Incorporation of GWAS data on genomic prediction accuracies assessed in the small, unadmixed, unstructured population of Icelandic dairy cattle

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ssGBLUP has 29%, 40% and 63% higher prediction accuracy for milk, protein and fat yield over PBLUP in Icelandic cattle

Icelandic cattle

- > ca. 26,000 breeding cows with annual milk yield of ca. 6,500 kg
- Unadmixed, unstructured, and genomically distinct from other European cattle populations (Gautason et al., 2020)
- Most related to cattle from Finland and Norway

Genomic selection in Icelandic cattle

More than 8,000 bulls and cows genotyped (50k SNP chip) to:

- Assessgenomic prediction accuracies
- Develop strategies to improve prediction accuracies for small cattle breeds

Results

- At short distances, linkage disequilibrium (LD) in Icelandic Cattle higher than in Red Nordic and Holstein-Friesian cattle (Fig. 1.)
- Single step GBLUP (ssGBLUP) gives considerably higher accuracy for genotyped animals than pedigree based BLUP (PBLUP) for yield traits (Fig. 2)

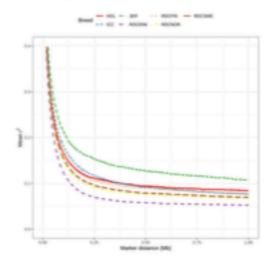
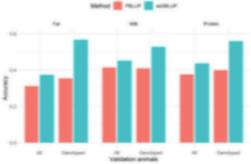


Fig. 2. Length of type and constaliants of markets for intervalue FIEL have pairs philled applied in also distance. We used 102 halos and CNL 420 markets for computing r^{-2} , formed under an architects (CL include). Gallo, SEL Constitution, 102 halos and CNL 420 millions, 102 halos and computer pairs (SEL 400 millions, 102 halos for Exactly, 102 halos for Exact



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Fig.2. Accessing of EBU hands on history and sublation split for pedge exclusion BLF [PELIP] and single strep EBLF [suEBLF] for exclusion and provide girls. 22 of exclusion in the presidence of surface step edge eductions. In the solid atom press.

Discussion and perspectives

- High LD could be due to long isolation of the breed and small founder population
- Higher gains in accuracy may partly be due to the relatively high LD at short distances
- Considerable genetic gain could be achieved by preselecting insemination bulls and bull dams
- Euture research: Effect of incorporating additional information (e.g. GWAS data, function al annotations) on genomic prediction accuracies

Methods

- Squared correlations among autosomal SNPs were computed using HD genotypes of icelandic bulls and six Nordic reference breeds. Squared correlations were averaged for intervals of 500 base pairs and plotted against marker distance.
- Breeding values were estimated for test day records of milk, fat and protein yield using PBLUP and ssGBLUP using a random regression test day model. Data were devided into validation and training set according to median birth date of half-sib groups. There were roughly 10,000 animals, 1113 of which were genotyped. We estimated accuracy of EBVs as:

$$r = \frac{cor(EBV_W + PE_W, EBV_t)}{h}$$

where PE, w, t and h stands for permanent environment, whole data, training data and square root of heritability.

References

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