

Genome-wide association of 16 milk fatty acids in Chinese and Danish Holstein populations

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Conclusion

- Joint population provides more power to detect significant SNP
- Few SNP showing significant different effects between two populations are detected

Data

- **Animal:** 784 Chinese Holstein cows (CN)
371 Danish Holstein cows (DK)
- **Common SNP:** 486,464 (BTA 1-29)

Models

- A single-SNP mixed model to detect SNP associated with fatty acids (FA)

$$y = \text{country} + \text{herd} + \text{parity} + b_1 * DIM + b_2 * e^{-0.05 * DIM} + qx + \alpha + e$$

- The following mixed model to detect differences in SNP effects

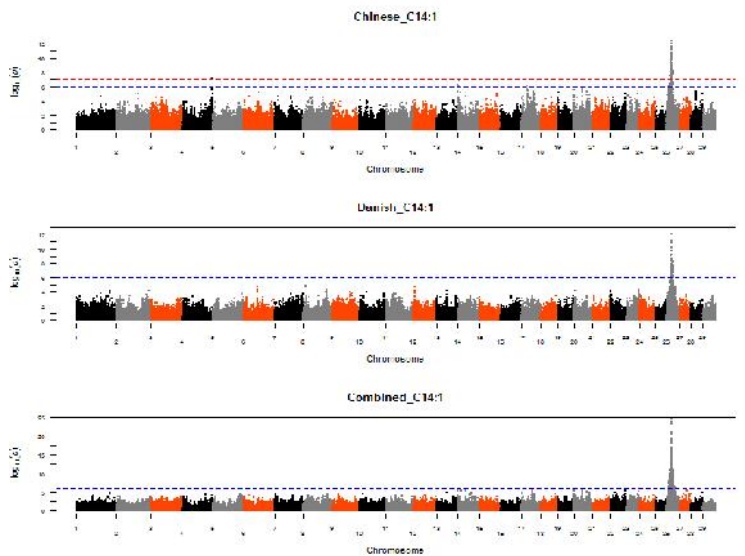
$$y = \text{country} + \text{herd} + \text{parity} + b_{CN(DK)} * DIM + d_{CN(DK)} * e^{-0.05 * DIM} + (q_{DK} + \Delta q * E)x + \alpha + e$$

E=0 for DK; E=1 for CN; Δq for difference in the SNP effect



Results

- **Figure1 Genome-wide association plots for FA C14:1**



- **Table1 Number of significant SNP associated with FA**

Trait	Genome-wide level				Chromosome-wide level			
	CN	DK	CN+DK	Diff*	CN	DK	CN+DK	Diff*
C8:0	0	0	0	0	0	3	1	0
C10:0	1	0	0	0	8	0	3	4
C12:0	0	0	0	0	2	0	1	3
C14:0	0	0	0	0	1	0	8	0
C14:1	167	59	354	0	312	122	528	3
C15:0	0	0	0	0	0	0	5	0
C16:0	0	0	2	0	8	2	13	0
C16:1	0	12	28	0	10	30	59	0
C18:0	8	0	1	3	146	1	29	33
C18:1n-9	0	0	6	0	10	0	19	2
C18:2n-6	1	0	4	0	18	6	29	2
C18:3n-3	0	0	0	0	0	2	0	10
CLA911	0	0	3	0	0	5	24	3
C14 index	253	175	501	0	406	287	776	3
C16 index	0	0	2	0	6	12	49	1
C18 index	17	0	6	0	173	5	53	1

* Significant differences in SNP effects between two populations