



Bundesforschungsinstitut für Kulturpflanzen Federal Research Centre for Cultivated Plants

The national program for the evaluation of genetic resources in cereals (EVAII) – a blueprint for a public private partnership

<u>A. Serfling¹</u>, H.-U. Leistner¹, E. Schliephake¹, L. Frese², F. Ordon¹

¹ Institute for Resistance Research and Stress Tolerance, Quedlinburg, Germany ² Institute for Breeding Research on Agricultural Crops, Quedlinburg, Germany

Development of EVA II



In 2001 launch of EVA II, the National Evaluation Program for Cereal Plant Genetic Resources, with the following objective:

- Establishment of an institutional network for the evaluation of wheat and barley PGR
- Generation of scientifcally more meaningful resistance data by
 - Evaluation of identical sets of germplasm at different locations
 - Use of standard methods and standard genotypes
- Composition of catch assortments of genotypes with defined resistances and integration into the network to facilitate virulence analysis of the main air-borne pathogens
- Integration of molecular genetic markers linked with resistance genes into the evaluation program
- Development of a dynamic information system for recording, analysis and provision of the data generated by the network

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Development of EVA II

EVA II agreement negotiated in 2001 and signed by 20 partners

- Content in alia
 - § 1 Indefinite duration, self-sustained network after a funding period of 3 years
 - § 2 Tasks of the partners and mode of operation
 - § 3 Coordination
 - § 4 Evaluation data delivery, public access embargo limited to three years
 - § 5 Public access via BIG (still under construction)
 - § 6 Extinction of use rights
 - § 7 IP
 - § 8 Non-disclosure
 - § 9 Affiliation of new partners (significant add on value required)
 - § 10 Liabilities
 - § 12 Duration
 - § 13 Final clause



EVAII partners

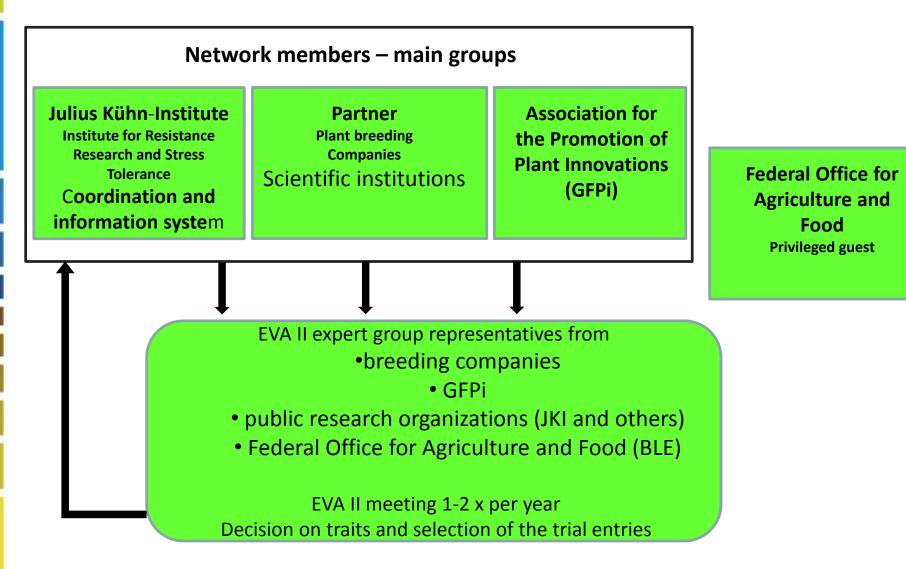




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- Pflanzenbau und Pflanzenzüchtung, Freising Landessaatzuchtanstalt der Universität Hohenheim Landwirtschaftliche Lehranstalten Triesdorf

Development of EVA II





Workflow: evaluation & documentation

- Selection of interesting diseases by the EVA II expert group
- Selection, ordering, multiplication and primary evaluation of the genotypes (coordinator)
- Dispatch of the composed trial entries along with the SMTA to partners
- Coordinator generates, database assisted, list for evaluation data recording and provides partners with the lists
- Assessment of the susceptibility on small-scale plots (1 plot x n locations)
- Import into the database, plausibility control by the coordinator and release of the results





Information system for EVA II



Support functions

- Facilitates the information flow between partners within the network
- Partners can search information by year, crop, disease or location or a combination thereof
- Facilitates sharing of results among network partners and allows immediate use of those data relevant to the specific program of a breeding company
- After 3 years, the data get part of the public domain



Workflow : evaluation & documentation



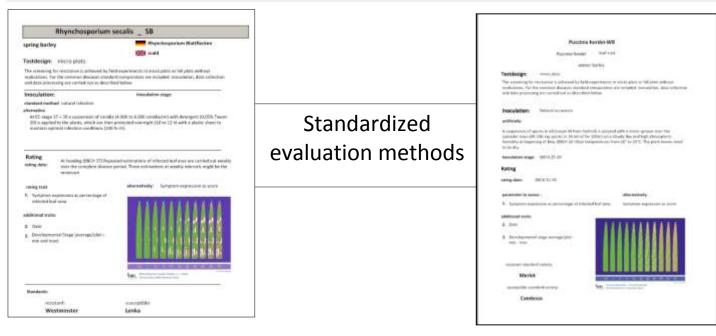
Management of the test set. Import of the genotype data in the multi crop passport descriptor format (FAO & EURISCO)

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Workflow : evaluation & documentation



| Year | Wheat | Barley |
|------|------------------------------------|----------------------------------|
| 2005 | Drechslera tritici-repentis (DTR); | Physiological leaf spots |
| | Septoria; Fusarium | |
| 2007 | Leaf rust | Rhynchosporium |
| 2009 | DTR (tan blotch) | Barley yellow dwarf virus (BYDV) |
| 2010 | Septoria; DTR | Leaf rust; Rhynchosporium |
| 2011 | Septoria; DTR | Leaf rust; Rhynchosporium |
| 2012 | Stripe rust | BYDV; Rhynchosporium; net blotch |



Workflow : evaluation & documentation

Export to Excel

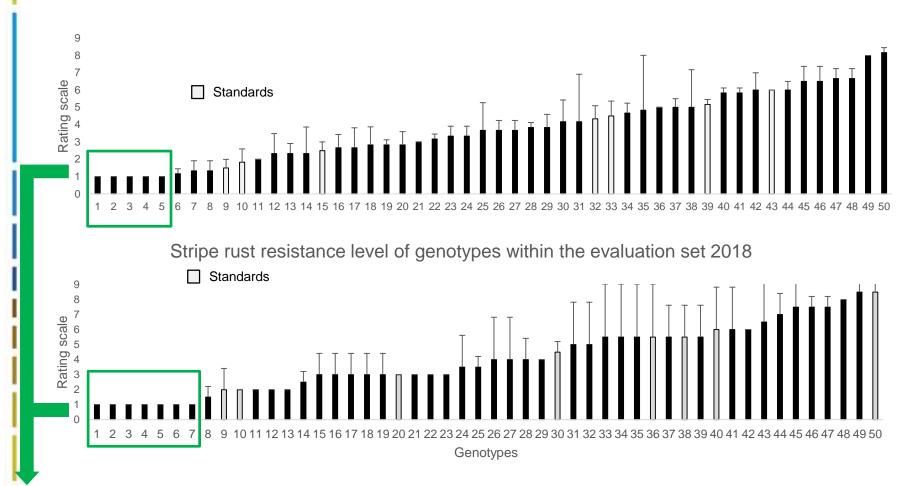


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Results of Evaluations in 2018



Stripe rust resistance level of genotypes within the evaluation set 2017



Data and genotypes evaluated as resistant are available for partners and usable for breeding.

Why EVAII as a blue print?



Eva II fullfills the basic demands for an evaluation system and does not put too much additional work for the private partners

The infrastructure is in place and working, and can be easily transferred to different crops

New features needed and challenges

Implement molecular data (GBS, Chip data etc.)

Implement screening protocols for more complex traits

Implement tools for genome wide association studies (GWAS)

Implemement tools for marker development



