RELATIONSHIPS AMONG SEMEN QUALITY TRAITS IN HOLSTEIN BULLS

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FRAMEWORK: Study of the male component of fertility in Holstein-Friesian

OBJECTIVE: To determine the genetic component of semen traits and to identify a reduced set of summary traits

MATERIAL AND METHODS:

Data from 511 bulls. Semen (2 ejaculates) collected from 1990 to 2007 in an AI centre

Table. 1. Description of data recorded

	N	Mean	Median	S.D.	C.V.	Kurtosis	Min.	Max.
Volume	*24101	5.76	5	2.69	46.80	2.57	1	20
	**22368	5.06	5	2.54	50.30	3.94	1	20
Concentration	*23484	1335	1370	631	47.20	-0.15	0	3815
	**21845	966	1370	516	53.40	-0.17	0	3548
Mass motility	*23926	4.14	4	0.83	20.30	-0.33	0	5
	**22213	4.02	4	0.83	20.70	-0.42	0	5
Individual motility	*24047	82.4	90	16.7	20.30	11.04	0	99
	**22318	81.1	85	18.1	22.40	8.77	0	90
Post thawing quality	22922	48.1	50	13.6	28.30	2.32	0	95

* First ejaculate
** Second ejaculate

Multi trait Model:

$$y_{ijklmno} = W\_f_i + NE\_f_j + AC\_cov^2_k + DPC\_cov^2_l + p\_r_m + a\_r_n + e_{ijklmno}$$

f= fixed; r=random; cov =covariate

W_f_i= Year-Week of collection (i=1,..,934)
NE_f_j= No ejaculate (j=1, 2)
$AC\_cov^2_k$=Age at collection (k=1, 2)
$DPC\_cov^2_l$=Days to previous collection (l=1, 2)
p_r_i = Permanent environmental (bull, m=1,.., 511)
a_r_m = Additive genetic (n=1,.., 1297)

Analyses: REML (VCE 6.0) – Principal Components (SAS 9.1)

RESULTS

Table.2 . Estimated heritabilities and repeatabilities (diagonal) and correlations (off diagonals) between characters. Standard deviations in brackets.

	Genetic					Permanent					Phenotypic				
Volume	**0.18**	**-0.01**	**0.18**	**0.32**	**0.18**	**0.10**	**-0.18**	**0.02**	**0.08**	**0.01**	**1.00**	**0.10**	**0.12**	**0.10**	**0.10**
	(0.01)	(0.06)	(0.08)	(0.27)	(0.18)	(0.01)	(0.02)	(0.02)	(0.03)	(0.04)					
Concentration		**0.16**	**0.87**	**0.80**	**0.67**		**0.18**	**0.83**	**0.88**	**0.82**		**1.00**	**0.68**	**0.60**	**0.30**
		(0.02)	(0.02)	(0.07)	(0.09)		(0.02)	(0.02)	(0.03)	(0.04)					
Masal motility			**0.16**	**0.82**	**0.84**			**0.18**	**0.81**	**0.83**			**1.00**	**0.72**	**0.43**
			(0.02)	(0.03)	(0.10)			(0.03)	(0.01)	(0.05)					
Individual motility				**0.08**	**0.80**				**0.26**	**0.89**				**1.00**	**0.40**
				(0.02)	(0.10)				(0.03)	(0.05)					
Post thawing quality					**0.16**					**0.30**					**1.00**
					(0.03)					(0.06)					

Table 3. Results of principal components analyses

	Genetic					Phenotypic				
Principal component	Eigenvalues	Difference	%	Cumulative		Eigenvalues	Difference	%	Cumulative	
1	3.54	2.53	71	71		2.61	1.61	52	52	
2	1.01	0.59	20	91		1.00	0.25	20	72	
3	0.41	0.37	8	99		0.75	0.37	15	87	
4	0.05	0.04	1	100		0.38	0.13	7	94	
5	0.01		0	100		0.25		5	100	
Traits	Eigenvectors					Eigenvectors				
	Prin1	Prin2	Prin3	Prin4	Prin5	Prin1	Prin2	Prin3	Prin4	Prin5
Volume	0.17	0.94	0.17	0.01	0.25	0.09	0.99	0.03	0.11	-0.07
Concentration	0.47	-0.34	0.53	-0.08	0.62	0.50	-0.15	0.37	-0.68	-0.35
Mass motility	0.53	-0.04	0.05	-0.68	-0.51	0.56	0.01	0.13	-0.07	0.82
Individual motility	0.52	-0.01	0.13	0.73	-0.42	0.53	-0.04	0.14	0.70	-0.45
Post thawing quality	0.45	-0.02	-0.82	0.03	0.35	0.38	-0.03	-0.91	0.16	-0.10

CONCLUSIONS

- Routine semen traits show moderate heritability and therefore could respond to selection (except individual motility ?)
- Two components explain most of the observed genetic and phenotypic variability: Quantity and Quality
- Relationship with actual bull ability to fecundate cows must be evaluated (A.I. results)

ACKNOWLEDGEMENTS

- The financial support of the Project INIA-FEDER: RTA2007-0071 is greatly acknowledged. S. Karoui is funded by an INIA scholarship