

**Objet:** FW: Abstract submitted: #78619491

**Date:** vendredi, 28 février 2025 à 10:53:06 h heure normale d'Europe centrale

**De:** Vasiljevic, Stefan (VETSUISSE)

**À:** Vasiljevic, Stefan (VETSUISSE)

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**Date :** vendredi, 28 février 2025 à 10:27

**À :** "Vasiljevic, Stefan (VETSUISSE)" <[stefan.vasiljevic@unibe.ch](mailto:stefan.vasiljevic@unibe.ch)>

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Dear Stefan Vasiljevic,

your Abstract #78619491 has been submitted and will be reviewed in the next days.

Thank you for submitting your abstract, we have received your contribution in good order.

Details of the Abstract are reported below:

### **Identifying QTL for hoof and leg conformation in Swiss dairy cattle**

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**Objectives:** To evaluate the h2 of hoof and leg conformation traits and to identify underlying QTL and candidate variants in Swiss Holstein (HO) and Brown Swiss (BS) cattle.

**Materials & Methods:** The dataset included 115k HO and 75k BS animals. Microarray-derived genotypes, own performance records and dEBVs for hoof and leg conformation traits were provided by the Association of Swiss Cattle Breeders. For HO, analyzed traits included bone quality (BQ), rear legs rear view (RLRV), rear legs side view (RLSV), heel depth (HDE), hoof angle (HAN), and locomotion (LOC), and for BS, traits examined were RLRV, RLSV, HDE, and HAN. The SNP data were imputed to the sequence level resulting in genotypes for 37M SNVs in HO and 26M SNVs in BS. A subset of 730k biallelic markers was extracted from the imputed data to conduct association tests. Own performance records were corrected for non-genetic factors with the lme4 R package. Analyses used the 730k SNPs, with variance component estimation and MLMA conducted using GCTA. Additive GWAS analyzed both, corrected phenotypes and dEBVs. Non-additive (dominant and recessive) models were applied on corrected phenotypes only. QTL-harboring chromosomes underwent a second MLMA incorporating all imputed SNPs.

**Results:** The estimated  $h^2$  using corrected phenotypic data for HO and BS ranged from 0.13 to 0.28 and from 0.10 to 0.26, respectively. In HO, nine additive QTL associated with hoof and leg conformation (LOC, BQ, HDE) were identified on chromosomes 5, 6, 7, 11, 14, and 18. Furthermore, the non-additive GWAS revealed a recessive QTL on chr 22 for BQ. In BS, GWAS identified additive QTL on chr 2, 13, 18, 25, and 26 for HDE and RLRV.

**Conclusion:** This study confirmed moderate  $h^2$  for hoof and leg traits in two cattle breeds. Our analyses revealed a genetic complexity underlying hoof and leg conformation traits in HO and BS cattle and identified several significant additive, but also for the first time non-additive QTL associated with these traits.

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