right]}$$



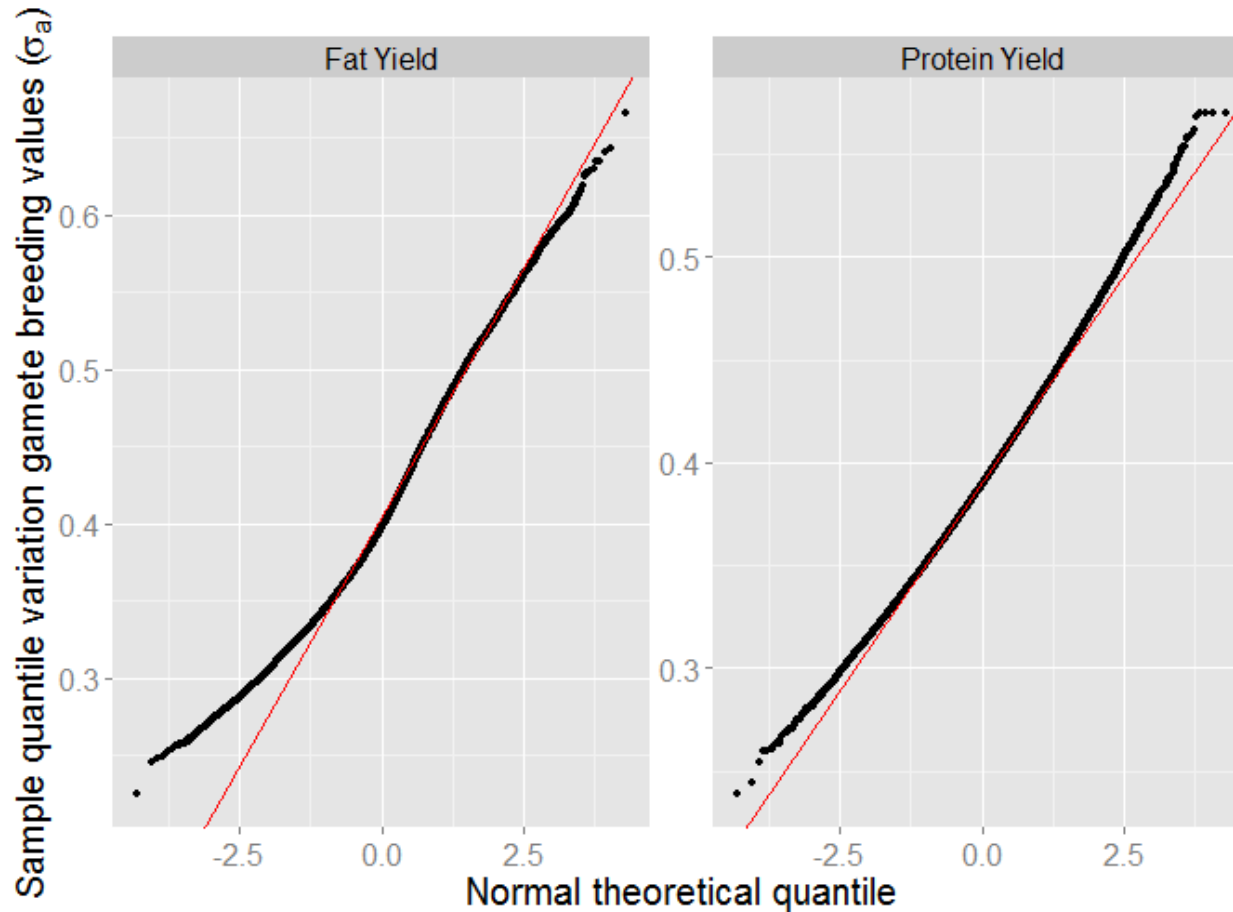
Results

Relation between mean (MGBV) & variation of gamete breeding values (VGBV)



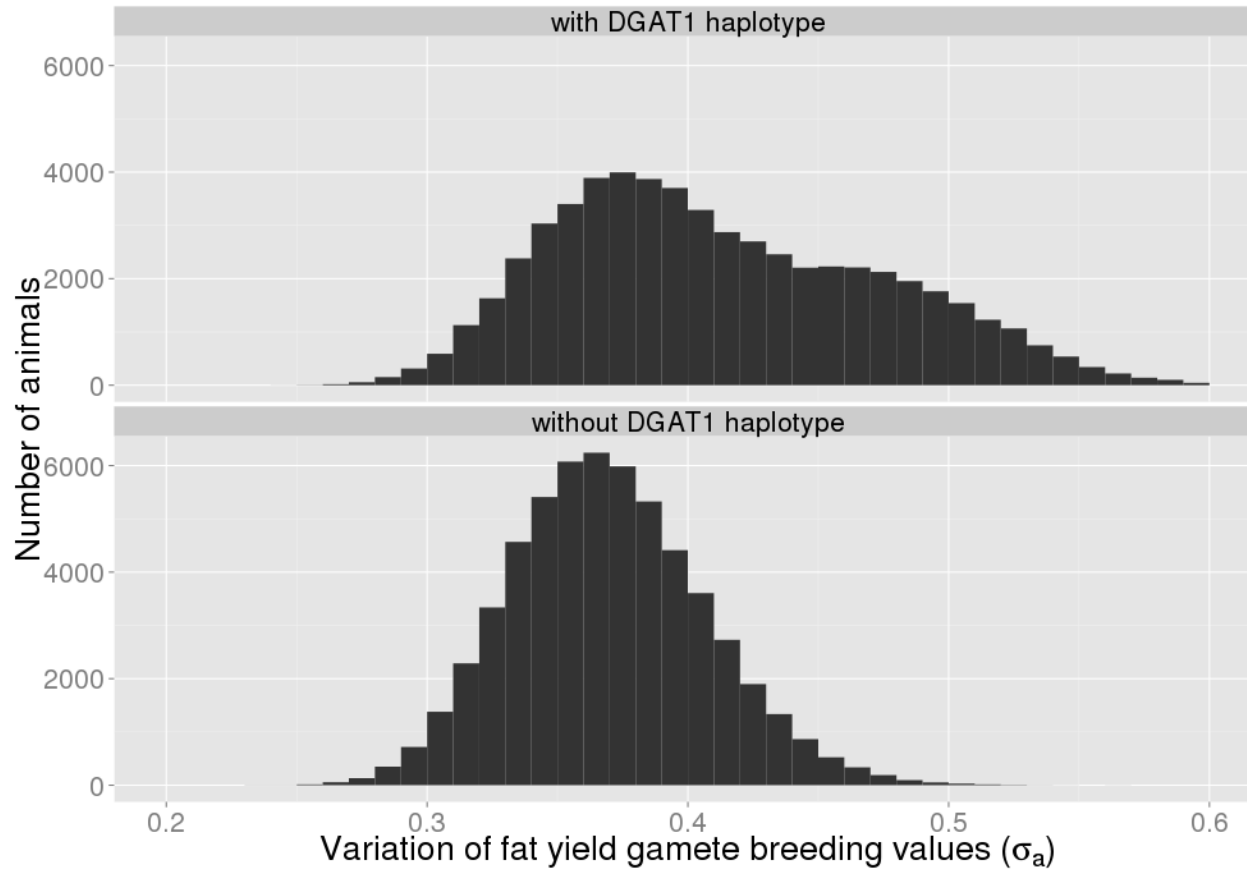
Results

Q-Q Plots for the variation of the gamete breeding values (VGBV)



Results

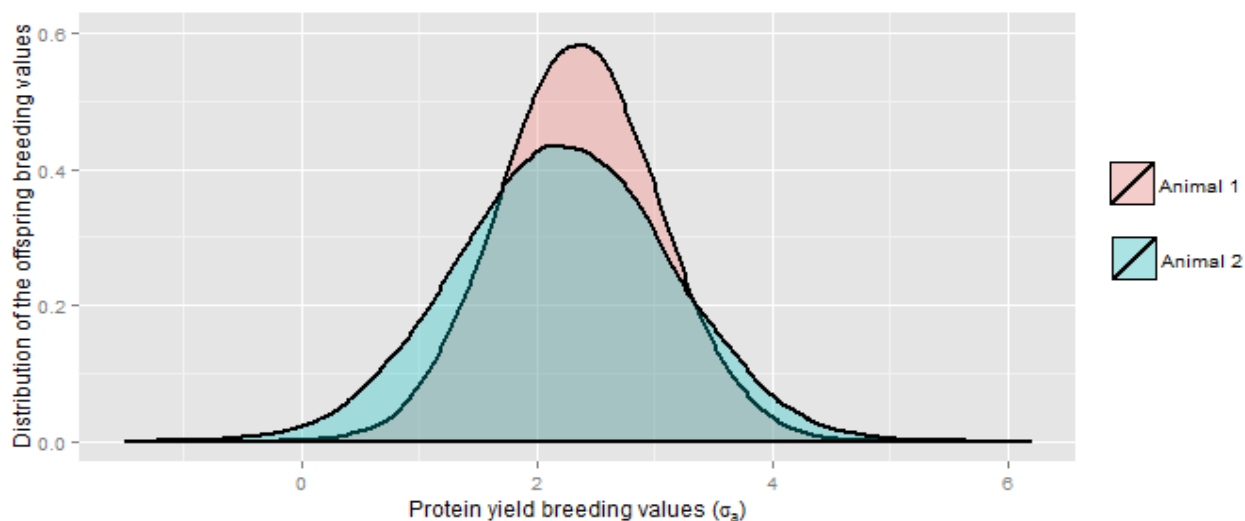
Distribution of VGBV for fat yield with & without the DGAT1 region



Results

Examples for specific matings (protein yield)

Sperm (σ_a)		Ovar (σ_a)		Offspring (σ_a)		$>1\sigma_a$		$>2\sigma_a$		$>3\sigma_a$		$>4\sigma_a$	
MGBV	VGBV	MGBV	VGBV	E(mBV)	E(vBV)	p(%)	N	p(%)	N	p(%)	N	p(%)	N
1.81	0.29	0.55	0.39	2.36	0.68	98	2	70	6	17	36	1	860
1.68	0.52			2.23	0.91	91	3	60	8	20	31	3	262



Results

gBAP: A genomic mating software for breeding associations to produce future candidates

■ Input:

- MGBV (DGV/2) and VGBV monthly estimated for all genotyped bulls & cows
- Imputed genetic defect state for all animal

■ Output:

- Recommendation of optimized mating combinations:
 - E(GEBV), Prob. of extreme offspring
 - Benefit: Low computation time for costumer

Animal	DGV	VGBV
12400001398471	146	4.502
528000086331385	142	3.496
82672792700100	142	4.234
84000009177608	142	3.864
84000009990078	142	3.628
84000001699263	142	3.996
52800072777802	143	4.329
52800076877223	143	4.190
52800082493602	143	4.305
84000009474087	143	3.702
52800078611632	144	4.622
52800076876554	144	4.144
52800086061225	144	4.188

cow	bull	DGV_OFF	Variation	p(>152)
12400001398471	52800086331385	144	7.99	10.56
12400001398471	82672792700100	144	8.73	12.62
12400001398471	84000009177608	144	8.36	11.59
12400001398471	84000009990078	144	8.13	10.94
12400001398471	84000001699263	144	8.50	11.99
12400001398471	52800072777802	144	8.83	14.10
12400001398471	52800076877223	144	8.69	13.72
12400001398471	52800082493602	144	8.80	14.04
12400001398471	84000009474087	144	8.20	12.34
12400001398471	52800078611632	145	9.13	16.22
12400001398471	52800076876554	145	8.64	14.90
12400001398471	52800086061225	145	8.69	15.01



Conclusions

- Offspring groups of sires vary and prediction of the distribution is possible
 - Useful information to increase/decrease the probability to get extreme offspring

- Farmers benefit from genomic selection:
 - Imputing LD to 50K: reduce costs and screening of the whole herds is possible
 - Screening the herds for genetic properties (polled, red factor)
 - Screening and managing recessive alleles/ haplotypes (HH1,HH2,HH3)

- New tools (i.e. gBAP) to handle all genomic information and to find the most suitable mating partners are needed
 - gEBV
 - Variation
 - Genetic defects (HH1,HH2,HH3,...)
 - Genetic properties (polled, coat colour..)
 -





Acknowledgements

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Thank you for attendance !

Results

Correlation between variation of gamete breeding values for different traits and inbreeding coefficients

	$VGBV_{PY}$	$VGBV_{FY}$	F_G	F_P
$VGBV_{PY}$	1	0.41	-0.19	-0.09
$VGBV_{FY}$		1	-0.10	-0.06
F_G			1	0.52
F_P				1

$VGBV_{PY}$: Variation gamete breeding values protein yield

$VGBV_{FY}$: Variation gamete breeding values fat yield

F_G : genomic inbreeding coefficient

F_P : pedigree inbreeding coefficient

