UNIVERSITY OF HOHENHEIM

# Breeding progress of nitrogen use efficiency of cereal crops, and winter oilseed rape in long-term variety trials


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# Overview

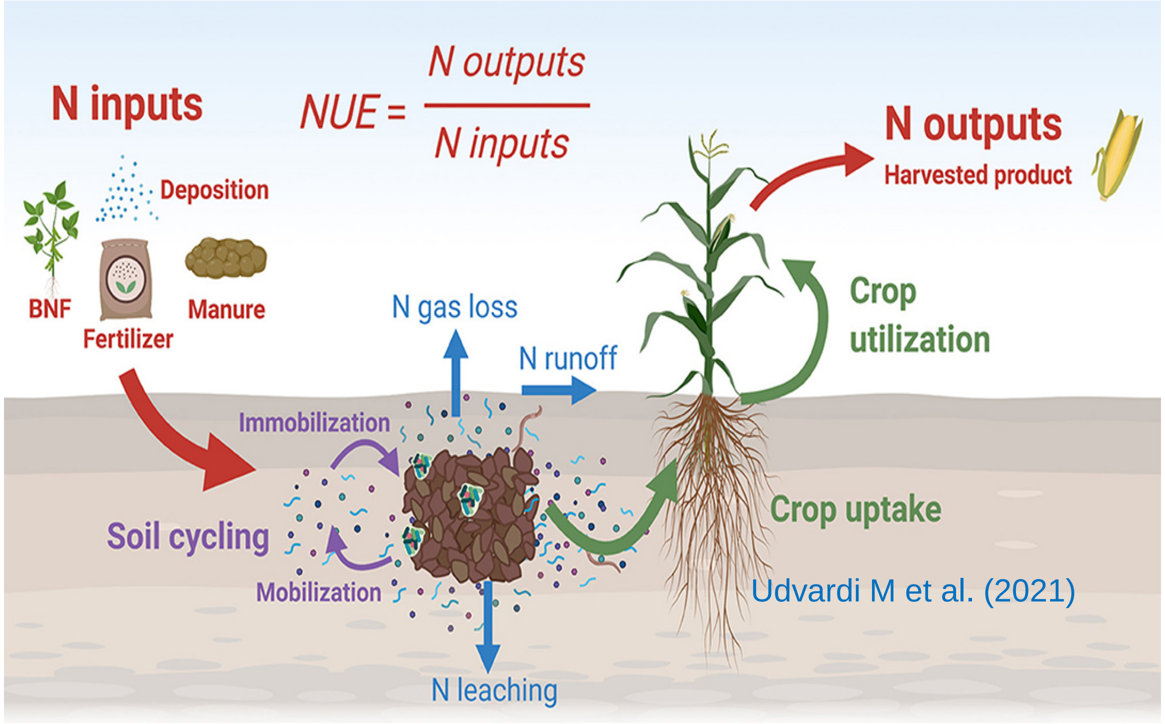
- Background
- Trials
- Key questions
- Overall trend and breeding progress
- Genotypic, environmental and G × E variation
- Genotypic, environmental and G × E correlation
- Heritability of variety means over testing period
- Conclusions

# Background (1)

- Introduction of growth control chemicals and short straw (rh) genotypes allowed for higher N fertilizaten rates
- Adverse environmental impact increased with more intensive cropping systems
- About 208 kg total N per ha used in agricultural land in Germany,, output of N with the harvested crops accounts for 67% (139 kg N per ha), resulting in a considerable budget surplus of 33% (69 kg N per ha) (BMEL 2022)
- EU policy measures (Farm-to-Fork Strategy 2020): reduction of N surplus by 50% and N fertilizer use by 20% until 2030
- Increasing world population (about 10 Billion until 2050) → increasing global demand for food and non-food agricultural products
- Improved varieties with higher yield and quality with less nitrogen use are needed, i. e. higher nitrogen use efficiency (NUE)

# Background (2)

Nitrogen use efficiency (NUE), a complex and dynamic process during yield building
Interaction between soil, environment, plant and crop management




N inputs

available N =
N fertilization rate + Nmin)

Outputs

Grain yield,
N yield (N accumulated in grain)

Nitrogen use efficiency

NUE=(N) Yield/ available N

# Key questions

- Was breeding progress achieved for NUE and related traits in registration trials?
- How large is the evironmental impact on variation of NUE compared to the genotypic ?
- How closely linked is grain yield (GYLD) and grain protein concentration (GPC) with grain nitrogen yield (NYLD)?
- Is there a potential to improve NUE in registration trials?

# Trials (1)

- Trials were treated according to crops good local agronomic practice (N, P, K, fungicides growth regulators, pesticides)
- All varieties of a trial received identical treatment, one N-level per trial
- Trial data assessed 1983 – 2021
  - Total N application rates (N fertilization rate kg ha$^{-1}$)
  - Soil mineralized N (Nmin kg ha$^{-1}$)
  - Soil fertility points (0 sand, 120 best soil)
  - Pre-crops (cereals, mais, foliage, legumes)
- Testing period 3 years (testing cycle)
- One to three trial series per year ( S1, S2, S3 varieties in first, second and third testing year), Spring wheat (all varieties in one series)





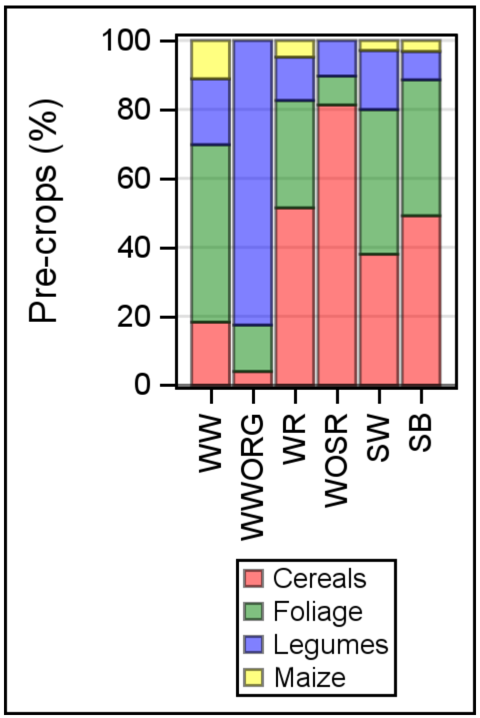
# Trials (2)

| Crop | Code | First year | Obser-vations | No. of trials | No. of varieties |
|---|---|---|---|---|---|
| Winter wheat | WW | 1983 | 25290 | 897 | 852 |
| Winter wheat organic[§] | WWORG[§] | 2013 | 842 | 69 | 31 |
| Winter rye hybrid varieties | WR Hyb | 1989 | 7712 | 569 | 244 |
| Spring wheat | SW | 1983 | 9546 | 640 | 155 |
| Spring barley | SB | 1983 | 18619 | 836 | 738 |
| Winter oil seed rape | WOSR | 1995 | 25655 | 696 | 797 |

[§] Winter wheat under organic testing regimen

# Trials (3)

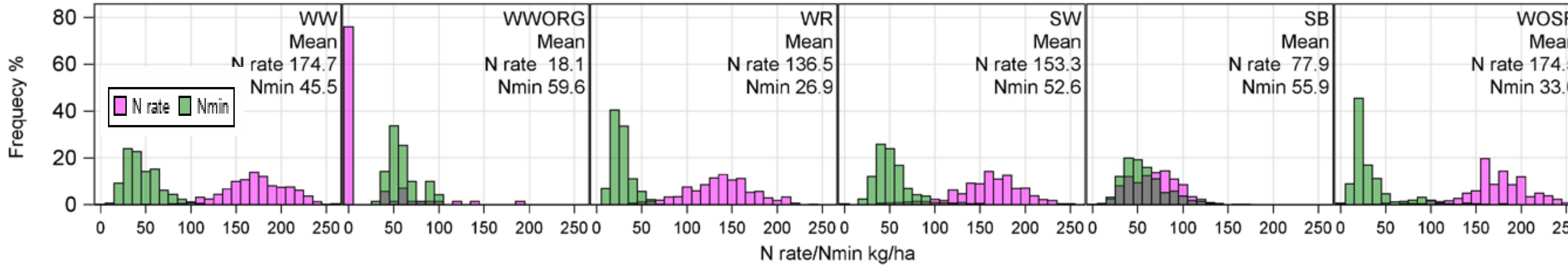
Pre-crops

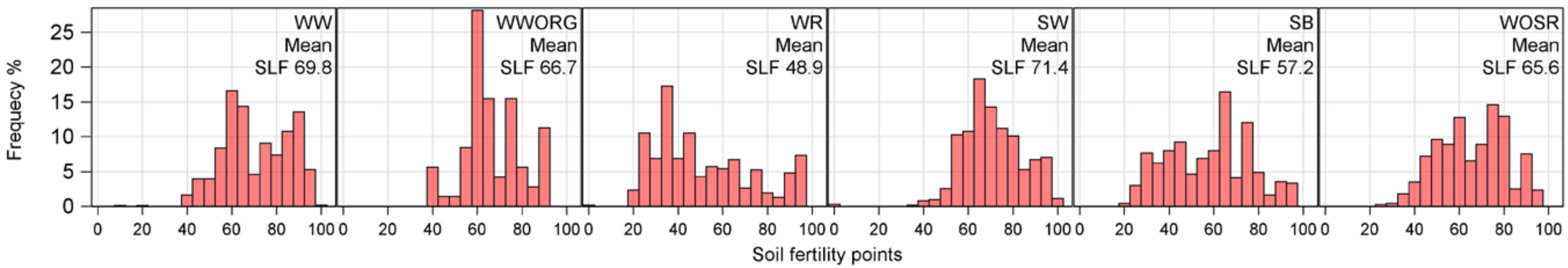



*WW* Winter wheat; *WWORG* Winter wheat organic; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat;
*SB* Spring barley; *WSOR* Winter oil seed rape; *SLF* Soil fertility points

# Trials (4)

N fertilization rates, Nmin and soil fertilty




*WW* Winter wheat;; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat; *SB* Spring barley; *WOSR* Winter oil seed rape; *ORG* organic
*SLF* Soil fertility points

## Trials (5)

Prediction of Nmin by BLUP from data 2019 – 2021
using a backward model selection procedure

$$y_{jkl} = \mu + (CP)_{im} + \delta_m a_{jkl} + \eta_i c_{jkl} + L_j + Y_k + (LYT)_{jkl} \qquad (1)$$

| | | |
|---|---|---|
| $y_{jkl}$ | observed Nmin per location *j*, year *k* and trial *l* | |
| $(CP)_{im}$ | trial categorical effect for crop *i* and pre-crop *m* | |
| $a_{jkl}$ | covariable | soil fertility points |
| $c_{jkl}$ | covariable | N rate |
| $L_j$ | random effect | location |
| $Y_k$ | random effect | year |
| $(LYT)_{jkl}$ | random effect | residual error |

Coefficient of determination $R^2$=41.5%

# Overall trend and breeding progress (1)

## Basic model

$$y_{ijkl} = \mu + G_i + Y_k + L_j + LYT_{jkl} + (GL)_{ij} + (GY)_{ik} + \epsilon_{ijkl} \qquad (2)$$

| | |
|---|---|
| $y_{ijkl}$ | variety × location × year × trial |
| $G_i$ | genotype |
| $L_j$ | location |
| $Y_k$ | year |
| $LYT_{jkl}$ | trial within location and year |
| $(GL)_{ij}$ | G × L interaction |
| $(GY)_{ik}$ | G × Y interaction |
| $\epsilon_{ijkl}$ | residual error |

## NUE and related traits

- Grain yield (GYLD) dt $ha^{-1}$
- Grain protein concentration (GPC) %
- N yield (NYLD) kg N $ha^{-1}$ (derived from GYLD and N concentration converted from GPC)
- NUE of
  - N yield ($NYLD_{NUE}$) kg N in grain per kg available N (N fertilization rate +Nmin)
  - grain yield ($GYLD_{NUE}$) kg grain per kg available N

# Overall trend and breeding progress (2)

## Overall model

Let genotypes be confounded with years, then effects $G_i$ and $(GL)_{ij}$ not nested within years are dropped in the basic model

$$y_{ijkl} = \mu + Y_k + L_j + (LYT)_{jkl} + (GY)_{ik} + \epsilon_{ijkl}$$

Overall model

$$y_{ijkl} = \mu + \alpha_1 t_k + \alpha_2 t_k^2 + Y'_k + L_j + (LYT)_{jkl} + (GY)_{ik} + \epsilon_{ijkl} \qquad (3)$$

$$E(y_{ijkl}) = \mu + \alpha_1 t_k + \alpha_2 t_k^2.$$

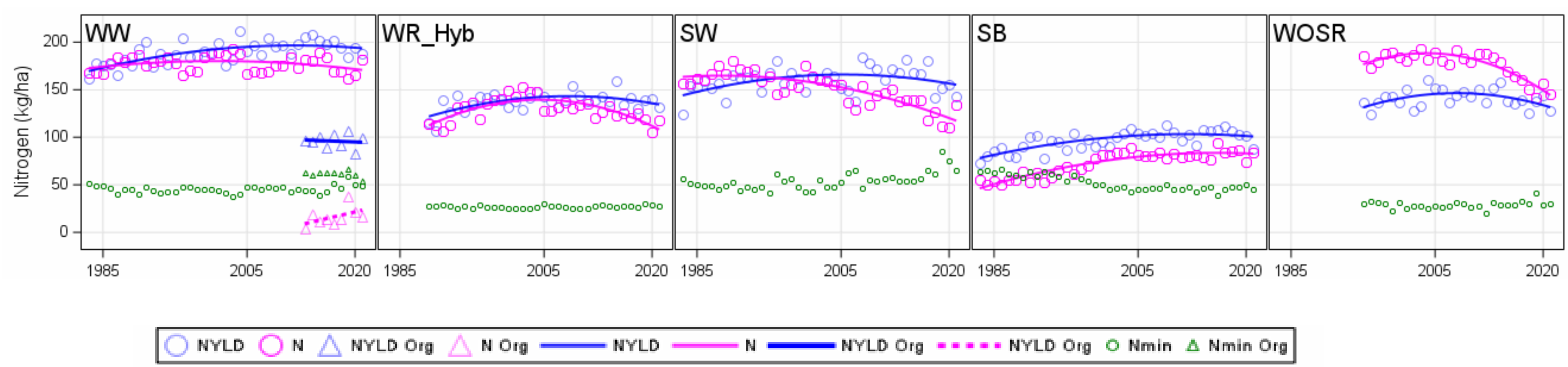
Overall trend function

$$Diff = E(y_{ijkl} | t_k = 2021) - E(y_{ijkl} | t_k = 1995) = \alpha_1 (2021 - 1995) + \alpha_2 (2021^2 - 1995^2)$$

Overall breeding progress

| | |
|---|---|
| $y_{ijkl}$ | variety × location × year × trial observation |
| $L_j$ | location |
| $Y_k$ | year |
| $t_k$ | harvest year |
| $Y'_k$ | deviation from overall trend, $t_k$ harvest year |
| $LYT_{jkl}$ | trial within location and year |
| $(GY)_{ik}$ | G × Y interaction |
| $\epsilon_{ijkl}$ | residual error |

# Overall breeding progress (1995 – 2021) (1)




*WW* Winter wheat;; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat; *SB* Spring barley; *WOSR* Winter oil seed rape; *SLF* Soil fertility points
*NYLD* nitrogen yield; *Nmin* soil mineralized nitrogen; *Org* organic wheat;

# Overall breeding progress (1995-2021) (4)

| | N yield kg $ha^{-1}$ | | | | | N kg $ha^{-1}$ | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Crop** | **1995** | **2021** | **Diff** | **%** | **sig** | **1995** | **2021** | **Diff** | **%** | **sig** |
| Winter wheat | 187.4 | 194.0 | 6.6 | 3.5 | ns | 180.3 | 170.0 | -10.3 | -5.7 | ns |
| Winter rye Hyb | 134.1 | 135.1 | 1.1 | 0.8 | ns | 130.4 | 107.8 | -22.6 | -17.4 | *** |
| Spring wheat | 160.9 | 155.0 | -5.9 | -3.6 | ns | 164.6 | 111.2 | -53.4 | -32.4 | *** |
| Spring barley | 94.3 | 102.3 | 8.0 | 8.5 | * | 67.2 | 78.5 | 11.3 | 16.8 | ** |
| Winter oil seed rape | 131.4 | 131.6 | 0.1 | 0.1 | ns | 176.9 | 143.5 | -33.4 | -18.9 | *** |
| | **Grain protein conc. %** | | | | | **Grain yield dt $ha^{-1}$** | | | | |
| | **1995** | **2021** | **Diff** | **%** | **sig** | **1995** | **2021** | **Diff** | **%** | **sig** |
| Winter wheat | 13.1 | 12.5 | -0.6 | -4.4 | ** | 95.4 | 103.3 | 7.9 | 8.3 | ** |
| Winter rye Hyb | 10.5 | 9.3 | -1.2 | -11.2 | *** | 84.9 | 96.6 | 11.6 | 13.7 | ** |
| Spring wheat | 14.0 | 13.9 | 0.0 | -0.2 | ns | 76.8 | 74.4 | -2.3 | -3.0 | ns |
| Spring barley | 10.8 | 10.3 | -0.5 | -4.5 | ns | 64.0 | 72.4 | 8.4 | 13.2 | ** |
| Winter oil seed rape | 18.8 | 17.4 | -1.4 | -7.6 | ** | 44.8 | 48.6 | 3.8 | 8.5 | * |
| | **NUE of N yield kg $kg^{-1}$** | | | | | **NUE of Grain yield kg $kg^{-1}$** | | | | |
| | **1995** | **2021** | **Diff** | **%** | **sig** | **1995** | **2021** | **Diff** | **%** | **sig** |
| Winter wheat | 0.85 | 0.91 | 0.06 | 7.3 | * | 43.0 | 48.3 | 5.2 | 12.2 | *** |
| Winter rye Hyb | 0.89 | 1.00 | 0.11 | 11.9 | ns | 56.4 | 71.6 | 15.2 | 27.0 | *** |
| Spring wheat | 0.76 | 0.88 | 0.12 | 16.0 | * | 36.2 | 42.4 | 6.2 | 17.1 | * |
| Spring barley | 0.76 | 0.83 | 0.07 | 8.7 | ns | 51.9 | 59.0 | 7.2 | 13.9 | * |
| Winter oil seed rape | 0.66 | 0.77 | 0.12 | 17.9 | *** | 20.9 | 27.3 | 6.4 | 30.8 | *** |

Cosiderable
progress for NUE achieved in
registration trials
despite N fertilizer reduction

ns not signifcant
* signifcant a 5%-level
** signifcant a 5%-level
*** signifcant a 5%-level

# Genotypic, environmental and G ⊠ E variation (1)

Basic model

$$y_{ijkl} = \mu + G_i + Y_k + L_j + LYT_{jkl} + (GL)_{ij} + (GY)_{ik} + \epsilon_{ijkl}$$

Extended model

$$y_{ijkl} = \mu + \beta r_i + G_i' + \gamma_1 t_k + \gamma_2 t_k^2 + Y_k' + L_j + LYT_{jkl} + (GL)_{ij} + (GY)_{ik} + \epsilon_{ijkl} \quad (4)$$

genetic trend

$r_i$ first trial year of variety i

non-genetic trend

$t_k$ harvest year k

**Variance components**

Genotypic $\sigma^2_{G'}$

Environmental $\sigma^2_E = \sigma^2_L + \sigma^2_{Y'} + \sigma^2_{LTY'}$

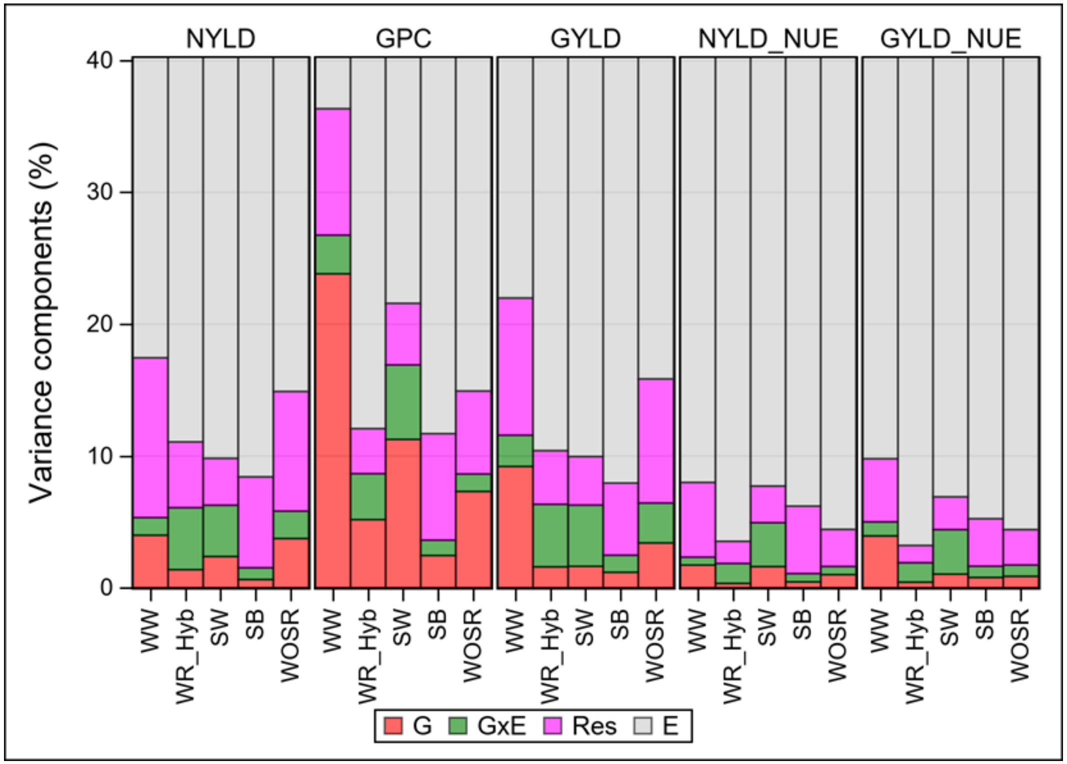
G ⊠ E $\sigma^2_{G'E} = \sigma^2_{G'L} + \sigma^2_{G'Y'}$

Residual $\sigma^2_\epsilon$

Marginal $\sigma^2_M = \sigma^2_{G'} + \sigma^2_E + \sigma^2_{G'E} + \sigma^2_\epsilon$

# Genotypic, environmental and G ⍰ E variation

Genotypic, environmental and G ⍰ E variation as per cent of total variation




Environmental variation is extremely dominating over genotypic variation

*WW* Winter wheat;; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat; *SB* Spring barley; *WOSR* Winter oil seed rape;
*NYLD* Nitrogen yield in grain; *GPC* Grain protein concentration; *GYLD* Grain yield; *NYLD_NUE* ($GYLD_{NUE}$) Nitrogen fertilizer use efficiency of nitrogen yield; *GYLD_NUE* ($GYLD_{NUE}$) Nitrogen fertilizer use efficiency of grain yield;
*G* Genotype; *Res* Residual; *G ⍰ E* Genotype ⍰ environment ; *E* Environment ;

# Genotypic, environmental, and G × E correlation (1)

Decomposition of the correlation between two traits (U, V) due to the random effects of the extended model

$$y_{ijkl} = \mu + \beta r_i + G_i' + \gamma_1\, t_k + \gamma_2 t_k^2 + Y_k' + L_j + LYT_{jkl} + (GL)_{ij} + (GY)_{ik} + \epsilon_{ijkl} \quad (4)$$

by a univariate approach (Piepho et al. 2014)

1. Computing variance components of random effects according to the extended model for trait $U$ and $V$ and for the difference $U - V$ between both traits.
2. Computing covariances between the random effects of trait $U$ and $V$ from variance components by using the equation
   $var(U - V) = var(U) + var(V) - 2cov(U,V) \Rightarrow$
   $(cov(U,V) = \frac{1}{2}(var(U) + var(V) - var(U - V))$
3. $r_{UV} = cov(U,V) / \sqrt{var(U)var(V)}$

# Genotypic, environmental, and G □ E correlation (2)

| **Correlation coefficients** | | **Calculated by** |
|---|---|---|
| Genotypic correlation | $r_G$ | variance and covariance of $G_i$ |
| Environmental correlation | $r_E$ | sum of variances and covariances of $L_J$, $Y_k$ and $(LYT)_{jkl}$ |
| G□E correlation | $r_{G□E}$ | sum of variances and covariances of $(GL)_{ij}$ and $(GY)_{ik}$ |
| Residual correlation | $r_{□}$ | variance and covariance of $\epsilon_{ijkl}$ |
| Marginal correlation | $r_M$ | sum of variances and covariances over all individual random effects of the extended model |

# Genotypic, environmental, and G ⨯ E correlation (3)

| | | WW | WR Hyb | WOSR | SW | SB | Mean |
|---|---|---|---|---|---|---|---|
| Observations | n | 19089 | 4730 | 25524 | 3867 | 13318 | |
| Genotypes | $n_G$ | 682 | 212 | 797 | 108 | 543 | |
| NYLD GYLD | $r_G$ | 0.28 | 0.08 | 0.68 | 0.40 | 0.32 | 0.35 |
| | $r_{GxE}$ | 0.76 | 0.81 | 0.36 | 0.88 | 0.75 | 0.71 |
| | $r_E$ | 0.84 | 0.76 | 0.86 | 0.90 | 0.79 | 0.83 |
| | $r_e$ | 0.79 | 0.74 | 0.54 | 0.84 | 0.70 | 0.72 |
| | $r_M$ | 0.79 | 0.75 | 0.81 | 0.89 | 0.78 | 0.80 |
| NYLD GPC | $r_G$ | 0.33 | 0.68 | 0.62 | 0.66 | 0.45 | 0.55 |
| | $r_{GxE}$ | 0.13 | 0.29 | -0.02 | -0.20 | 0.20 | 0.08 |
| | $r_E$ | 0.26 | 0.38 | 0.40 | 0.14 | 0.47 | 0.33 |
| | $r_e$ | 0.35 | 0.48 | 0.33 | 0.19 | 0.58 | 0.38 |
| | $r_M$ | 0.26 | 0.39 | 0.40 | 0.16 | 0.47 | 0.34 |
| GYLD GPC | $r_G$ | -0.81 | -0.69 | -0.21 | -0.42 | -0.70 | -0.57 |
| | $r_{GxE}$ | -0.52 | -0.28 | -0.16 | -0.61 | -0.45 | -0.40 |
| | $r_E$ | -0.31 | -0.31 | -0.11 | -0.28 | -0.15 | -0.23 |
| | $r_e$ | -0.25 | -0.12 | -0.09 | -0.34 | -0.10 | -0.18 |
| | $r_M$ | -0.38 | -0.31 | -0.11 | -0.30 | -0.16 | -0.25 |

- Nitrogen yield is stronger correlated with grain yield than with protein concentration
- Selection for higher nitrogen yield does not counteract with selection for higher grain yield and protein concentration

*WW* Winter wheat;; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat; *SB* Spring barley; *WOSR* Winter oil seed rape;
*NYLD* Nitrogen yield in grain; *GPC* Grain protein concentration; *GYLD* Grain yield; *n* Number of observations; $n_G$ Number of genotypes
*G* Genotype; ⨯ Residual; *G ⨯E* Genotype ⨯ environment ; *E* Environment ; *M* Marginal

# Genotypic, environmental, and G × E correlation (4)

| | | WW | WR Hyb | SW | SB | WOSR | Mean |
|---|---|---|---|---|---|---|---|
| Observations | $n$ | 19089 | 4730 | 3867 | 13318 | 21564 | |
| Genotypes | $n_G$ | 682 | 212 | 108 | 543 | 797 | |
| NYLD with $NYLD_{NUE}$ | $r_G$ | 1.00 | 1.01 | 1.00 | 1.00 | 1.00 | 1.00 |
| | $r_{GxE}$ | 0.98 | 1.00 | 0.98 | 0.99 | 0.93 | 0.98 |
| | $r_E$ | 0.59 | 0.42 | 0.68 | 0.83 | 0.33 | 0.57 |
| | $r_e$ | 0.98 | 0.89 | 0.98 | 0.99 | 0.92 | 0.95 |
| | $r_M$ | 0.63 | 0.44 | 0.70 | 0.84 | 0.37 | 0.60 |
| GYLD with $GYLD_{NUE}$ | $r_G$ | 1.00 | 0.99 | 1.00 | 1.00 | 1.00 | 1.00 |
| | $r_{GxE}$ | 0.97 | 0.96 | 0.99 | 0.99 | 0.96 | 0.97 |
| | $r_E$ | 0.61 | 0.41 | 0.71 | 0.80 | 0.30 | 0.57 |
| | $r_e$ | 0.98 | 0.93 | 0.98 | 0.99 | 0.92 | 0.96 |
| | $r_M$ | 0.65 | 0.44 | 0.73 | 0.81 | 0.35 | 0.60 |

Rank of genotypic values for varieties of grain and nitrogen yield is the same as rank of NUE (Laidig et al. 2024)

*WW* Winter wheat;; *WR* Winter rye, *Hyb* hybrid varieties; *SW* spring wheat; *SB* Spring barley; *WOSR* Winter oil seed rape; *NYLD* Nitrogen yield in grain; *GYLD* Grain yield; *NYLD_NUE* ($GYLD_{NUE}$) Nitrogen fertilizer use efficiency of nitrogen yield; *GYLD_NUE* ($GYLD_{NUE}$) Nitrogen fertilizer use efficiency of grain yield; *n* Number of observations; $n_G$ Number of genotypes *G* Genotype; *Res* Residual; *G × E* Genotype × environment ; *E* Environment ; *M* Marginal

# Genotypic, environmental, and G □ E correlation (4)

## Proof that $r_G$ □ 1 and $r_{G□E}$ □ 1 (Laidig et. al. 2024)

Consider two random variables *Wij* and *Uij* = *Wij*/*Nj*, where *Wij* = grain yield of *i*th genotype in *j*th environment and *Nj* = nitrogen input in *j*th environment. For *Wij*, we assume the random-effects model

$$W_{ij} = \mu + G_i + L_j + GL_{ij} \qquad (1)$$

with independent random effects having zero mean and variances $var(G_i) = \sigma_G^2$, $var\left(L_j\right) = \sigma_L^2$ and $var\left(GL_{ij}\right) = \sigma_{GL}^2$. Here, we will investigate what can be said about the covariance of effects for *Wij* and *Uij* assuming model (1) for *Wij*. For simplicity, we will assume that *Nj* is independent of all effects in the model for *Wij*. This could be relaxed by assuming a covariance with *Lj*, but this is not expected to have any substantive bearing on the subsequent derivation, as will be explained briefly at the end. The model for *Uij* can be written as

$$U_{ij} = \frac{\mu + G_i + L_j + GL_{ij}}{N_j} = \mu'_j + G'_{ij} + L'_j + GL'_{ij} \quad (2)$$

where $\mu'_j = \frac{\mu}{N_j}$, $G'_{ij} = \frac{G_i}{N_j}$, $L'_j = \frac{L_j}{N_j}$ and $GL'_{ij} = \frac{GL_{ij}}{N_j}$.

A challenge in the subsequent derivation is that all effects in (2) involve the random variable *Nj*, hence we need to check if there are correlations among the effects. It will be useful to make use of the laws of total variance and total covariance (Rudary 2009). Let *X*, *Y* and *Z* be three random variables. Then the law of total variance states that

$$var(Y) = E[var(Y|X)] + var[E(Y|X)].$$

The law of total covariance states that

$$cov(X,Y) = E[cov(X,Y|Z)] + cov[E(X|Z), E(Y|Z)] .$$

**Proof that $r_G$ ⍰ 1 and $r_{G⍰E}$ ⍰ 1** (Laidig et. al. 2023)

*continued*

If we identify $Z$ with $Nj$, and $X$ and $Y$ with any of the two effects in (2), then it emerges from the law of total covariance that the effects in (2) must all be uncorrelated from one another. For example, we find that

$$cov\left(G'_{ij}, L'_j\right) = E\left[cov\left(G'_{ij}, L'_j \middle| N_j\right)\right] + cov\left[E\left(G'_{ij} \middle| N_j\right), E\left(L'_j \middle| N_j\right)\right] = E\left[\frac{1}{N_j^2} cov\left(G_i, L_j\right)\right] + cov[0,0] = 0$$

Before we consider covariances among effects for $W_{ij}$ and $U_{ij}$, we need to transition (2) into a model of the same form as (1). To do so, we may define

$$\mu'_j = \mu'' + F''_j,$$

where $\mu'' = E\left(\mu'_j\right)$ and $F''_j = \mu'_j - \mu''$. Similarly, we define

$$G'_{ij} = G''_i + H''_{ij},$$

where $G''_i = E\left(G'_{ij} \middle| G_i\right)$ and $H''_{ij} = G'_{ij} - E\left(G'_{ij} \middle| G_i\right)$ . With these definitions, we can rewrite (2) as

$$W_{ij} = \mu'' + G''_i + L''_j + GL''_{ij}, \qquad (3)$$

where $L''_j = L'_j + F''_j$ and $GL''_{ij} = GL'_{ij} + H''_{ij}$.

## Proof that $r_G$ □ 1 and $r_{G□E}$ □ 1 (Laidig et. al. 2023)

*continued*

With this reparameterization, we can now study covariances among effects between models (1) and (3), using the law of total covariance and the delta method (Johnson et al. 2003).

(i) $cov(G_i, G_i'') = E\left[cov(G_i, G_i'')|N_j\right] + cov\left[E\left(G_i|N_j\right), E\left(G_i''|N_j\right)\right] \approx \frac{\sigma_G^2}{\varphi_N}$

(ii) $cov\left(L_j, L_j''\right) = E\left[cov\left(L_j, L_j''\right)\middle|N_j\right] + cov\left[E\left(L_j\middle|N_j\right), E\left(L_j''\middle|N_j\right)\right] \approx \frac{\sigma_L^2}{\varphi_N}$

(iii) $cov\left(GL_{ij}, GL_{ij}''\right) = E\left[cov\left(GL_{ij}, GL_{ij}''\right)\middle|N_j\right] + cov\left[E\left(GL_{ij}\middle|N_j\right), E\left(GL_{ij}''\middle|N_j\right)\right] \approx \frac{\sigma_{GL}^2}{\varphi_N}$

where $\varphi_N = E\left(N_j\right)$. Similarly, the variances of the random effects in (3) can be approximated as follows:

(i) $var(G_i'') \approx \frac{[E(G_i)]^2}{\varphi_N^4}\sigma_N^2 + \frac{\sigma_G^2}{\varphi_N^2} = \frac{\sigma_G^2}{\varphi_N^2}$

(ii) $var\left(L_j''\right) = var\left(L_j' + F_j''\right) \approx \frac{\sigma_L^2}{\varphi_N^2} + \frac{\mu^2\sigma_N^2}{\varphi_N^4}$

(iii) $var\left(GL_{ij}''\right) = var\left(GL_{ij}' + G_{ij}' - E\left(G_{ij}'\middle|G_i\right)\right) \approx \frac{\sigma_{GL}^2}{\varphi_N^2} + var\left[G_i\left(\frac{1}{N_j} - \frac{1}{\varphi_N}\right)\right] \approx \frac{\sigma_{GL}^2}{\varphi_N^2}$

where $\sigma_N^2 = var\left(N_j\right)$. From these results, the correlations can be approximated as

(i) $corr(G_i, G_i'') \approx 1$

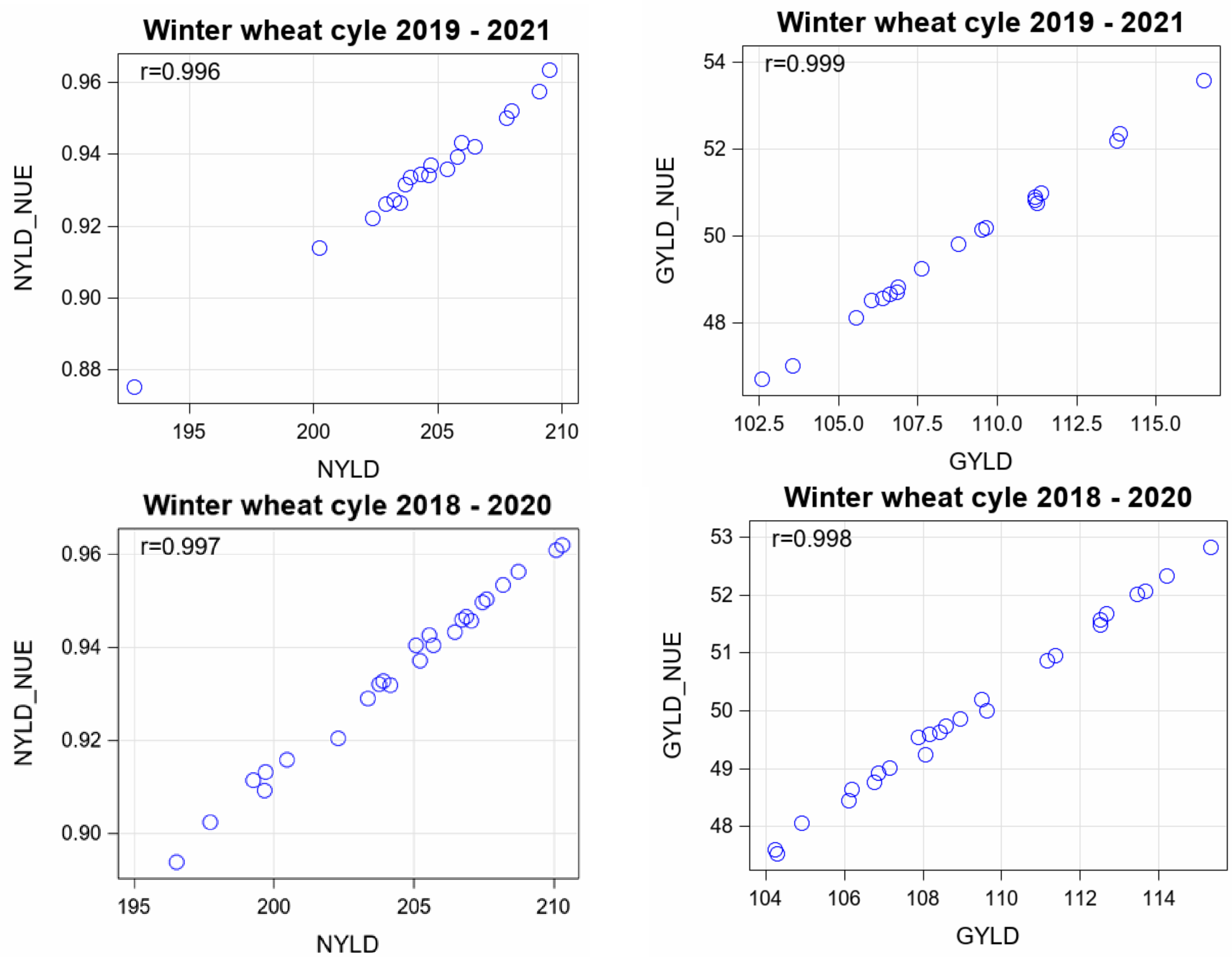
(ii) $corr\left(L_j, L_j''\right) \approx \frac{1}{\sqrt{\left(1+\frac{\mu^2\sigma_N^2}{\varphi_N^2\sigma_L^2}\right)}} < 1$

(iii) $corr\left(GL_{ij}, GL_{ij}''\right) \approx 1$

As noted before, we have assumed here that $L_j$ and $N_j$ are uncorrelated. If a covariance is allowed, this will only affect the correlation $corr\left(L_j, L_j''\right)$, but it will still be the case that $corr\left(L_j, L_j''\right) < 1$.

# Genotypic, environmental, and G ⍰ E correlation (5)

Examples: Correlation between cycle means (LS means) of varieties




*NYLD* Nitrogen yield in grain;
*GYLD* Grain yield;
*NYLD_NUE* NUE of nitrogen yield;
*GYLD_NUE* NUEof grain yield;




## Heritability (1)

Broad sense heritability of 3-year cycle means

$$h^2 = \sigma^2_{G'} / \left( \sigma^2_{G'} + \frac{v_d}{2} \right), \qquad (5)$$

where $\sigma^2_{G'}$ is the genotypic variance and
$v_d$ is the average variance of a difference between the BLUE-means of two varieties tested in the same 3-year cycle (Piepho & Möhring 2007).

# Broader sense heritability of cycle means ( 3 years)

| | Number of locations | | | | | | | NYLD | GPC | GYLD | NUE of NYLD | NUE of GYLD |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Crop | $n$ | $n_1$ | $n_2$ | $n_3$ | $n_{12}$ | $n_{13}$ | $n_{23}$ | $H^2$ | $H^2$ | $H^2$ | $H^2$ | $H^2$ |
| Winter wheat | 24 | 8 | 8 | 8 | 0 | 0 | 4 | 0.83 | 0.96 | 0.90 | 0.82 | 0.90 |
| Winter rye Hyb | 24 | 8 | 8 | 8 | 0 | 0 | 6 | 0.61 | 0.89 | 0.65 | 0.54 | 0.63 |
| Spring wheat | 21 | 7 | 7 | 7 | 5 | 6 | 5 | 0.74 | 0.90 | 0.62 | 0.69 | 0.59 |
| Spring barley | 23 | 8 | 8 | 7 | 0 | 0 | 3 | 0.57 | 0.78 | 0.72 | 0.56 | 0.72 |
| Winter oil seed rape | 36 | 9 | 13 | 14 | 0 | 1 | 7 | 0.85 | 0.94 | 0.80 | 0.84 | 0.79 |
| Mean | 25.7 | 7.9 | 8.8 | 8.9 | 1.0 | 1.4 | 5.0 | 0.72 | 0.89 | 0.74 | 0.69 | 0.73 |

N yield equally reliable as grain yield,
should be given higher attention in registration trials

Since 2023, N yield of winter wheat varieties is reported as quality trait in the Descriptive Variety List

$n$ Number of trials per cycle; $n_1$, $n_2$, $n_3$ number of locations in cycle year 1, 2 and 3; $n_{12}$, $n_{13}$, $n_{23}$ overlapping locations

*NYLD* Nitrogen yield in grain; *GYLD* Grain yield; *GPC* Grain protein concentration; *NUE* N use efficiency





# Conclusions

- N fertilizer rate was considerably reduced in the last 26 years (in all crops except spring barley)
- Grain yield increased despite lower N fertilzer rates
- N accumulated in grain was not significantly reduced, despite reduced N fertilizer rates
- Considerable breeding progress achieved for NUE
- Rank order of genotypic values of varieties for grain and N yield is identical with NUE, i.e., selection for high grain and nitrogen yield is equivalent to high NUE
- Heritability of N yield is about as high as for grain yield, therefore N yield should be considered as additional criterion in registration trials

## Literature

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