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inter**g**enomics

INTERBULL

Comparison of genetically and genomically estimated variance

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Aim

Describing the pattern of estimated genetic variance for several populations and traits, using different types of relationship matrices.

Material, phenotypes

- Brown Swiss Cattle

- 6 populations

- 34 traits

- National-, international-predicted genetic merits (PGM)

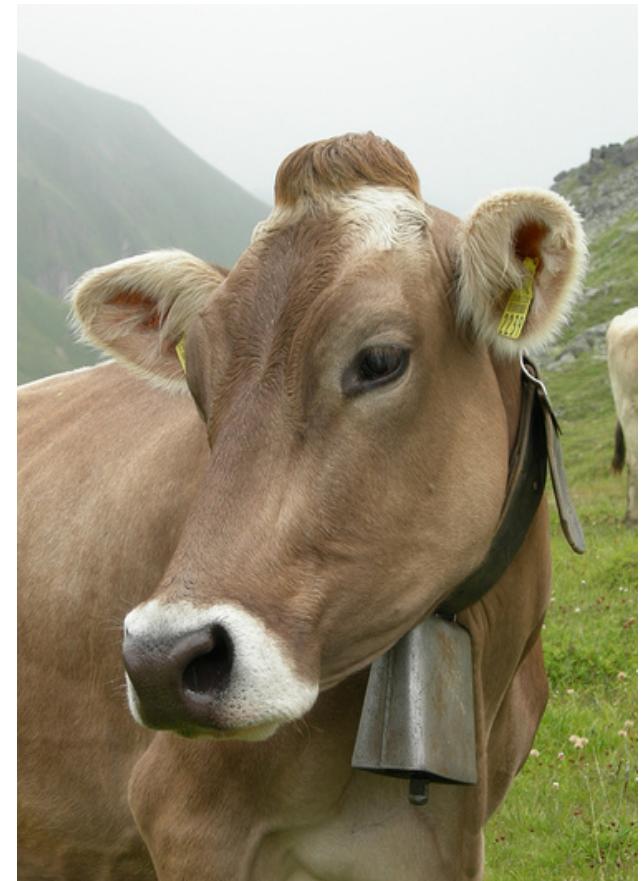- 175 population – trait combinations

Photo: www.brownswiss.org

Material, genotypes

- 8794 genotyped bulls

- Illumina Bovine BeadChip
  (LD, 50k ver.1, 50k ver.2 and HD)

- Imputation 55,172 SNPs
  FindHap (VanRaden, 2011)

- After edits 45,743 SNPs

Methods

Variance of observations

Method	Phenotype	Rel. matrix	Observation
V_{NPGM}	Dau. rec.	nA	nPGM
V_{IPGM}	nPGM	iA	iPGM
V_{DGV}	iPGM	G (vanRaden,2011)	DGV

REML estimation

Method	Phenotype	Rel. matrix
V_{MACE}	nPGM	iA
V_{GCTA}	iPGM	G (Yang, 2011)

Results, mean few traits

Trait	V_{NPGM}	V_{IPGM}	V_{DGV}	V_{MACE}	V_{GCTA}
Protein	186	190	208	284	150
Somatic cell score	53	56	60	73	36
Female fertility	34	35	51	75	20
Stature	37	38	46	55	31

Absolute values
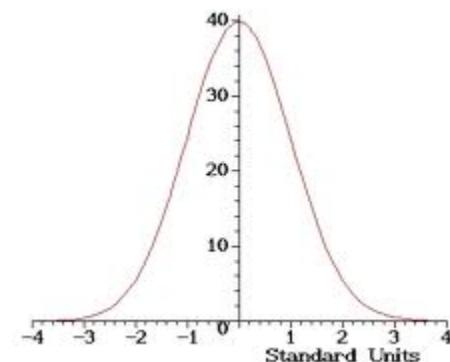
Results, mean few traits

Trait	V_{NPGM}	V_{IPGM}	V_{DGV}	V_{MACE}	V_{GCTA}
Protein	100	101	118	146	77
Somatic cell score	100	107	114	148	68
Female fertility	100	105	181	195	43
Stature	100	104	115	131	72

Standardized values
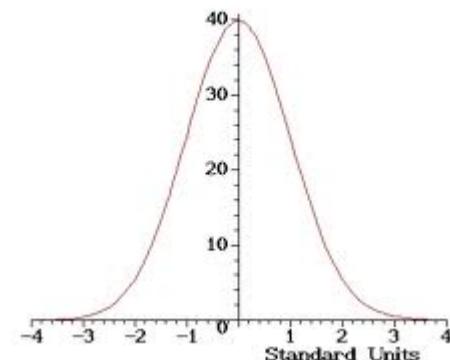
Results, per population

Pop.	Protein				Stature			
	V_{IPGM}	V_{DGV}	V_{MACE}	V_{GCTA}	V_{IPGM}	V_{DGV}	V_{MACE}	V_{GCTA}
CHE	100	106	123	70	101	105	121	67
DEA	100	119	136	80	104	149	147	82
FRA	102	81	127	62	112	106	115	63
ITA	106	157	200	111	104	110	154	86
SVN	94	122	101	49	98	114	101	53
USA	103	122	187	91	104	104	150	83

Standardized values

Results, correlation

	V_{IPGM}	V_{DGV}	V_{MACE}	V_{GCTA}	h2
V_{NPGM}	0.966	0.980	0.986	0.988	0.138
V_{IPGM}		0.936	0.931	0.943	0.148
V_{DGV}			0.993	0.998	0.135
V_{MACE}				0.998	0.127
V_{GCTA}					0.131

	h2
V_{MACE} - V_{GCTA}	-0.698

Conclusion

Photo: Genetic-Austria.at

- Differences between traits

- Differences between populations within trait

- Differences between populations between traits

- Low correlation between heritability and the methods

- High correlation between heritability and the change in estimated variance with genetic and genomic methods

Thank you for your attention