Changes in genomic predictions when new information is included

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Introducing

• Persistence of genomic evaluations depends on the amount of data and population parameters

• Persistence may be high when the data is large enough
  - Chromosome segments can be well estimated
  - 10,000 to 15,000

• Stable predictions
  - e.g., > 15k genotyped bulls with high accuracy
• Stability of GEBV when more data is included is a desirable feature

• Fluctuations over time due to limited accuracy and decay of genomic information

• Small changes without additional information is a special requirement
• Evaluate changes in EBV and GEBV when new data is added on a monthly basis from December/2016 to December/2017
Materials and Methods

• Birth Weight (BW = 8,186,503)
• Weaning Weight (WW = 8,881,124)
• Post-Weaning Gain (PWG = 4,386,184)

• 10,129,980 animals in the pedigree
• 484,074 animals with genotypes

• 3-Trait model used in routine evaluations
• BLUP
• ssGBLUP using APY with 20K size core
New data by month

- **BW Dec/2016 (7,900,946) → 285,557 → Dec/2017 (8,186,503)**
- **WW Dec/2016 (8,630,227) → 250,897 → Dec/2017 (8,881,124)**
- **PWG Dec/2016 (4,298,754) → 87,430 → Dec/2017 (4,386,184)**
- **Genotypes Dec/2016 (392,999) → 91,075 → Dec/2017 (484,074)**
Correlations among predictions one year later

Correlation Dec/2016 - Dec/2017

All: 0.99 0.99
Own records: 0.99 1.00
No own records: 0.99 0.99
New records: 0.99 0.97
No new records: 0.99 1.00
Young: 0.99 1.00

Corr_GEBV
Corr_EBV
Distribution of differences of predictions

Minor changes, close to zero for 50% of animals

Outliers shown larger changes

Average changes greater for GEBV

Maximum changes greater for EBV

Changes are expressed in additive genetic standard deviation units
Distribution of differences of predictions over a year

![Graph showing distribution of differences over a year](image-url)
Average (maximum) changes in predictions over a year

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Conclusions

- The genomic evaluations are stable over a year because of large historical data and limited new data.
Thank you!!!