

Changes in genomic predictions when new information is included

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Introduction

- 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

Introduction

- 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

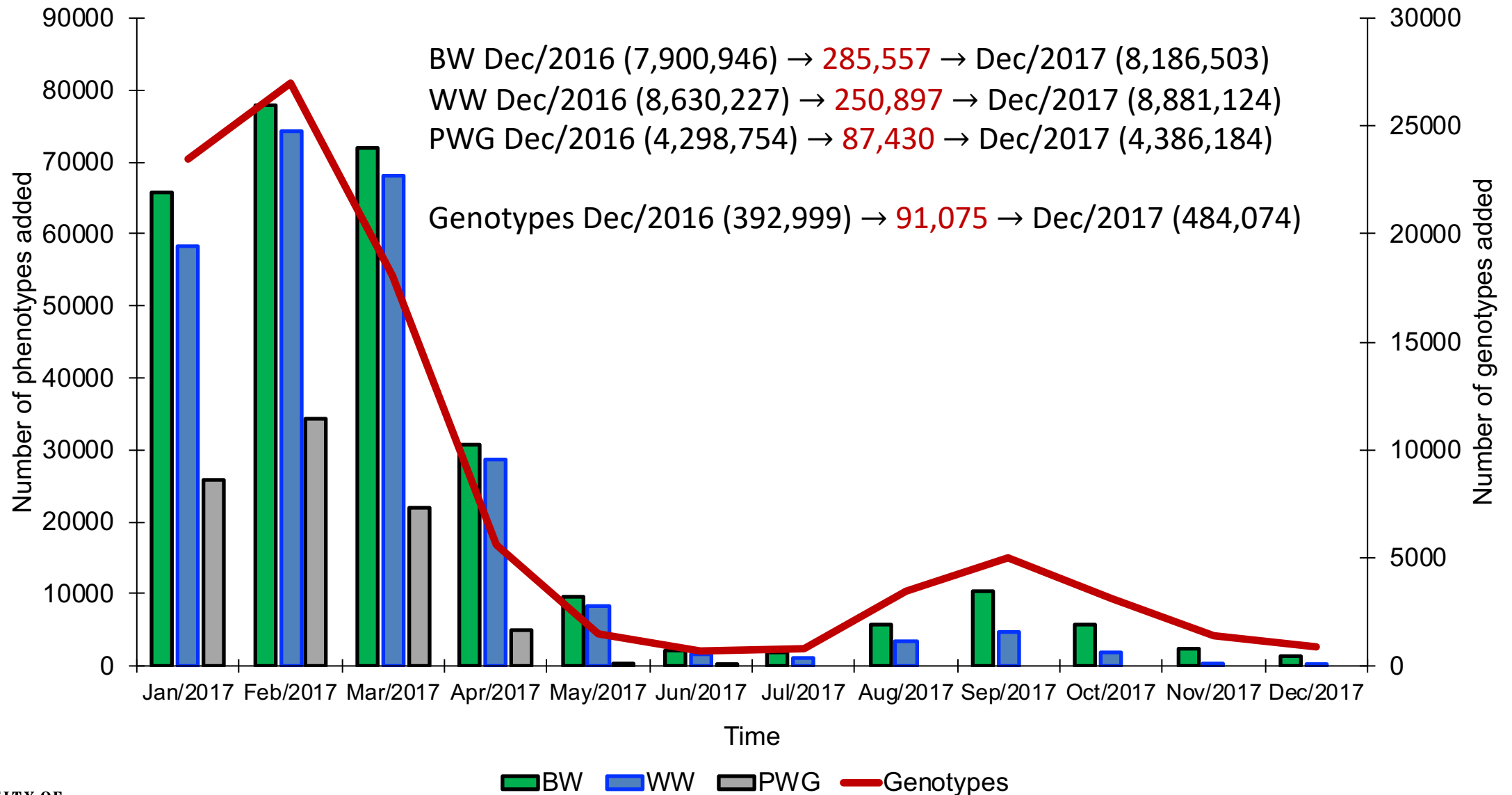
Objective

- **Evaluate changes in EBV and GEBV when new data is added on a monthly basis from December/2016 to December/2017**

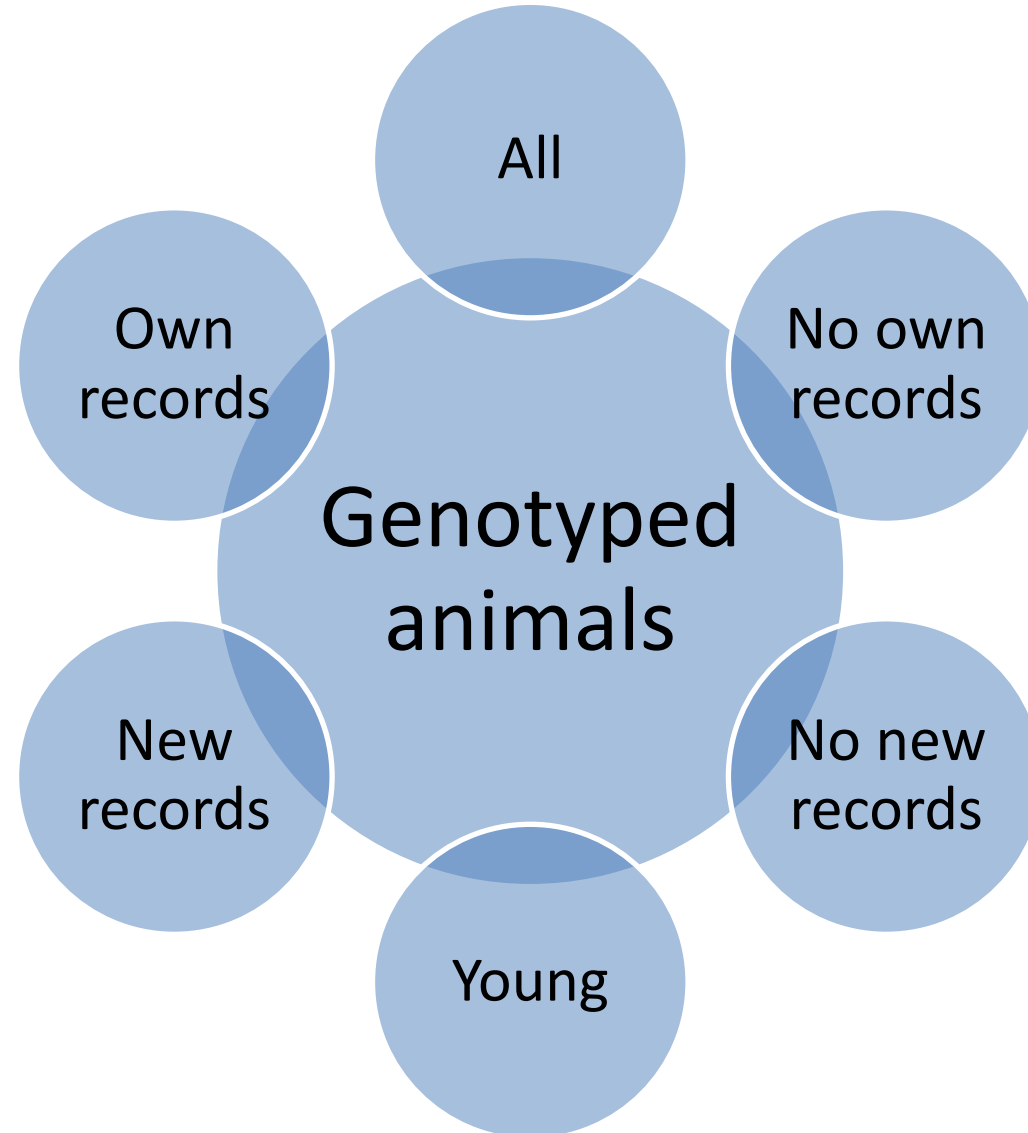
Materials and Methods

- 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

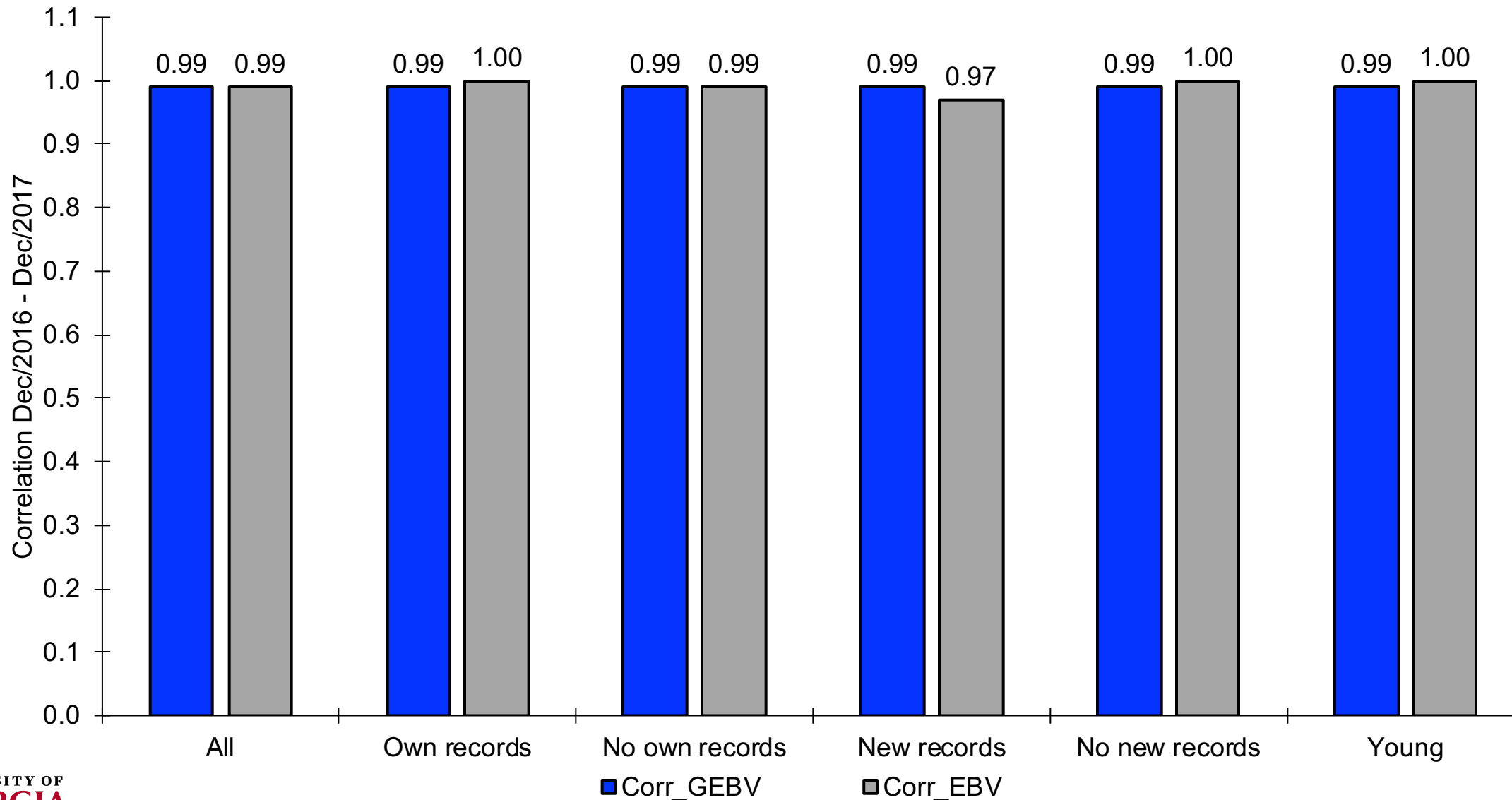
New data by month



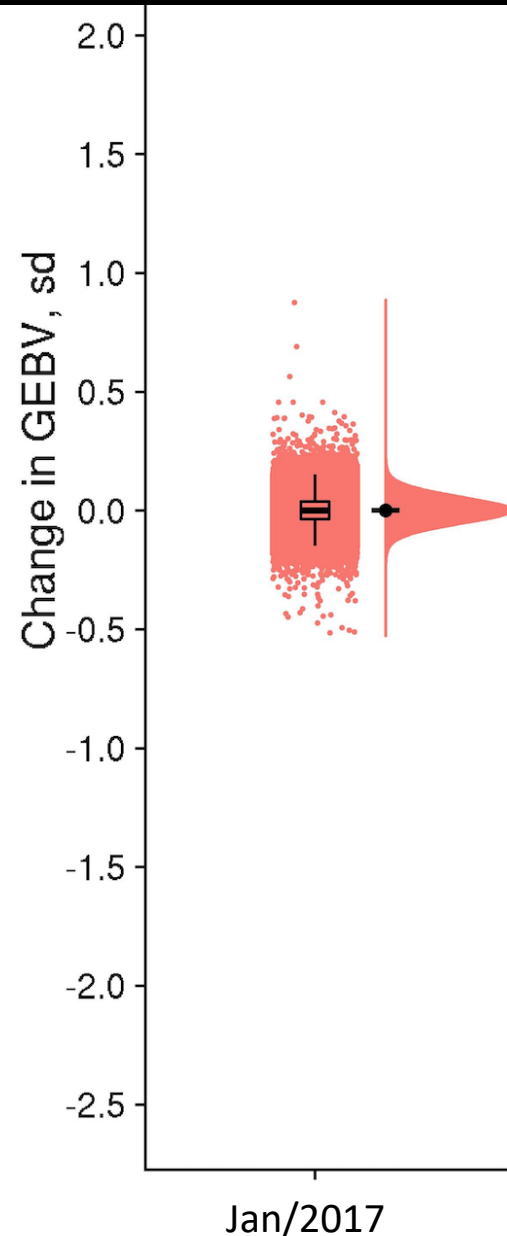
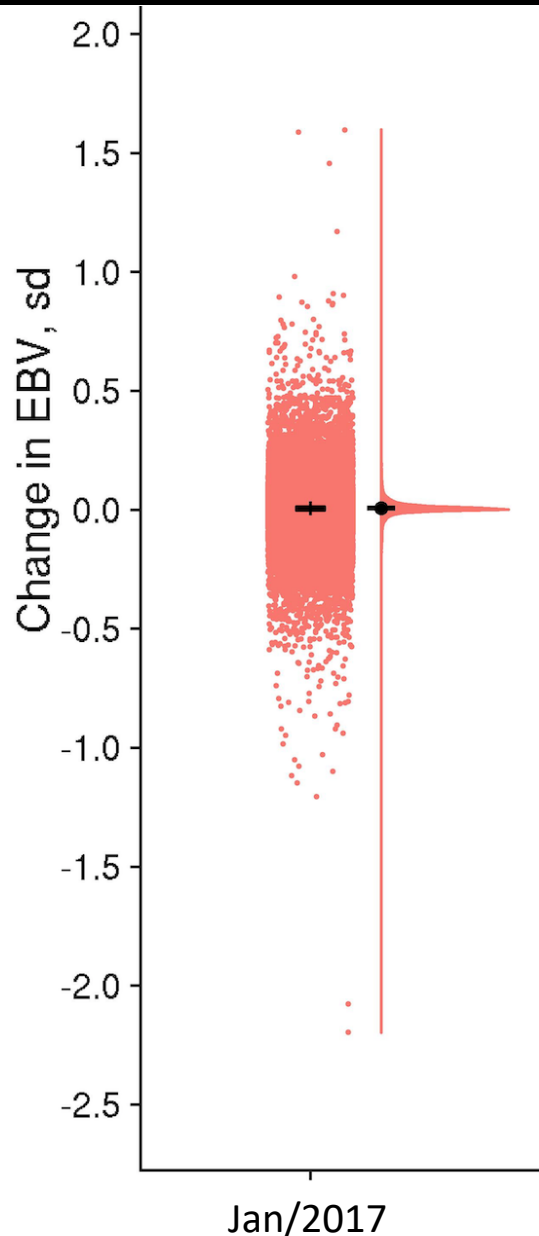
Comparison groups



Correlations among predictions one year later



Distribution of differences of predictions



Minor changes, close to zero for 50% of animals

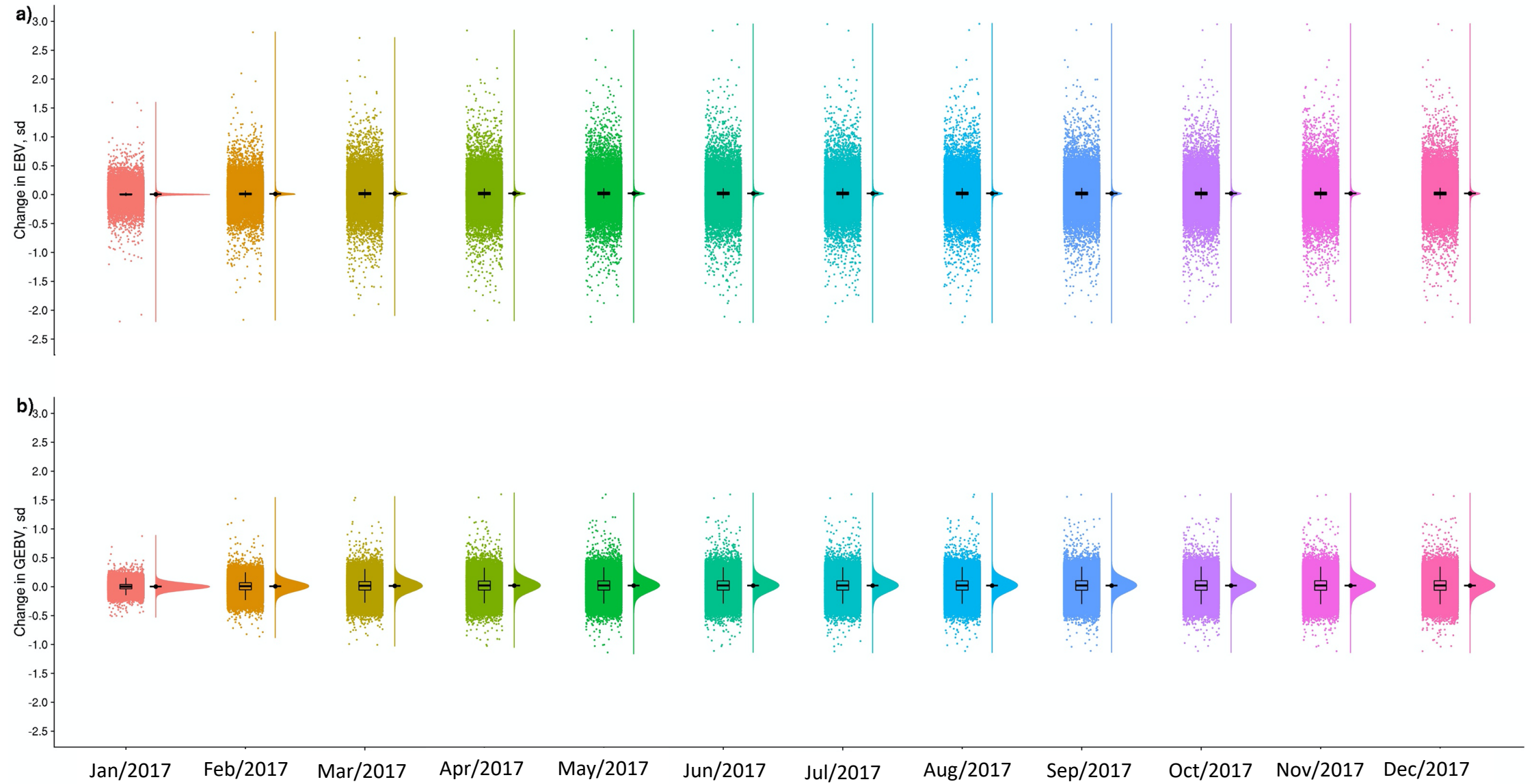
Outliers shown larger changes

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



Average(maximum) changes in predictions over a year

Contrast	Genotyped animals					
	All	Records	No records	New records	No new records	Young
Dec/2016-Jan/2017_EBV	0.02(2.20)	0.02(2.20)	0.01(0.70)	0.04(2.20)	0.02(1.15)	0.02(0.70)
Dec/2016-Jan/2017_GEBV	0.05(0.88)	0.05(0.88)	0.04(0.25)	0.05(0.88)	0.05(0.45)	0.05(0.25)
Dec/2016-Dec/2017_EBV	0.06(2.95)	0.06(2.95)	0.04(1.44)	0.12(2.95)	0.05(1.39)	0.05(0.69)
Dec/2016-Dec/2017_GEBV	0.10(1.59)	0.10(1.59)	0.10(0.53)	0.11(1.59)	0.10(0.75)	0.10(0.53)

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Conclusions

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



Thank you!!!

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