

Validation Working Group report

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Need for new genomic validation

- **Problem:**
 - Validation bulls are a pre-selected subset of bulls born
 - Analysis of new data must account for previous selection
 - But the new data should be independent of previous data
- **Solution:**
 - Compute final GEBVs including new and truncated data
 - Then deregress to isolate the new vs. truncated data

Progress

- **Genomic validation software revised by Pete Sullivan**
 - February: Predict (deregressed) **GEBV** instead of **EBV** or **DYD**
 - Feb Workshop reports from (**DEU, NLD, USA, CAN**)
 - March, August: Allow **B1 > 1.2**, pass/fail/**hiSE**, easier use
- **Studied other options for genomic deregression and weighting**
- **Reviewed trend validation tests I, II, and III**
- **Simulation results of Judith Himmelbauer (Zuchtdata, Austria)**

Small data validation (from Feb): **USA Guernsey**

Trait	Bulls	B1	S.E.(B1)	R ² GEBV	R ² PA	Pass / Fail
Milk	19	0.92	0.22	51	36	Pass
Fat	19	0.51	0.18	32	34	Fail
Protein	19	0.77	0.25	36	26	Pass
SCS	18	1.48	0.43	42	19	Fail
Longevity	7	0.52	0.52	37	5	Pass
DPR (int)	19	0.62	0.62	18	30	Fail

USA summary from February Workshop

- Larger breeds and more heritable traits had more stable results
- Smaller breeds and less heritable traits are hard to validate. Tests often fail:
 - B_1 more or less than expected from S.E., which may be underestimated.
 - Upper biological limit of 1.2 should allow for S.E. of B_1
 - R^2 of parent average may exceed GEBV with small sample sizes

Retest with new deregression – HOL milk

- Deregression was too small
- Compared $EDC_{dif} / (EDC_{total} + k)$ to previous $EDC_{dif} / (EDC_{dif} + k)$
- Example: applied to USA HOL milk, same table as VanRaden (2021)
- B1 is further from 1.0 with larger S.E. and thus more tests failed, but t-test values are similar
- Model R^2 more similar to DYD R^2
- DYD ignores genomic selection

Dep.	Var.	t-test		R^2	
		B1	B0	Resid	Model
DYD	1.027	1.9	-14.4	0.10	59
DRPo	0.990	-0.9	-16.5	0.02	69
DRPn	0.985	-1.1	-16.7	0.03	60
GEBV	0.992	-0.8	-16.3	0.02	72

Possible weight revision

- Deregression formula was revised and new weighting option was considered
- $y = Xb + Zu + e$
- Solve to obtain b^{\wedge} and u^{\wedge} , the observed residuals e^{\wedge} can be computed as:
- $e^{\wedge} = y - Xb^{\wedge} - Zu^{\wedge}$
- y could be weighted by $\text{Var}(e^{\wedge})$ including PEV, but MME use only $\text{Var}(e)$.
- Choice probably makes little difference since young bull REL very similar.
- Simulation could verify if $\text{Var}(e)$ is more precise than $\text{Var}(e^{\wedge})$.

LR regression

- Predict later published **GEBV** from earlier published **GEBV**
 - Simple to use without deregression, weights, or precomputed REL
 - Similar to Verify program used for all **EBVs** since 2002
 - Klei et al. (2002 Interbull Bulletin) used REL to compute expected change
 - GVerify is applied to **GEBVs** to check consistency from 4 months earlier
- Can apply Verify to 4-year instead of 4-month truncated **EBVs** (TMACE)
- Use a series of truncation times to get smaller S.E. in small populations

Current validation tests

- Tests **I**, **II**, and **III** check for bias in proven bull genetic **trend**
- Test **IV** checks for stability of **EBV variance** (MS)
 - Pre-selected bulls have reduced variance of MS
 - Tests often pass because software checks mean squared error (bias squared plus variance) instead of variance
- **Genomic** validation checks if young bull **GEBV** match later **DYD**
- Perform both the **EBV** and **GEBV** validations in the revised `gebvtest.py` program? (Being explored by Pete)

Status of trend tests I, II, and III

- **Test I:** Difference of first vs. all lactation genetic trends
 - Still useful for repeated records models with single EBV
- **Test II:** Difference in DYD across time
 - Few people get DYD for difficult traits or single-step models
- **Test III:** Trend in 2nd crop daughters by year of birth
 - Less useful because few proven bulls are returned for years of service
 - Instead, check trends for young bulls as they add daughters?
 - Make math more precise using regression instead of year counts?

Status of genomic validation

- Revised **gebvtest.py** is ready:
 - Uses later GEBV or **deregressed GEBV** instead of later **DYD** or **deregressed EBV** as dependent variable (better for ssGBLUP)
- Future options for genomic validation:
 - Add **regression on age** to test if genetic trend in young bulls changes when they later add daughter records
 - Add other regressions such as for **PA** or inbreeding
 - Estimate S.E. for R^2 by bootstrapping ([Legarra et al, 2014](#))

Simulation results

- Himmelbauer et al. (J. Dairy Sci., accepted 2023)
- Genomic pre-selection biases tests of **DYD** or deregressed **EBV**
- Tests of **GEBV** and **dGEBV** do account for selection
- Most tests identify direction but not size of true bias
- Use cows instead of bulls to validate small populations?
 - Similar to using foreign bulls to validate domestic **GEBV**
 - **YD** of cows still predict well due to less selection

Summary and questions

- The working group did a lot of work.
- Do new tests produce too many FAILing grades (use 0.8 to 1.2)?
- Should all GEBV tests now use the revised instead of previous software?
- Any other revisions needed this year?
- Mäntysaari et al. (2010) “**Interbull validation test for genomic evaluations**” is the most cited Interbull Bulletin paper of all time (184 citations). Happy retirement to Esa!

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Summary of GENO forms from 20 countries

Category	Most	Next	Next	Next	Least
Year sent:	14: 2015-19	3: 2010-14	3: 2020-23		
	(USA-yield-2017)	AUS, IRL, NZL	ESP, NOR, SLO		
Model:	11: GBLUP/SNPBLUP	5: Bayesian	3: Single-Step	1: Haplotype	
		USA, NLD, CHE, SLO, HUN	BEL, CZE, NOR	FRA	
SNP list:	14: 50K only	4: 60K	2: 60K NLD		
		USA, GBR, ITA, NOR	NLD, HUN		
Reference:	11: Bulls only	9: Cows/bulls			
Polygenic %:	6: No answer	4: Yes, ??%	4: 20%	4: 10%	2: 0%
	BEL, CZE, ESP, IRL, ITA, NZL	FRA, JPN, NLD, HUN	AUS, CAN, DEU, POL	USA, GBR, NOR, SLO	DFS, CHE