

Genome-wide association study for milk, fat and protein yields in different lactation stages in Canadian Holstein and Jersey cattle



holivier@uoguelph.ca

Hinayah Rojas de Oliveira^{1,2}, F. F. Silva¹, L. F. Brito², J. Jamrozik^{2,3}, D. A. L. Lourenco⁴ and F. S. Schenkel²



¹Universidade Federal de Viçosa, Minas Gerais, Brazil; ²CGIL - University of Guelph, Ontario, Canada; ³Canadian Dairy Network, Ontario, Canada; ⁴University of Georgia, Georgia, USA



Introduction

- Several countries currently use random regression models in their official genetic evaluations
- Typically EBVs based on test-day records are more accurate than those based on the cumulative 305-d models
- Most GWAS for production traits have been carried out using cumulative 305-d yields
- However, using lactation-day yields in GWAS may allow for assessing:
 - Genomic regions with substantial effect on different lactation stages
 - Differences in groups of candidate genes along the lactation curve

Materials and Methods

- A total of 10,798 Holstein and 973 Jersey cattle were used
- Random regression coefficients for each animal were predicted based on the GBLUP method
- Direct genomic values (DGV) for each lactation stage were obtained by summing up the predicted DGV of the specific days: 1) from 5 to 95, 2) from 96 to 215, and 3) from 216 to 305 days
- Moving SNP-by-SNP windows of 20 adjacent SNPs that explained more than 0.50% of total additive genetic variance were considered for further analyses
- Candidate gene analyses were performed via Ensembl database, using the Variant Effect Predictor tool
- The gene functions were obtained from the National Center for Biotechnology Information database (NCBI), and QTLdb - Animal Genome Databases

OBJECTIVES

- To identify important genomic regions associated with milk (MY), fat (FY) and protein (PY) yields in different lactation stages of Canadian Holstein and Jersey cattle; 2) to investigate prospective candidate genes across breeds and lactation stages for the production traits

Results

Table 1. Number of important genomic windows (N), mean and maximum (Max) proportion of explained genetic variance in each lactation stage, trait and breed.

Trait	Stage	Jersey			Holstein		
		N	Mean (%)	Max (%)	N	Mean (%)	Max (%)
Milk	1	16	0.51	0.56	29	0.53	0.59
	2	16	0.57	0.69	51	0.55	0.71
	3	21	0.55	0.62	50	0.56	0.72
Fat	1	30	0.58	0.88	20	1.93	4.86
	2	10	0.55	0.61	25	2.87	8.74
	3	8	0.53	0.58	22	2.53	7.07
Protein	1	6	0.52	0.53	9	0.99	1.46
	2	10	0.53	0.58	14	1.05	1.94
	3	13	0.54	0.58	10	0.93	1.52

- Lower number of windows was found for PY in comparison to MY and FY in both breeds
- Number of important windows tended to be higher for Holsteins than for Jerseys for all analyzed traits
- Genomic regions associated with milk production traits in different lactation stages were located on chromosomes BTA5, BTA11, BTA14 and BTA20 for Jerseys, and on chromosomes BTA5, BTA14 and BTA20 for Holsteins
- Different sets of candidate genes were found across breeds and lactation stages

Table 2. Candidate genes for each trait, lactation stage and breed. Genes in bold were already reported in the literature.

Trait	Stage	Jersey		Holstein	
		BTA	Genes	BTA	Genes
Milk	1	5	IGF-I , NT5DC3, PAH, TXNRD1	14	CYHR1 , DGAT1 , eef1d , MAF1 , MAPK15, RHPN1, SCRIB, VPS28 , ZC3H3
	2	5	CHST11, NT5DC3, PAH, TXNRD1	14	CYHR1 , DGAT1 , eef1d , MAF1 , MAPK15, RHPN1, SCRIB, VPS28 , ZC3H3
	3	5, 20	NT5DC3, PAH, PRKAA1, PTGER4, TTC33, TXNRD1	14	CYHR1 , DGAT1 , eef1d , MAF1 , MAPK15, RHPN1, SCRIB, VPS28 , ZC3H3
Fat	1	5, 14, 20	ANO6, IGF-I , PAH, SLC38A1 , DGAT1 , GPBP1	5, 14	DGAT1 , KLHL42 , POLDIP3, SEP3, TMTC1 , TOX
	2	5	IGF-I , NT5DC3, PAH	5, 20	ADAMTS12, CCDC91 , KLHL42 , LARGE1, MRPS35, POLDIP3, TMTC1
	3	5	ASCL1, GLT8D2, HCFC2, HSP90B1, IGF-I , NT5DC3, PAH, PARPBP, PMCH, STAB2, TDG	5, 20	ADAMTS12, CCDC91 , KLHL42 , LARGE1, MRPS35, PTHLH, TMTC1
Protein	1	5, 11	NCK2, PAH	14	CYHR1, DGAT1 , MAF1, VPS28
	2	5, 11	NCK2, PAH, SLC20A1	14	CYHR1, DGAT1 , MAF1, SCRIB, VPS28
	3	11	NCK2, SLC20A1	14	CYHR1, DGAT1 , MAF1, VPS28

CONCLUSIONS

Genomic regions associated with MY, FY and PY were identified for different lactation stages in Holsteins and Jerseys. The sets of prospective candidate genes differed substantially across breeds and lactation stages. Further studies using alternative methodologies will assist to validate these findings.