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Genomic Evaluation for Foot and Claw disorders in Czech Holstein

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Session VI: New traits [2]

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projects MZE-RO0723 and QK1910320.

Objectives

Predict **Genomic Breeding Values**
for resistance to **Foot and Claw Disorders**
using a **Multi-trait** Animal Linear model
With **Linear Type Traits**.

Supported by The Ministry of Agriculture of the Czech Republic:
projects MZE-RO0723 and QK1910320.

Cooperating organizations

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Diary of Diseases and Medication

A source of the records of diagnoses (Dg)

Diagnoses defined in accordance with ICAR

Launched in 2017

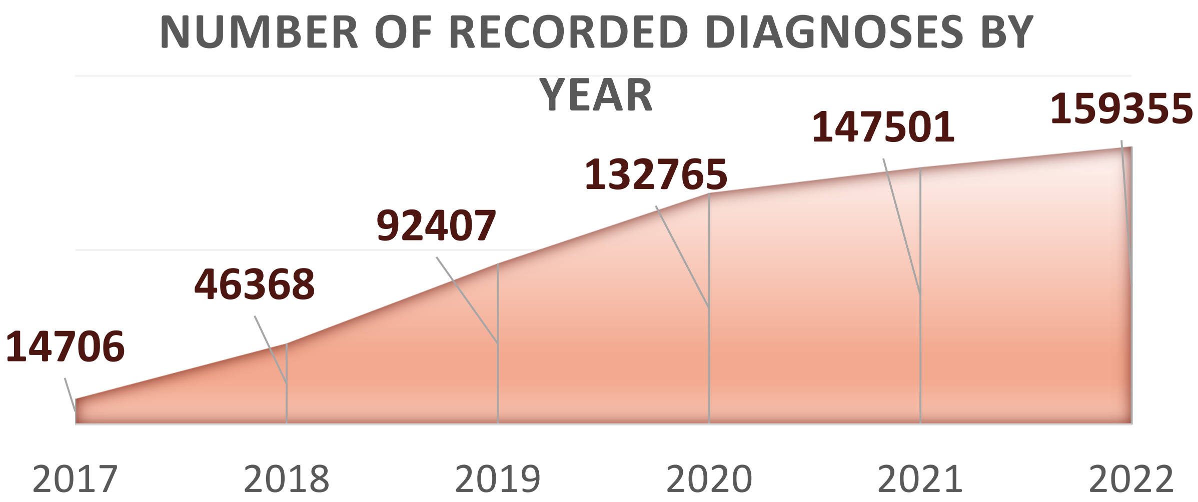
620 000 records of Dg

185 000 diseased animals

400 000 monitored cows

340 agricultural enterprises

Voluntary recording



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Foot and claw disorders definition

- **Infectious digital disorders** (IDD) included dermatitis digitalis and interdigitalis, interdigital phlegmon, and heel horn erosion;
- **Claw horn lesions** (CHL) included ulcer, white line disease, horn fissure, double sole etc.;
- **Overall claw disorders** (OCD) comprised all the recorded Foot and claw disorders.

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Short description of datasets

Infectious digital disorders	40,859 cows 71,219 lactations 12.52 % LIR 46 herds
Claw horn lesions	25,143 cows 44,265 lactations 13.30 % LIR 30 herds
Overall prevalence of claw disorders	57,567 cows 100,903 lactations 17.00 % LIR 64 herds

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Linear animal model for foot and claw disorders

- y_{ijkl} = $parity\_agegroup_i + herd\_year\_season_j + pe_k + a_l + e_{ijkl}$, (1)

where

- y_{ijkl} is the analysed CD trait; **0/1 occurrence in lactation**
- $parity\_agegroup_i$ is the effect of parity combined with age at calving class
- $herd\_year\_season_j$ is the combined effect of herd,year and season of calving
- pe_k is the random permanent environmental effect on cow traits across parity;
- a_l is the random additive genetic effect of animal,
- e_{ijkl} is the random residual effect

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Linear animal model for linear type traits

$$y_{ijklm} = \text{herd\_year\_season}_i + \text{classifier}_j + \beta_1 age_k + \beta_2 age_k + \beta_1 s_l + \beta_2 s_l + a_m + e_{ijklm}, \qquad (2)$$

where

y_{ijklm} is the linear type trait; **scored in the first lactation**

herd_year_season of scoring$_i$ is the combined effect of herd, year and season of scoring

classifier$_j$ is the effect of classifier

$\beta_1 age_k + \beta_2 age_k$ are linear and quadratic regressions on the age at scoring

$\beta_1 s_l + \beta_2 s_l$ are linear and quadratic regressions on the days in milk at scoring

a_m is the random additive genetic effect of animal,

e_{ijklm} is the random residual effect

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Genomic Data

- Single-step genomic BLUP (ssGBLUP)
- Program package BLUPF90 (Misztal et al. 2018)

- Genomic matrix: 12,959 animals; from that 5 374 bulls
- The Illumina BovineSNP50

- Number of effective SNPs (after QC): 36,520
- Number of effective Individuals (after QC): 12,672

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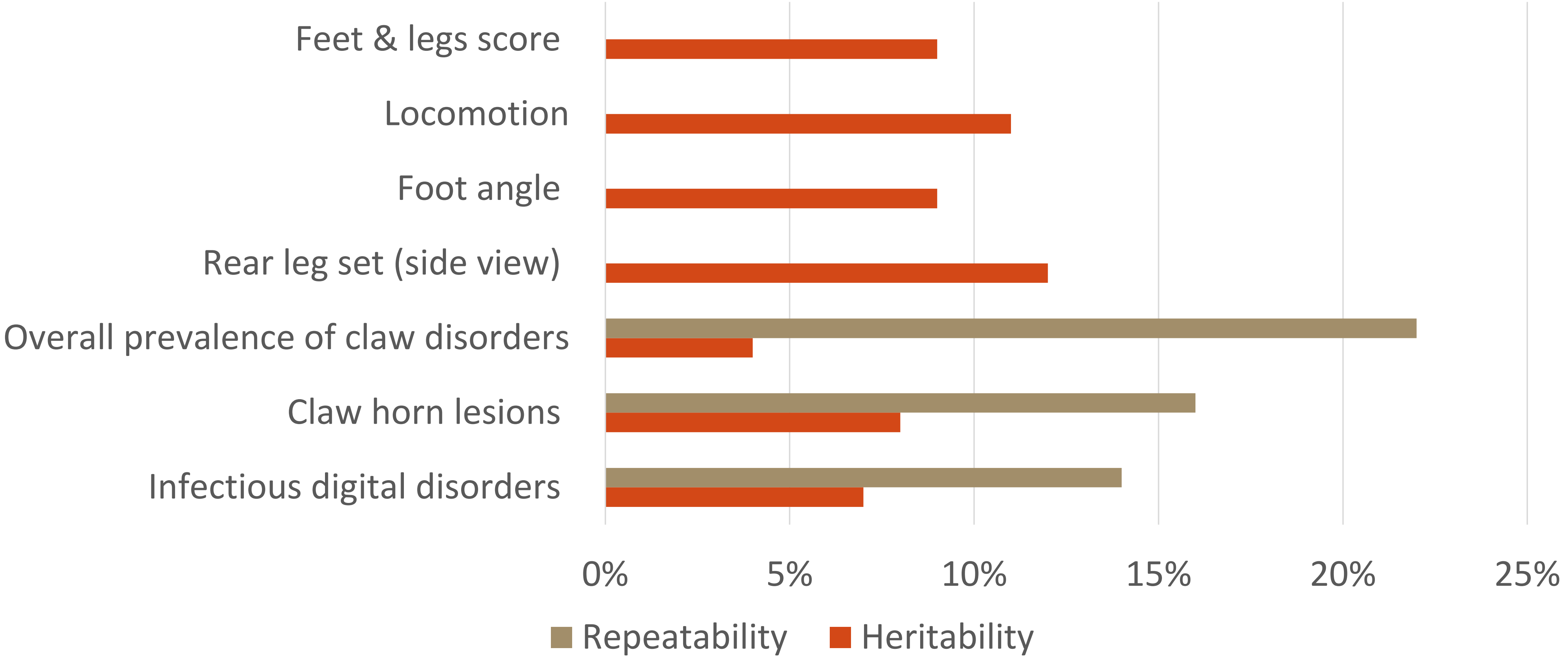
Heritability and repeatability



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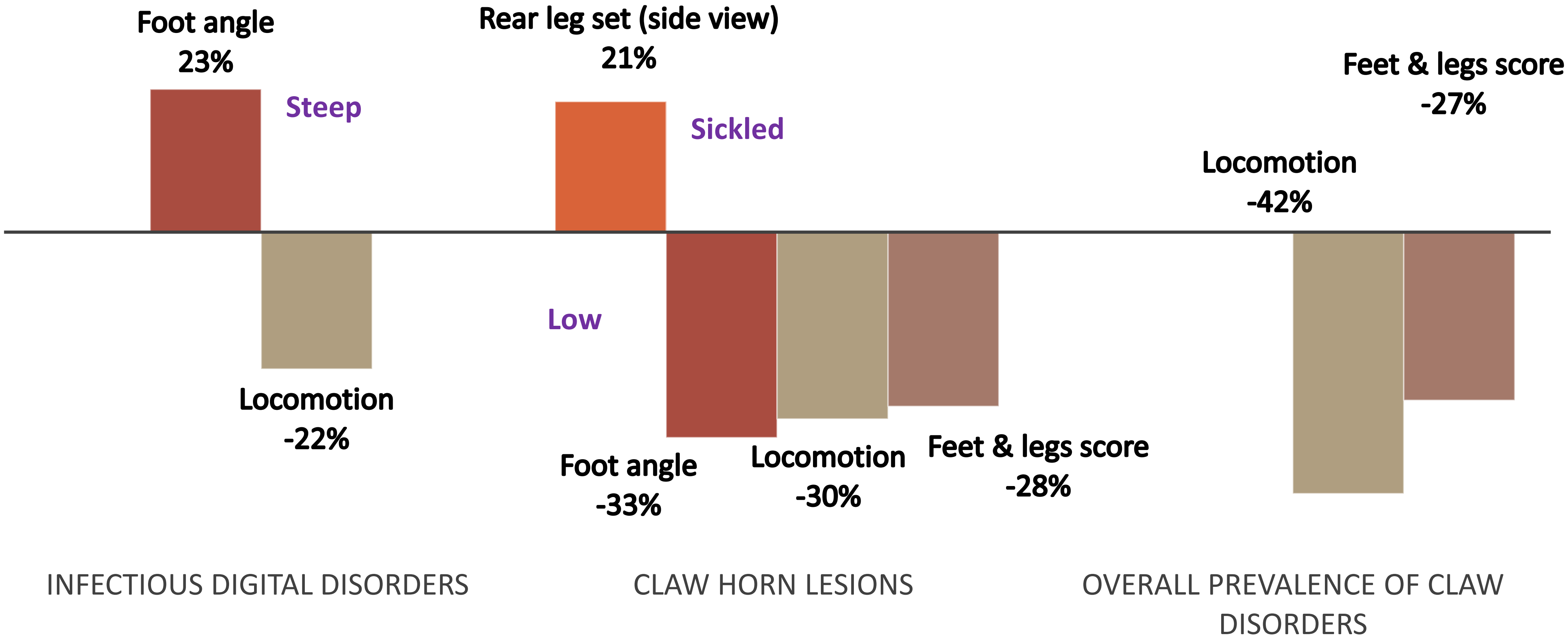
Genetic correlations with linear type traits



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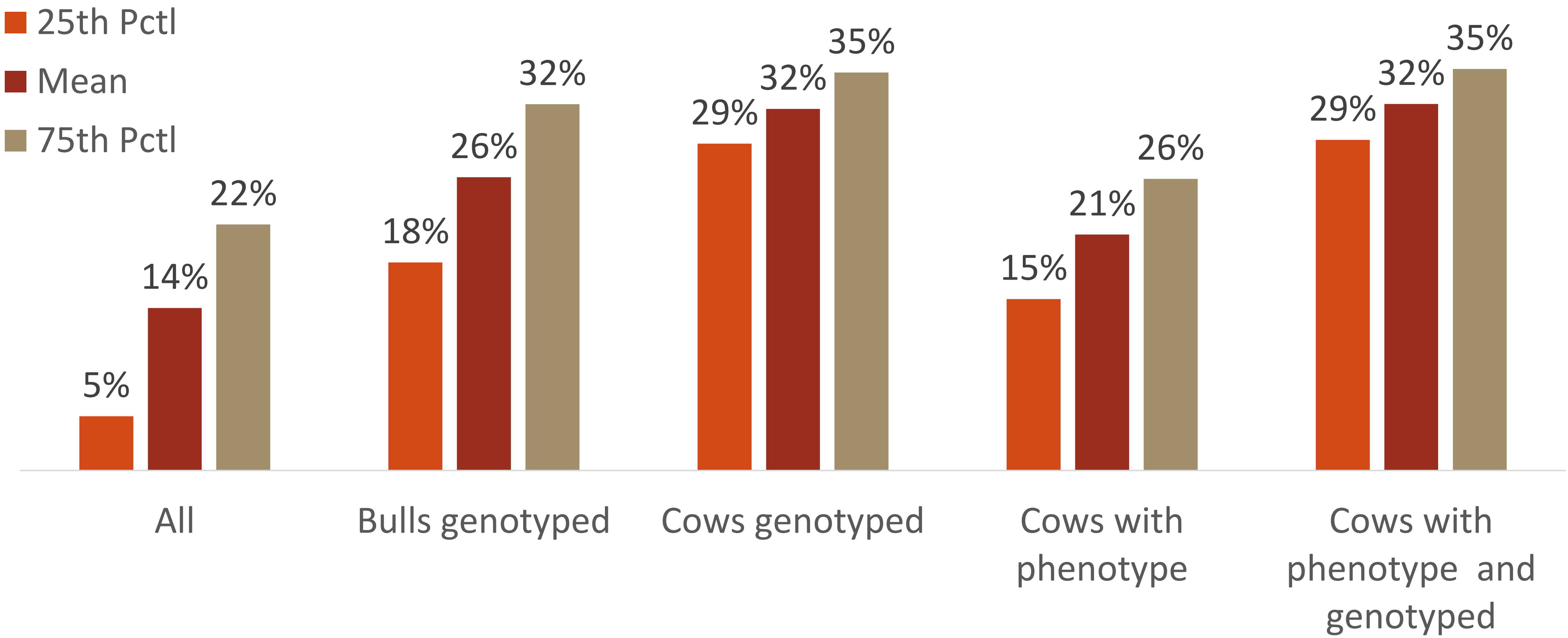
Accuracies of Breeding values for Infectious Digital Disorders by Multitrait Animal Model



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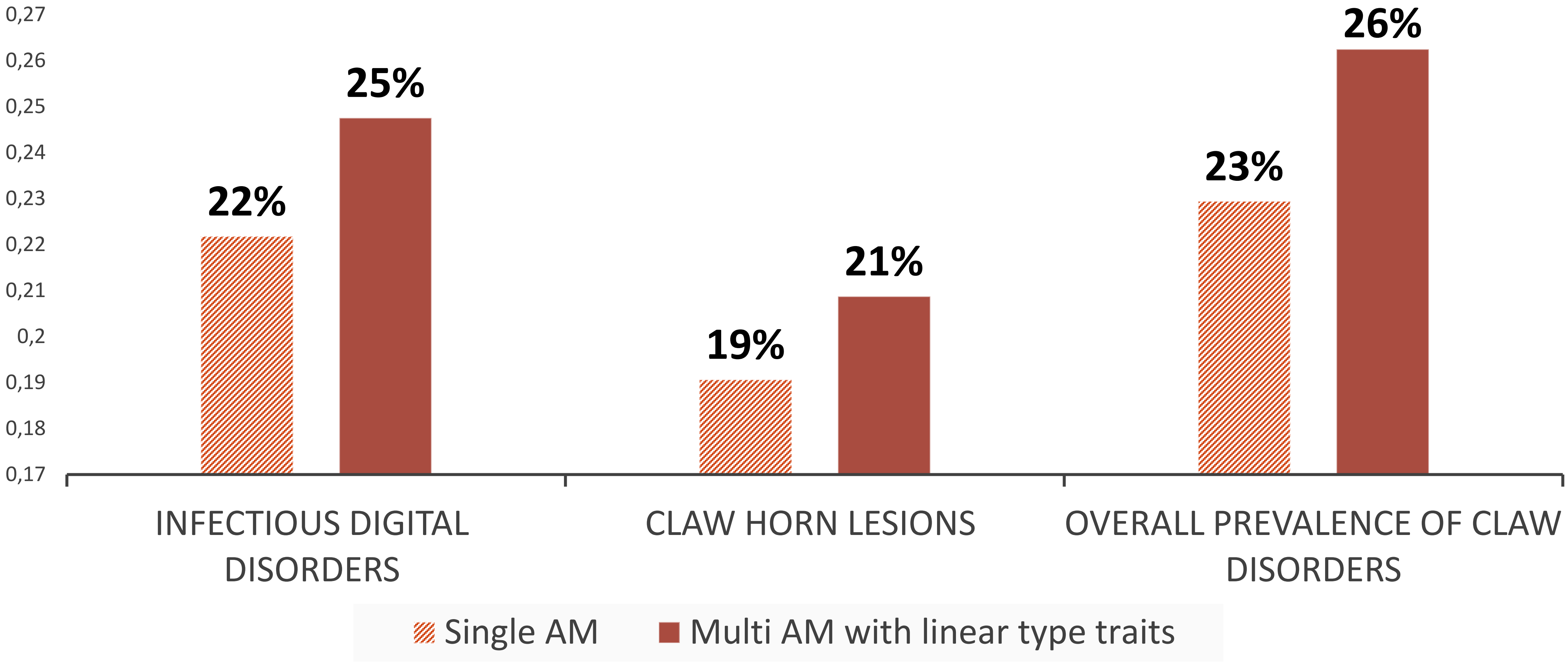
Increase in average accuracies of genomic breeding values by Multitrait Animal Model for young genomic bulls (186)



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Recapitulation of 2023

1. Accessible and functional health data monitoring system: Web application Diary of Diseases and Medication
2. Genomic breeding values are implemented: for Clinical mastitis (CM) and three group traits of Foot and claw disorders
3. Health index including economic values of health traits is established

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Future

- Increasing awareness of the benefits of monitoring cows' health data among farmers
- Consequently, to upturn the proportion of monitored animals for health in dairy cattle in the Czech Republic
- Improving breeding values estimation methods for health, e.g. using the weighted ssBLUP method
- Shortening the lactation period during which the occurrence of a health trait will be monitored
- Extend selection to other health traits, e.g. Reproductive disorders or genetic analysis of calf health

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Thank you

For your attention

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