UNIVERSITÄT
HOHENHEIM

Connecting Variety Trialling Systems Across Two Countries

Waqas Malik, Hans-Peter Piepho

8-12 Sep. 2025, Poznan, Poland

Introduction

- A key step in crop improvement is the evaluation of variety candidates coming out of plant breeding programmes regarding their Value for Cultivation and Use (VCU) in multi-environment trials.
- In Europe, before acceptance to a country's national list, crop variety candidates must undergo testing for VCU in multi-environment trials.

Introduction

- A key step in crop improvement is the evaluation of variety candidates coming out of plant breeding programmes regarding their Value for Cultivation and Use (VCU) in multi-environment trials.
- In Europe, before acceptance to a country's national list, crop variety candidates must undergo testing for VCU in multi-environment trials.
- This testing for VCU is done by examination offices (EO) at the national level in many European countries.

Introduction

- A key step in crop improvement is the evaluation of variety candidates coming out of plant breeding programmes regarding their Value for Cultivation and Use (VCU) in multi-environment trials.
- In Europe, before acceptance to a country's national list, crop variety candidates must undergo testing for VCU in multi-environment trials.
- This testing for VCU is done by examination offices (EO) at the national level in many European countries.
- Ususally, VCU trials last 2 to 3 years and involve 5 to 15 locations per year.

Introduction

- Typically, candidate varieties developed by plant breeders are submitted only to the EO of a single country in Europe.

Introduction

- Typically, candidate varieties developed by plant breeders are submitted only to the EO of a single country in Europe.
- Once a variety is accepted to the national list of a country, it can be marketed in that country.

Introduction

- Typically, candidate varieties developed by plant breeders are submitted only to the EO of a single country in Europe.
- Once a variety is accepted to the national list of a country, it can be marketed in that country.
- Moreover, it may be marketed in other European countries as well, even if it has not been tested for VCU in that country.

Introduction

- Typically, candidate varieties developed by plant breeders are submitted only to the EO of a single country in Europe.
- Once a variety is accepted to the national list of a country, it can be marketed in that country.
- Moreover, it may be marketed in other European countries as well, even if it has not been tested for VCU in that country.
- Up to that point, no performance assessment has been conducted in those other countries.

Objective

- We investigate how VCU trialling systems of two countries can be connected and integrated.

Objective

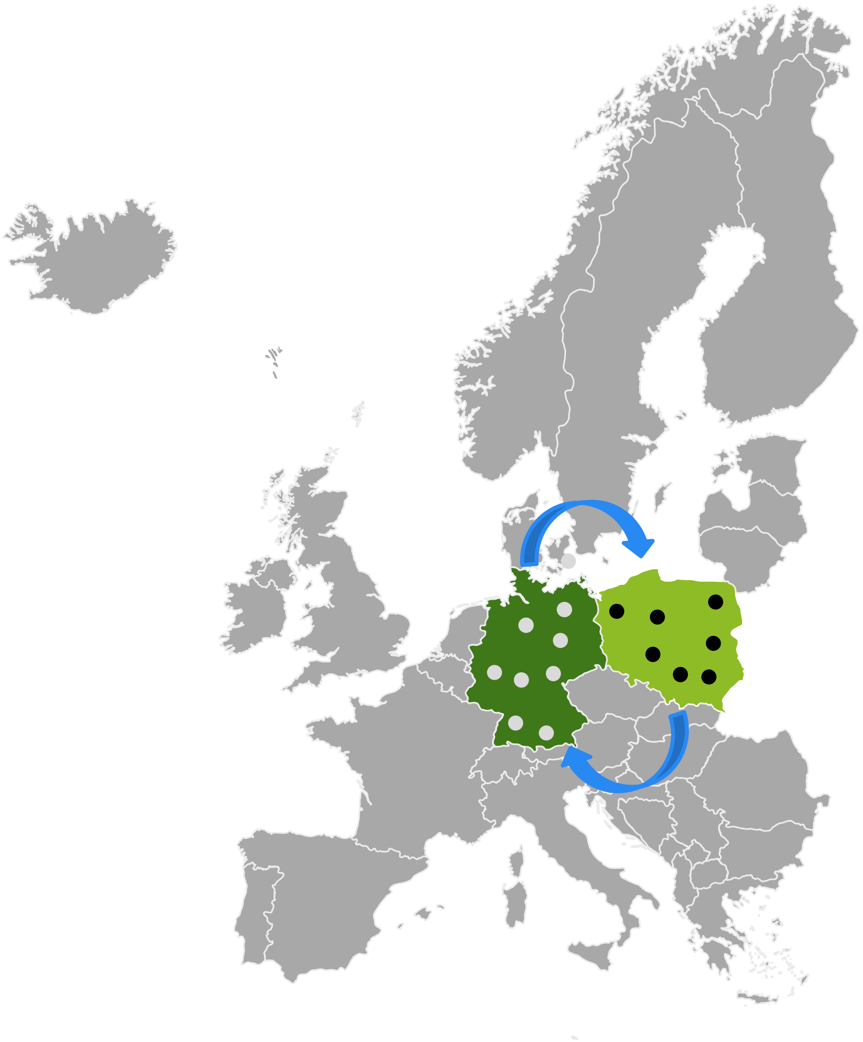
- We investigate how VCU trialling systems of two countries can be connected and integrated.
- So that performance can be assessed for both countries without altering the capacity of the trialling systems.

Objective

- We investigate how VCU trialling systems of two countries can be connected and integrated.
- So that performance can be assessed for both countries without altering the capacity of the trialling systems.
- We highlight the benefit of a joint analysis of data from two countries, and show how the efficiency of each country's VCU testing system can be improved—without altering the overall capacity of the systems.

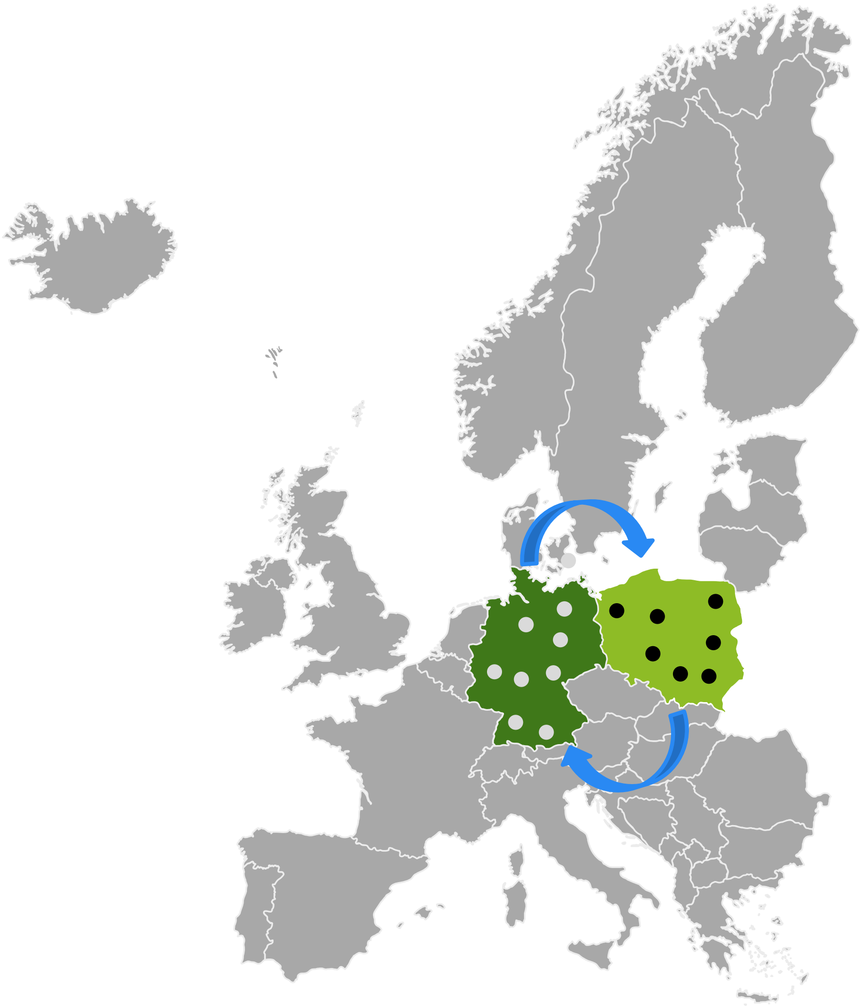
Joint analysis

- A joint analysis of data allows assessing the similarity in performance of those varieties tested in both countries.



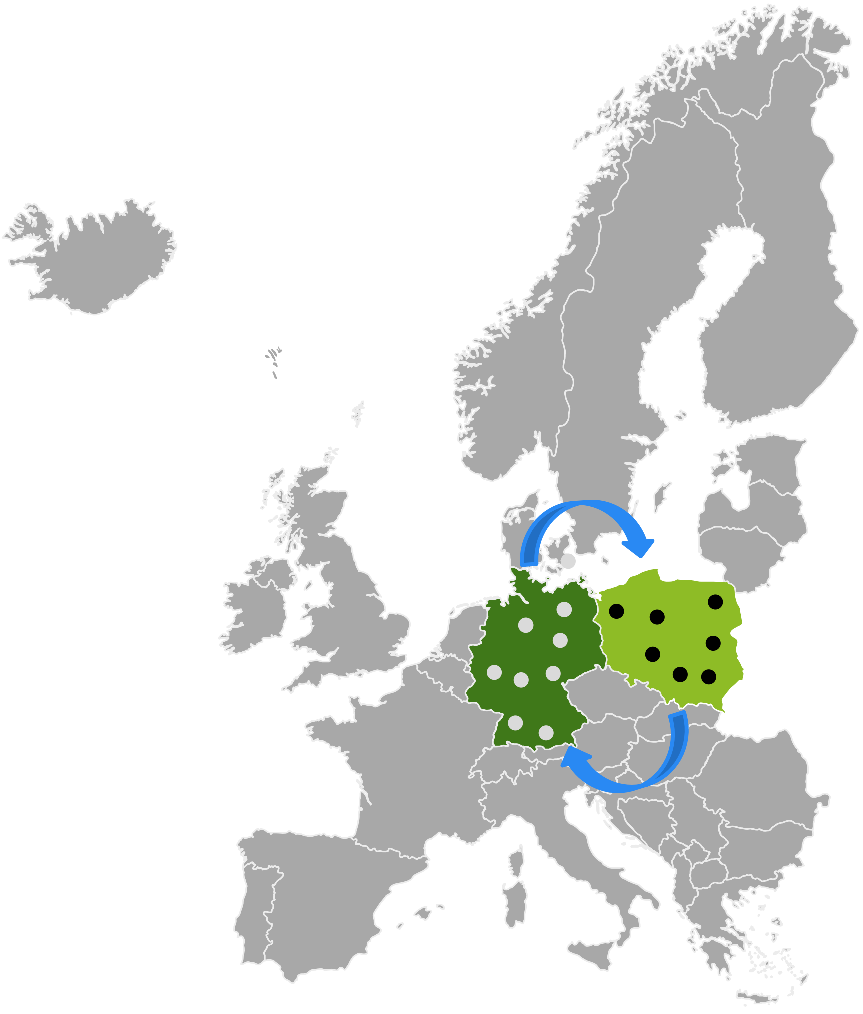
Joint analysis

- A joint analysis of data allows assessing the similarity in performance of those varieties tested in both countries.
- Varieties that are in common between countries can be regarded as checks providing some degree of connectivity between countries.



Joint analysis

- A joint analysis of data allows assessing the similarity in performance of those varieties tested in both countries.
- Varieties that are in common between countries can be regarded as checks providing some degree of connectivity between countries.
- This gives us an opportunity to borrow strength from the neighboring countries.



Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- $yield_{ijkl}$ is the mean yield of the *i*-th variety in the *j*-th location, *k*-th year and *l*-th country.
- μ_l is the fixed intercept for the *l*-th country.

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- $yield_{ijkl}$ is the mean yield of the *i*-th variety in the *j*-th location, *k*-th year and *l*-th country.
- μ_l is the fixed intercept for the *l*-th country.
- g_{il} is the random effect for the *i*-th variety in the *l*-th country.
- y_{kl} is the random effect for the *k*-th year in the *l*-th country.
- s_{jl} is the random effect for the *j*-th location in the *l*-th country.

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- $yield_{ijkl}$ is the mean yield of the *i*-th variety in the *j*-th location, *k*-th year and *l*-th country.
- μ_l is the fixed intercept for the *l*-th country.
- g_{il} is the random effect for the *i*-th variety in the *l*-th country.
- y_{kl} is the random effect for the *k*-th year in the *l*-th country.
- s_{jl} is the random effect for the *j*-th location in the *l*-th country.
- $(gy)_{ikl}$, $(sy)_{jkl}$, $(gs)_{ijl}$ and $(gsy)'_{ijkl}$ are random interactions.

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- Three random effects for which a correlation between countries is allowed

• g_{il} for the *i*-th variety in the *l*-th country	$\text{var}\begin{pmatrix} g_{i1} \\ g_{i2} \end{pmatrix} = \begin{pmatrix} \sigma_{g1}^2 & \rho_g \sigma_{g1}\sigma_{g2} \\ \rho_g \sigma_{g2}\sigma_{g1} & \sigma_{g2}^2 \end{pmatrix}$

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- Three random effects for which a correlation between countries is allowed

• g_{il} for the *i*-th variety in the *l*-th country	$\mathrm{var}\begin{pmatrix} g_{i1} \\ g_{i2} \end{pmatrix} = \begin{pmatrix} \sigma_{g1}^2 & \rho_g \sigma_{g1} \sigma_{g2} \\ \rho_g \sigma_{g2} \sigma_{g1} & \sigma_{g2}^2 \end{pmatrix}$
• y_{kl} for the *k*-th year in the *l*-th country	$\mathrm{var}\begin{pmatrix} y_{k1} \\ y_{k2} \end{pmatrix} = \begin{pmatrix} \sigma_{y1}^2 & \rho_y \sigma_{y1} \sigma_{y2} \\ \rho_y \sigma_{y2} \sigma_{y1} & \sigma_{y2}^2 \end{pmatrix}$

Joint statistical model

- A joint model for combined analysis of two or more countries data

$$yield_{ijkl} = \mu_l + g_{il} + y_{kl} + (gy)_{ikl} + s_{jl} + (sy)_{jkl} + (gs)_{ijl} + (gsy)'_{ijkl}$$

- Three random effects for which a correlation between countries is allowed

- g_{il} for the *i*-th variety in the *l*-th country	$\mathrm{var}\begin{pmatrix} g_{i1} \\ g_{i2} \end{pmatrix} = \begin{pmatrix} \sigma_{g1}^2 & \rho_g\sigma_{g1}\sigma_{g2} \\ \rho_g\sigma_{g2}\sigma_{g1} & \sigma_{g2}^2 \end{pmatrix}$
- y_{kl} for the *k*-th year in the *l*-th country	$\mathrm{var}\begin{pmatrix} y_{k1} \\ y_{k2} \end{pmatrix} = \begin{pmatrix} \sigma_{y1}^2 & \rho_y\sigma_{y1}\sigma_{y2} \\ \rho_y\sigma_{y2}\sigma_{y1} & \sigma_{y2}^2 \end{pmatrix}$
- $(gy)_{ikl}$ for the *i*-th variety in the *k*-th year and *l*-th country	$\mathrm{var}\begin{pmatrix} (gy)_{ik1} \\ (gy)_{ik2} \end{pmatrix} = \begin{pmatrix} \sigma_{gy1}^2 & \rho_{gy}\sigma_{gy1}\sigma_{gy2} \\ \rho_{gy}\sigma_{gy2}\sigma_{gy1} & \sigma_{gy2}^2 \end{pmatrix}$

Assess the performance of the networks

- Using variance components from historical data
- We computed prediction error variances of a difference for BLUPs of two varieties in the same country using the plug-in approach of Stroup (2002)

$$vd_{ii'(l)} = [(\hat{g}_{il} - \hat{g}_{i'l}) - (g_{il} - g_{i'l})]$$

Assess the performance of the networks

- Using variance components from historical data
- We computed prediction error variances of a difference for BLUPs of two varieties in the same country using the plug-in approach of Stroup (2002)

$$vd_{ii'(l)} = [(\hat{g}_{il} - \hat{g}_{i'l}) - (g_{il} - g_{i'l})]$$

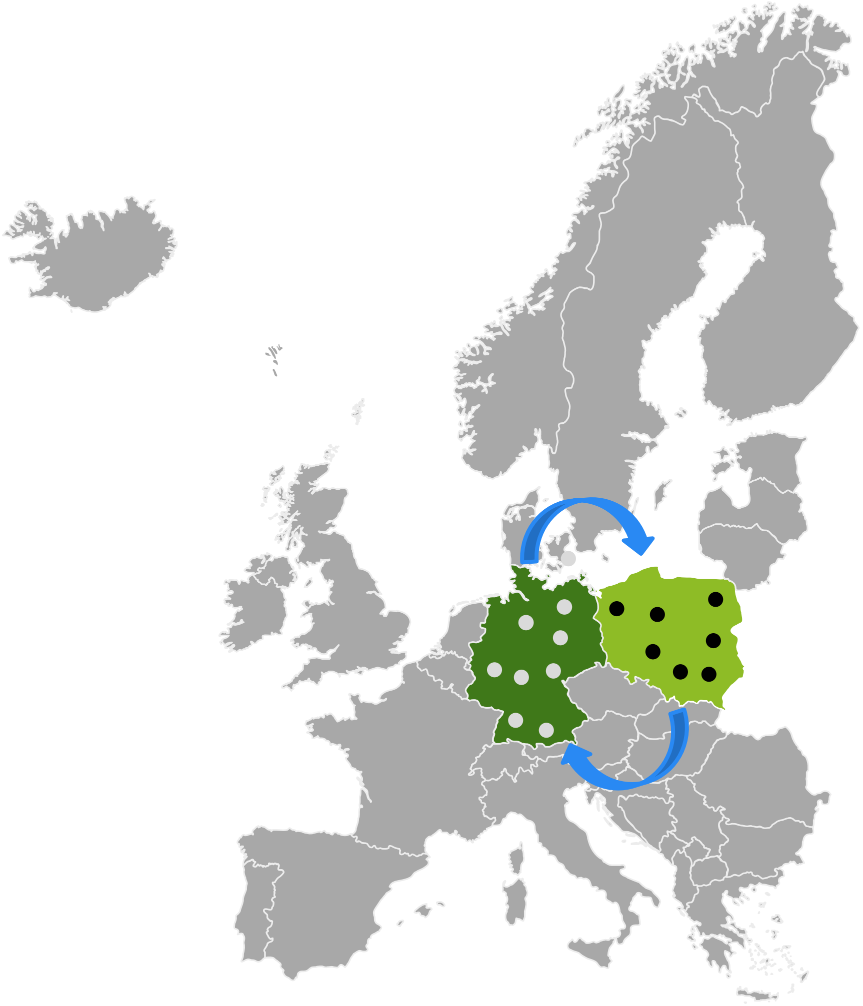
- From these variances of a difference, we computed pairwise heritabilities as given in Piepho et al (2024).

$$h^2_{ii'(l)} = 1 - \frac{vd_{ii'(l)}}{\mathrm{var}(g_{il} - g_{i'l})}$$

Historical maize VCU trial data in Germany and Poland

- Grain maize datasets of registered varieties from German and Polish VCU trials (Malik, 2022)
- Variety means per year and location are provided in the dataset

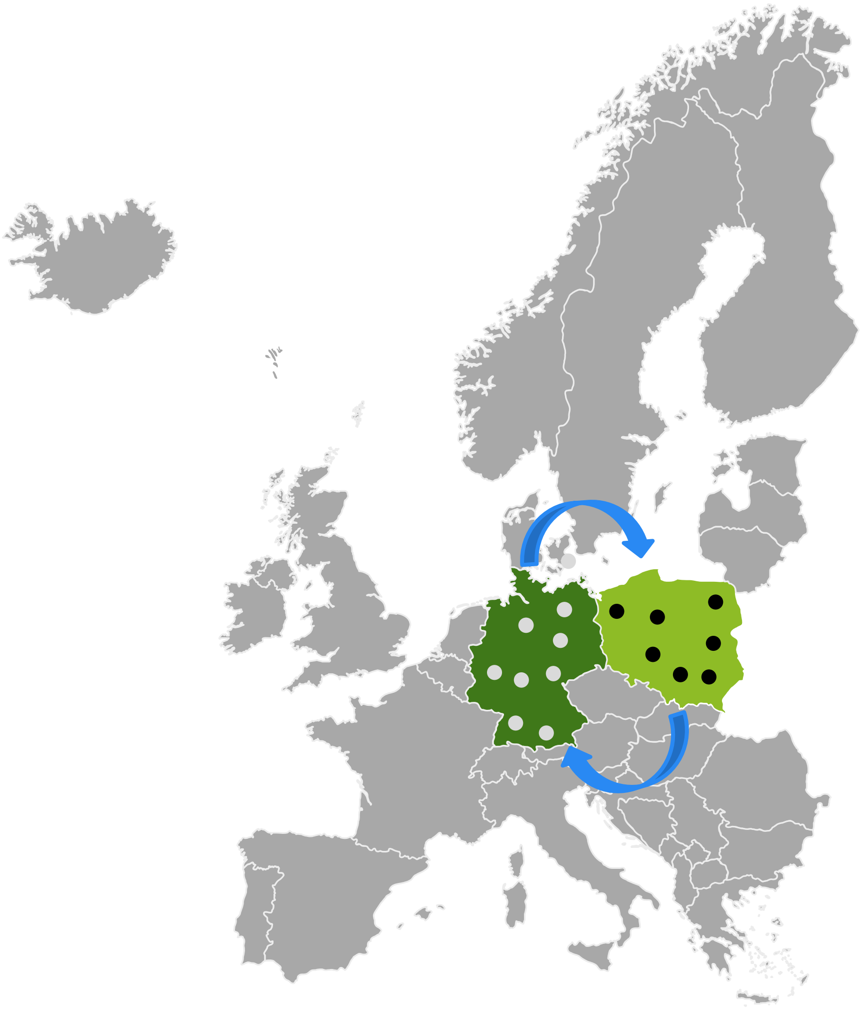
	Germany	Poland
Years	1987 – 2016	1994 – 2017
Varieties	350	634
Locations	121	32
Common varieties	43	



Joint analysis of German and Polish VCU trials

- Variance components from Malik (2022)

	Germany	**Poland**	$\rho_{(\text{Germany,Poland})}$
G	11.292	15.021	0.890
Y	59.706	191.284	0.812
GY	5.144	6.269	0.126
S	99.976	89.923	
GS	4.356	8.462	
YS	155.660	172.154	
Residual (GLY`)	27.775	27.359	



Evaluating alternative design options

- We assume 3 years of testing and the same number of 12 locations each year in a country.
- Each trial is assumed to have a testing capacity of 200 plots.

Evaluating alternative design options

- We assume 3 years of testing and the same number of 12 locations each year in a country.
- Each trial is assumed to have a testing capacity of 200 plots.
- In total, the systems of the two countries combined require a total capacity of 200 × 3 × 12 × 2 = 14,400 plots.
- Furthermore, we assume that a total of 180 varieties are tested across the two countries.

Evaluating alternative design options

- Three MET designs across both countries will be considered.
  1. This MET design reflects the current practice with assuming 100 varieties tested in each country, from which 20 varieties are tested in both countries (180 varieties in total). For simplicity, we assume completely randomized design with two replicates.

Evaluating alternative design options

- Three MET designs across both countries will be considered.

  1. This MET design reflects the current practice with assuming 100 varieties tested in each country, from which 20 varieties are tested in both countries (180 varieties in total). For simplicity, we assume completely randomized design with two replicates.

  2. We modify the design with all 180 varieties are tested in both countries and according to an incomplete block design with trials corresponding to incomplete blocks.

Evaluating alternative design options

- Three MET designs across both countries will be considered.

  1. This MET design reflects the current practice with assuming 100 varieties tested in each country, from which 20 varieties are tested in both countries (180 varieties in total). For simplicity, we assume completely randomized design with two replicates.

  2. We modify the design with all 180 varieties are tested in both countries and according to an incomplete block design with trials corresponding to incomplete blocks.

  3. In this MET design, we modify the individual trial design. As the capacity is 200 plots, we have 20 additional plots, on which 20 of the 180 varieties can be duplicated, leading to a partially replicated (p-rep) design.

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability $(h^2_{ii'})$	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability $(h_{ii'}^{2})$	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210
3	Germany		Germany	0.82091	0.82091
4	Germany		Poland	0	0.65024

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability ($h^2_{ii'}$)	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210
3	Germany		Germany	0.82091	0.82091
4	Germany		Poland	0	0.65024
5	Poland		Germany	0	0.65389
6	Poland		Poland	0.82552	0.82552

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability ($h^2_{ii'}$)	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210
3	Germany		Germany	0.82091	0.82091
4	Germany		Poland	0	0.65024
5	Poland		Germany	0	0.65389
6	Poland		Poland	0.82552	0.82552
7	Germany	Poland	Germany	0.40636	0.73278
8	Germany	Poland	Poland	0.40864	0.82552

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability $(h^2_{ii'})$	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability ($h^2_{ii'}$)	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210

MET design (2): All 180 varieties tested in both countries, 100 varieties per trial

1	Germany + Poland		Germany	0.79682	0.84406
2	Germany + Poland		Poland	0.80479	0.84758

Assessing the performance of the networks

MET design (1) (status quo): 20 varieties in common + 80 varieties in each country

Comparison type	Test country		Prediction for	Heritability $(h^2_{ii'})$	
	Variety 1	Variety 2		Analysis scenario 1 (Correlation=0)	Analysis scenario 2 (Correlation=unstructured)
1	Germany + Poland		Germany	0.82091	0.85993
2	Germany + Poland		Poland	0.82552	0.86210

MET design (2): All 180 varieties tested in both countries, 100 varieties per trial

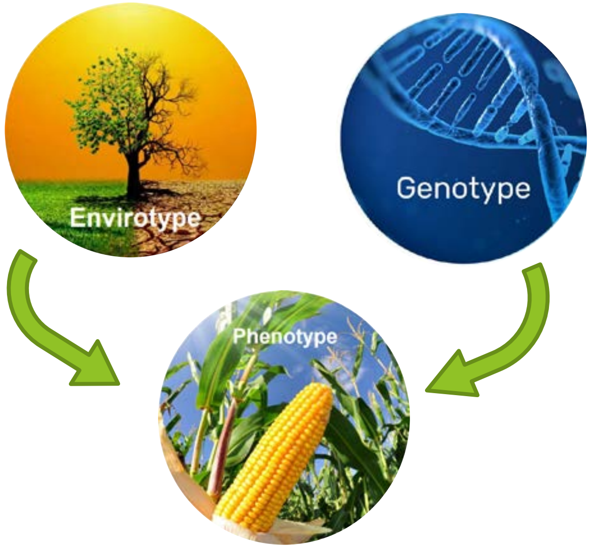
1	Germany + Poland	Germany	0.79682	0.84406
2	Germany + Poland	Poland	0.80479	0.84758

MET design (3): All 180 varieties tested in both countries, 180 varieties per trial, p-rep design per trial

1	Germany + Poland	Germany	0.83136	0.86674
2	Germany + Poland	Poland	0.83332	0.86769

Incorporating marker and environmental information

- Leveraging marker and environmental information allows for more precise estimation of genetic effects.
- Environmental information (covariates) from environmental data and soil properties.
- Fitting the same model but with regression on environmental covariates.



Conclusion

- Varieties that are in common can be regarded as checks providing some degree of connectivity between countries.
- Countries can benefit from combining the data from the other countries.

Conclusion

- Varieties that are in common can be regarded as checks providing some degree of connectivity between countries.
- Countries can benefit from combining the data from the other countries.
- If countries collaborate, greater precision can be achived by integrating the p-rep design.
- Extension of the integration to more than two countries is straightforward.

Conclusion

- Varieties that are in common can be regarded as checks providing some degree of connectivity between countries.
- Countries can benefit from combining the data from the other countries.
- If countries collaborate, greater precision can be achived by integrating the p-rep design.
- Extension of the integration to more than two countries is straightforward.
- More precision can be achieved by adding marker and enviromental information.

Reference

- Malik, W.A., Buntaran, H., Przystalski, M., Piepho, H.P. (2022) Assessing the between-country genetic correlation in maize yield using German and Polish official variety trials. *Theoretical Applied Genetics* 135, 3025–3038.
- Piepho, H.P., Malik, W.A. (2024) Connecting variety trialling systems across two countries, *Plant Breeding*.
- Piepho, H.P., Williams, E., Prus, M. (2024) Assessing the efficiency and heritability of blocked tree breeding trials. *Tree Genetics & Genomes* 20, 33.
- Stroup, W.W. (2002) Power Analysis Based on Spatial Effects Mixed Models: A Tool for Comparing Design and Analysis Strategies in the Presence of Spatial Variability. *Journal of Agricultural Biological and Environmental Statistics* 7: 491–511.

UNIVERSITÄT
HOHENHEIM

Thank You for your Attention !

w.malik@uni-hohenheim.de

piepho@uni-hohenheim.de