Patterns of genetic variation between autosomes and sex chromosomes in *Bos taurus* genome

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Conclusions

- sex chromosomes → lower variant density than autosomes, because of lower recombination rates
- X chromosome → less extreme functional consequences of variants than on autosomes
- Y chromosome → loss of recombination leads to the accumulation of nonsynonymous mutations
- long noncoding regions → lower variant density
- high recombination rate → high density of SNPs and InDels

Objectives

Mining patterns of genetic variation between autosomes and sex chromosomes in the bovine genome

Data set

- WGS of 217 cattle (Illumina)
- 7 breeds
- ARS-UCD1.2_Btau5.0.1Y genome
- annotation files — Btau_5.0.1 and ARS-UCD1.2

Methods

quality control → trimming → alignment → post-alignment processing → SNP/InDel calling → variant annotation

Statistical analysis:
- variant density on each chromosome
- InDel length
- Ka/Ks ratio
- nucleotide divergence
- Tajima's D

Results

- 23,655,295 SNP/3,758,781 InDel
- numbers of SNPs and InDels → not uniformly distributed across 100kb non-overlapping windows ($P < 0.001$)
- on BTA12 and BTA13 → regions with high variant density
- Ka/Ks ratio → BTA = 0.79
  BTX = 0.62
  BTY = 2.00