ECPGR Activity Grant Scheme
Proposal Form

Third Call – Phase XI (2024–2028)

Activity Proposal

Activity	
Full title	**Multi-environment validation, mapping, and marker development for resistance to fungal diseases in barley and wheat**
Acronym (or short title)	**ValoResWB -**
Duration of Activity (in months)	24
Start date – End date *Please indicate start date not earlier than 3 months after deadline of Call*	September 1, 2026

Applying Working Group(s)

	Working Group	Indicate name and surname of Working Group Chair
1.	Wheat	Albrecht Serfling
2.	Barley	Nils Stein

Activity Coordinator

Activity Coordinator	
Name and Surname	Serfling, Albrecht
Working Group	Wheat
Nationality	Germany
Current position	Deputy head of institute, chair of wheat WG
Institute	Julius Kühn Institute, Institute for Resistance Research and Stress Tolerance
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Activity Partners (ECPGR-funded)

Please note that each partner needs to be a member of an ECPGR Working Group to be eligible for funding. For self-funded partners please use the separate box below.

Partner ID No.	Name and Surname	Institute	Country
1	Serfling, Albrecht	Julius Kühn Institut	Germany
2	Stein, Nils	IPK Gatersleben	Germany
3	Jan Svensson	Nordic Genetic Resource Centers (NordGen)	Sweden
4	Liliana Vasilescu	NARDI Fundulea	Romania
5	Gintaras Brazauskas	LAMMC	Lithuania
6	Marja Jalli	LUKE	Finland
7	Pavol Hauptvogel	NPPC	Slovakia
8	Rita Costa	INIAV	Portugal
9	Mara Bleidere	AREI	Latvia
10	Ernesto Igartua Arregui	CSIC	Spain
11	Maja Boczkowska	IHAR	Polska
12	Namuk Ergün	Central Research Institute for Field Crops	Turkey

Self-funded partners

Partner No.	Name and Surname	Institute	Country
1	Hackauf, Bernd	Julius Kühn Institut	Germany
2	Zetzsche, Holger	Julius Kühn Institut	Germany
3	Arzu Celik Oguz	Ankara University	Turkey
4	Aziz Karakaya	Ankara University	Turkey
5	Markus Herz	Bavarian State Research Institute for Agriculture	Germany
6	Alessandro Tondelli	CREA-GB Fiorenzuola d'Arda	Italy
7	Katarina Ondreičková	NPPC	Slovakia
8	René Hauptvogel	NPPC	Slovakia
9	Miriam Nadubinska	NPPC	Slovakia

Description of Activity (suggested max. 1,000 words)

Please address the following aspects:

– ***Background:*** Explain the context behind the choice of this Activity, e.g. why this has been prioritized or selected. If this is the continuation of a preceding Activity, please indicate how and why the new Activity will build on previous results/experiences.

Several wheat and barley genotypes resistant to different pathogens have been identified as a result of evaluation field trials conducted in the ECPGR EVA Wheat and Barley network from 2021 onwards. However, some of the trials were not repeated, and the heritability of the examined traits was low. Additionally, the background of these resistances is unknown, and marker information regarding resistance loci is only available from genome-wide association studies (GWAS) based on fewer than 100 genotypes or from only one environment. While some highly significant associations with improved resistance to Zymoseptoria, yellow rust and leaf rust (in wheat), as well as powdery mildew, leaf scald (Rynchosporium), net blotch (Pyrenophora teres) and Ramularia (in barley), were identified, the LOD values were often only slightly above the significance threshold and had a minor influence on phenotypic variance (e.g. resistance to Fusarium in wheat) in terms of reducing infestation. Furthermore, results were often only available for one of the three zones, meaning accessions previously evaluated as resistant should be tested repeatedly in several zones and locations. The aim of this project is therefore to confirm results from the EVA network and to promote the use of genebank accessions with resistances in breeding by following a three-step approach: (I) to make unknown but highly effective resistances that are not yet used in breeding varieties available for breeding in the future; (II) to develop closely linked markers; and (III) ideally, candidate gene identification via database alignment by using bioinformatics. We will create segregating F_2 populations from resistant and susceptible parents to the diseases under investigation to detect genetic patterns and examine the F_3 families of selfed F_2 plants to confirm observations. SNP marker data are available from the EVA project for the parent lines to be

investigated (wheat: 25k Illumina Infinium array; barley: 15k array). This technology is also available for the genotyping of segregating populations and for bulked segregant analysis, in order to detect resistances in F_3 families in more detail. The central aim of the project is to identify novel, highly effective resistances in genebank accessions and to gain knowledge about their genetic background, with the ultimate goal of accelerating the transfer of these resistances into future cultivars. The project plans to make the data generated by the investigation of accessions (originally SSDs from the Evaluations) available to EURISCO. If the opportunity arises in the future, data on derived materials (crosses) will be linked to the original accessions in EURISCO.

– ***Justification:*** Explain why this Activity is justified in terms of making progress towards achieving the ECPGR priority activities and the targets of the *Plant Genetic Resources Strategy for Europe*.

The project focuses on the conservation and management of European plant genetic resources (PGR), promoting their sustainable use and strengthening the germplasm information system that supports their conservation and use. The activity will continue activities of the EVA Wheat and Barley network, engaging both WG members of EVA as well as private sector partners in evaluation trials (Table 5.1, P1). It will confirm results and enriching datasets on these genetic resources, which will also be incorporated into EURISCO, applying an approach proposed by the EURISCO Advisory committee on the handling of SSD data (Table 4.3, P1). Generation of populations will facilitate the use of landraces in breeding programmes (Table 5.3, P2), by eliminating some of the undesired traits (lodging, tallness) and identifying novel resistance loci.

A selection of wheat and barley plant genetic resources will be cultivated and evaluated for resistance levels at various locations, then crossed with susceptible cultivars. These genetic resources can then be successfully used as a source of resistance for future breeding lines and cultivars. This will be in accordance with the EU Commission's Farm-to-Fork Strategy (F2F), which aims to strengthen the sustainability and resilience of food production systems by increasing diversity. The use of genetic resources to increase resistance levels aligns with the objectives of the ECPGR to promote the use of PGR in research and breeding, PGR documentation and information, and scientific and technical exchange and networking (Table 3, Targets 4 and 5, P2, https://www.ecpgr.org/fileadmin/templates/ecpgr.org/upload/ACTIVITY_GRANT_SCHEME_PHASEIX-X/3rd_Call_Phase_XI/Priority_ECPGR_activities_for_GrantScheme2025-26.pdf)..

– ***Rationale for the choice of partners:*** Explain why the selected partners are the most suitable to carry out the proposed Activity and briefly describe their respective roles in the Activity.

The WG members representing the different geographic zones of the EVA WB network will ensure broad climatic coverage. Some have provided PGR to EVA which will be used in this project, and they also have capacity and expertise to conduct disease trials in field or greenhouse conditions. Together with breeding companies from the EVA network, they will conduct repeated field trials in different locations to evaluate genotypes several times, in order to calculate the area under the disease progress curve and the average ordinate. For each trait, a set of five of the most resistant genotypes and one susceptible genotype will be cultivated and evaluated at least three times per growing season. With regard to the most relevant biotic stresses six traits affecting wheat (leaf rust, stripe rust, *Zymoseptoria*, *Pyrenophora*, powdery mildew and *Fusarium*) and five traits affecting barley (leaf rust, powdery mildew, *Pyrenophora*, *Rynchosporium* and *Ramularia*) will be investigated. The interests and research capabilities of the partners in recording and assessing diseases are taken into account in order to be able to make location-dependent, comparable statements about

resistance. Where necessary and possible, the project will also engage private sector partners from the EVA WB network to complement field trials with in kind contributions.

Self-funded JKI partners will contribute data on all traits, while other partners will focus on one or more traits depending on regional characteristics and the diseases that frequently occur at the trial site. All partners have experience of conducting field trials and recording and evaluating diseases in wheat and barley.

JKI and IPK will provide their expertise in molecular biology and data analysis, contributing to the genotyping of F3 populations, association analyses and marker development.

– ***Methodology or Approach:*** Explain how the partners will operate. Clearly explain who is expected to do what. Also explain the rationale for meeting (or not) as part of the Activity. Include a Gantt Chart, to illustrate the work breakdown structure of the project.

Field trials will be performed in the first and second years of the investigation (spring types SSDs in the first year and winter type SSDs, and F_3 families of winter and spring types in the second year). These trials will also be performed by the JKI's partner institute, the Institute for Breeding Research on Agricultural Crops. In 2026, the JKI will phenotype the F_2 populations generated from the evaluated resistant genotypes and establish F_3 families from each F_2 population genotype. During the second year of the project, F_3 families, each consisting of 20 genotypes derived from six crosses of the most resistant wheat genotypes, and five crosses from the mos resistant barley genotypes with a susceptible cultivar, will be sent to partners for rating. Therefore, each partner will rate a maximum of 120 wheat F_3 families derived from susceptible and resistant F_2 genotypes of winter SSD crosses, and a further 120 F_3 families derived from spring SSD crosses (if all six wheat traits and F_3 families of all types are investigated). Additionally, a maximum of 100 barley F_3 families will be derived from winter-type SSD crosses and 100 from spring-type SSD crosses (if all five barley traits and winter- and spring-type F_3 families are investigated). Together with the five most resistant SSDs for each trait, 30 winter-type SSDs and spring-type SSDs (wheat) and 25 winter-type barley SSDs and 25 spring-type barley SSDs will be grown in field trials (two replications). A maximum of 266 two-rowed field plots are therefore planned for winter wheat trials, 266 for spring wheat trials, 155 for winter barley trials and 155 for spring barley trials. These F_3 families, together with the parental lines, will be evaluated at least three times for each trait to calculate the area under the disease progression curve (AUDPC) and the area under the disease incidence curve (AO). Furthermore, leaf samples from F_3 families showing a uniform phenotype will be sent to JKI. The JKI will extract DNA for genotyping, followed by bulked segregant analysis based on the 25k Illumina array for wheat and the 15k Illumina array for barley. Partners will analyse one or more traits in field and/or greenhouse trials (selected according to their area of expertise and field trial capacity). Partners will conduct field trials to evaluate the parental lines and F_3 families. Ankara University will conduct field trials including parental lines and F_3 families, as well as analysing seedlings in greenhouse trials under controlled conditions. JKI will analyse both wheat and barley traits. Ankara University will analyse barley diseases (net blotch, spot blotch, leaf rust and Fusarium head blight of wheat). NPPC (Piešťany, Slovakia) will host trials in spring barley for powdery mildew (*Blumeria hordei*) and in winter wheat for powdery mildew (*Blumeria graminis*) and Septoria leaf blotch (*Zymoseptoria tritici*) under natural field conditions.IPK Gatersleben will perform a bulk segregant analysis using the 15k array to saturate the barley resistance-specific intervals. This will delimit resistance loci, allowing disease resistance genes to be identified. JKI will derive closely linked markers to develop highly resistance-specific KASPs, accelerating the transfer of resistance into cultivars. Crops, investigated by the partners depend on

the geographical regions, so that not all crops and types are analyzed at each location (Table 1). The schedule of activities is shown in Table 2.

Table 1. The crops will be analysed by the partners in field and greenhouse trials. Asterisks mark self-funded partners.

Partners	ID	Spring barley	Winter barley	spring wheat	winter wheat
Julius Kühn Institut	1	X	X	X	X
Julius Kühn Institut (GL)*	1	X	X	X	X
IPK Gatersleben	2	X			
Ankara University*	SF 3,4	X	X	X	X
Nordic Genetic Resource Centers (NordGen)	3	X		X	
NARDI Fundulea	4	X	X		
LAMMC	5	X		X	X
LUKE	6	X			
NPPC	7	X			X
INIAV	8	X		X	
AREI	9	X		X	X
LFL*	SF 5	X			
CREA-GB*	SF 6	X	X		
EEAD-CSIC	10	X	X	X	
IHAR	11	X	X	X	X
TAGEM-FCCRI (Ankara)	12	X	X	X	X

Table 2: Schedule of activities for the two-year project beginning in September 2026.

Year	2026	2027				2028		
Task Quarter (3 months)	4	1	2	3	4	1	2	3
Phenotyping of parental lines (greenhouse)								
Phenotyping and field trials of parental lines (field)								
Generation and phenotyping of F_2 populations								
Generation and phenotyping of F_3 families								
Genotyping, marker analysis, detection of candidate genes								
Development and validation of KASPs								

– ***Description of genetic material:*** If your Activity is focusing on genetic material, please describe in detail, as far as possible, who is providing this genetic material, its status and the number of accessions under investigation (for example: *This Activity aims at molecularly analysing / safety-duplicating / evaluating / collecting XY accessions (listed) of "Genus species", provided by genebank Z/ farmers in country W /to be collected in country P…, etc.*).

The wheat and barley genotypes planned for the project are SSD lines developed and evaluated in the EVA Wheat and Barley network. They originated from partner genebanks, JKI developed the SSDs where not yet available and distributed them to the evaluating partners under the terms of the SMTA. Phenotypic data from preliminary evaluations exist and were used to select SSD lines for the project. After the phenotyping of 30 wheat genetic resources (the five most resistant to each trait) and 25 resistant barley accessions, all will be crossed to specific susceptible cultivars for specific diseases (based on information from the German variety board). Crosses from the most resistant genotypes will be self-fertilised to generate a segregating F_2 population. The resulting F_3 families from each F_2 genotype will be distributed to partners for analysing resistance in different environments. The resistant genotypes used for the study have been delivered in the past by IPK Gatersleben (Germany), CREA (Italy), NARDI (Romania), Agroscope (Switzerland), IHAR (Poland), CRI (Czech Republic), NPPC (Slovakia) and BVAL (Austria).

– ***Expected impact.*** Clearly specify the expected impact from this Activity for the respective ECPGR priority activity, compared to the current state of progress of the respective *Plant Genetic Resources Strategy for Europe* target. Explain how the impact will be obtained.

Current state of progress

Marker trait associations were detected by partially non repeated sets of below of 100 genotypes. These associations provide the first indication of the possible locations of novel resistance genes in the analysed set. However, the genetic background of the resistance cannot be analysed based on available data.

Expected outputs of the activity

-Genotype data from F_2 genotype and F_3 families
-Analysis of the genetic background of resistances
-Closely linked markers, available as KASPs for accelerated breeding of resistant elite lines
-Crosses of resistant genotypes with elite cultivars (selected for favorable traits
-Possible selection of genotypes showing multiple resistances
-Knowledge about genetic background of resistances

In collaboration with the research and private breeding sector (2.4.3), it will have an impact on the ECPGR's priority activity of using innovative tools, such as predictive characterisation techniques and GWAS, to discover and test useful traits that contribute to food security and sustainable agriculture. Genotypic data will be generated, resistance will be mapped, the best resistance genes will be isolated, closely linked markers will be developed and resistant genotypes will be generated for use in breeding programmes.

– ***Links with other non-ECPGR projects or individuals*:** If applicable, clearly explain the objectives of the linked projects and the reasons for complementarity with the ECPGR Activity.

Non ECPGR projects are linked by the analysis of same traits and accessions from the same genbanks.

Project Genbank3.0 (project number 031B1300B, funded by the Federal Ministry of Research, Technology and Space) focused on mapping and validating new resistance loci against powdery mildew, yellow rust and leaf rust which had not yet been utilised in breeding programmes. The project aimed to establish a publicly accessible library of donors carrying rare resistance loci against various races of powdery mildew, yellow rust and leaf rust that have not yet been used in breeding. Some of the genotypes analysed in Genbank 3.0 have also been phenotyped and genotyped in EVA WB evaluations.

Project Rusthealth (project number 321-06.01-28-1-D1.20B-21, funded by the Federal Ministry of Agriculture, Food and Regional Identity) aims to expand the wheat population specifically to improve genetic diversity coverage of the current varieties' resistance spectrum. Some accessions overlap with the EVA WB evaluations.

The Horizon project AGENT (funded by the EU under grant agreement 862613) provided plant material to EVA WB, some of which is also included in this proposal. Existing phenotypic data for some diseases can also be exploited.

Expected products and related ECPGR Priority activity

List concrete products and results that are obtained by the Activity and the corresponding number(s) of the ECPGR Outcome(s) and/or Output(s) and/or Activities to which each product/result will contribute.

	Expected products/results	Corresponding contribution to *Plant Genetic Resources Strategy for Europe* target
1	Identification and validation of (multi-) resistant genetic resources*	Corresponding to table 5- Promoting sustainable use of PGR. Accessions will be further analyzed by a part of the existing EVA network and can be an example, how the EVA concept can be the basis for further analysis and breeding
2	Detection of unknown resistances to fungal diseases of wheat and barley*	Corresponding to the PGR strategy for Europe targests (Table 5, P1"….PGR in Europe are increasingly characterized and evaluated under standard conditions..."
3	Closely linked KASP markers for the accelareted transfer into cultivars*	Correspnding to the genotyping with suitable sets of molecular markers (Table 5)
4	Knowledge about resistance genes, inheritance of resistances, resistance mechanisms and possible long-term effectiveness of resistances*	Corresponding to Tables 3,4,5 due to coordinated use and assessment for future needs
5	Resistant F_3 plants from analyzed families are available for further breeding activities	Collections of PGR in Europe are increasingly characterized and evaluated under standard conditions (Table 5, Target 1 and 3, P1 and P2)

*Both data will be transferred to EURISCO and will be with the FAIR principles (Table 4, paragraph 3.)

Workplan for the proposed period of the Activity

Brief description of meetings and/or main actions of the Activity.

	Type of Action *(indicate if "meeting" or "other action")*
Phenotyping of parental lines (greenhouse)	Action Accessions that have already been evaluated in the EVA WB network will be phenotyped under controlled conditions (in a greenhouse), including inoculation with the following fungal wheat pathogens: *Zymoseptoria*, yellow rust, leaf rust (in wheat), powdery mildew (in both barley and wheat), leaf scald (*Rynchosporium*), net blotch (*Pyrenophora teres*) and *Ramularia* (in barley) are used to generate segregating F2 populations by crossing with susceptible elite cultivars. Isolates of each of these pathogens are available. Phenotyping and crosses will be performed by JKI and, later, by partners in field trials throughout the project.
Phenotyping and field trials of parental lines (field)	Action Field trials will be performed by each partner, except in the first quarter if the project starts before July. Spring types will be sown in spring depending on where the trial is conducted. The partners will consider the presence of pathogens and how to reliably detect them. JKI will phenotype the entire set of accessions and fungal pathogens.
Generation and phenotyping of F_2 populations	Action From each of the wheat and barley accessions evaluated as resistant, F_2 populations will be generated by crossing with a variety known to be susceptible to one of the diseases under investigation. These investigations will be conducted under greenhouse conditions at JKI and at the University of Ankara (Fusarium species).
Generation and phenotyping of F_3 families	Action From each of the F_2 plants, F_3 families will be generated by selfing. Clearly resistant and susceptible F_2 plants will be used to generate F_3 families. The F_3 families will be rated for their uniform resistance or susceptibility to individual pathogens (entire barley and wheat families and traits by JKI; selected families and pathogens by the partners depending on availability).
Genotyping, marker analysis, detection of candidate genes	Genotyping of all F_3 families of wheat and barley, as well as the parental lines and susceptible cultivars (a maximum of 272 wheat samples and 160 barley samples), will be performed using 25k and 15k SNP arrays. A bulk segregant analysis of wheat and barley families will identify resistance loci and candidate genes.
KASP marker design and validation	Based on the identified resistance loci, highly associated SNP markers will be used to design resistance-specific KASP markers within the candidate region(s). These markers will be validated by JKI in KASP assays using the parental lines.

Additional remarks

Indicate any additional remark(s) that is/are important for the evaluation/implementation of the proposed Activity

Remarks:
Discussions within the EVA Wheat and Barley network have highlighted that there is a need to involve the network also in basic pre-breeding activities. This proposal will use data generated by the EVA network to identify the most promising landraces for backcrossing with elite cultivars to make them more amenable to further analysis and breeding. The private sector partners agreed that adding this first pre-breeding step to the EVA workflow would be advantageous and a clear benefit of the collaboration.

Please send the completed form together with the budget table to the

Chair of the submitting Working Group for submission of the Activity proposal.