

Genetic and environmental variance among F2 families in a commercial breeding program for perennial ryegrass (*Lolium perenne* L.)



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FORASESELECT is a research consortium of DLF-Trifolium and Aarhus University, with the goal of implementing Genome Wide Selection (GWS) in perennial ryegrass

Aim of this study: Estimate the genetic parameters of agronomic characters in F2 populations in the current breeding program

Materials: 1453 F2 families:

- Originates from 76 parent populations and selected from 5 cycles of selection
- Farmed in 7 locations across Europe

Traits:

- Yields (first cut and remaining cuts)
- Rust resistance, winter survival, stem production, spring growth, density

Results:

Assuming $\text{Var}_A = 2 * \text{Var}_{ID}$:

h^2 within parent pops: $(2 * \text{Var}_{ID} / \text{Var}_{TOT})$

h^2 across parent pops: $(2 * V_{ID} + 2 * V_{PAR}) / \text{Var}_{TOT}$

Character	h^2 within	h^2 across	r_a with 1 st yr. tot
Dry matter (kg/m ²)			
1 st year – 1 st cut	0,22	0,31	
1 st year – remaining cuts	0,29	0,38	
1 st year – total	0,36	0,39	
2 nd year – 1 st cut	0,06	0,14	
2 nd year – remaining cuts	0,04	0,05	
2 nd year – total	0,05	0,07	
Spring growth	0,35	0,43	
Rust resistance	0,24	0,31	0.18
Stems production	0,00	0,00	
Density	0,07	0,15	0.44
Winter survival	0,08	0,12	



Statistical models:

$$Y = Xk + Xex + Zid + Zp + Z(id+lm) + Zc + e$$

and in case of more scoring per plot:

$$Y = Xk + Xex + Xs + Zid + Zp + Z(id+pl) + Zc + e$$

FIXED FACTORS:

k = check; ex = experiment (year + location + management);

s = scoring time;

RANDOM FACTORS:

id = F2 family; p = parents (P1 + P2); lm = location + management;

pl = plot within location/management; c = microenvironment within plot.

Analysis: REML (DMUAI)

Conclusions:

- Enough variance for further selection for yield
- High heritability in yield, spring growth, rust resistance
- Heritability is low in density and winter survival and very low in stems production
- Genetic correlation between yield and rust resistance is positive