Federal Ministry
for Economic Cooperation
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Progress Report BMZ Project Funding

General Information

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Closing date	End of February per year
Reporting period	The previous calendar year
Submit by e-mail to	beaf@giz.de

Notes on completing the entry form:

When completing the template, please follow the guide questions in italics, which can be overwritten.

Characters should be font size 11 in Arial. Please do not change the format nor submit a pdf.

Progress reports should not exceed 6 pages. Detailed research reports should be added in the form of annexes.

General direction:

If the period between the last progress report and the final report would be less than 3 months, the last progress report can be omitted.

1. Basic data

The IARC applicant	International Potato Center (CIP)
Project title	Accelerating the Development of Early-Maturing-Agile Potato for Food Security through a Trait Observation and Discovery Network
Funding type, GIZ Project Number and Contract Number	Project Funding, Project number: 14.1432.5-001.00 Contract Number: 81180345
Reporting Period	1 January–31 December 2017
Project Coordinator and Project Scientists	Project coordinator: Hannele Lindqvist-Kreuze, Av. La Molina 1895, Apartado 1558, La Molina, Lima, Peru. Phone number: +511 349 6017 (3065). Email: h.lindqvist-kreuze@cgiar.org Principal staff members: Merideth Bonierbale, Hannele Lindqvist-Kreuze, Elisa Salas, Elisa Mihovilovich, Junhong Qin, Hirut Getinet, Dorcus Gemenet
Project Partners	- Max Planck Institute for Molecular Plant Physiology (MPI-MP): Karin Koehl - Yunnan Academy of Agricultural Sciences (YAAS): Xianping Li - Gansu Agricultural University (GAU): Zhang Junlian - Heilongjiang Academy of Agricultural Sciences (HAAS): Sheng Wangmin - Ethiopian Institute of Agricultural Research (EIAR): Gebremedhin Woldegiorgis - Amhara Regional Agricultural Research Institute (ARARI): Alemu Worku

2. Progress Report

State of Project Implementation

Work Package 1: Phenotyping and genotyping
Output 1: Broad genetic diversity of advanced-bred lines genotyped and phenotyped in key environments

Activity 1.1. Extend and adapt phenotyping protocols for key adaptive traits
Milestone: Low-tech shoot phenotyping parameter identified from high-tech laser scanning data by month 24. *Status: ongoing*

Twenty-one potato genotypes were evaluated for drought tolerance under greenhouse and field conditions using four treatments and two stress levels during the seasons 2015–2017. At harvest, tuber and starch yield data were collected and used to calculate drought stress index. Plants under stress condition showed less above-ground mass as well as tuber yield. Tuber and starch yield of test genotypes were more affected by late stress (after flower initiation) than early stress (until flower initiation).The effect of water stress on plants was clearly observed from the analysis of laser scanning records.

According to the analysis of variance, genotype and genotype x water stress interaction

were significant in all test seasons, suggesting there is ample genetic variance in the population being studied for drought stress-related traits. The phenotyping parameters plant height, leaf area, and leaf movement were measured by laser scanner and used to calculate growth rate, amplitude of leaf movement, and downward and upward leaf movement. These variables were then used to estimate their relationships to the drought stress index of the potato genotypes in the different treatments. The statistical models tested were linear regression, stepwise regression, Lasso, hierarchical clustering, and polynomial model. Of these, the two degree polynomial model was better fitted to daily data of plant height and leaf areas as well as coefficients. Up to 0.4 (p=0.01) correlations were obtained between polynomial coefficients and tolerance level of test genotypes. The best parameters and statistical models will be tested in field trials in 2018 season.

Milestone: Field validation of new parameter on multiple sites by months 30. *Status: **ongoing.*** See full report attached (Gedif 2017 progress report.pdf).

Milestone: Phenotyping protocols refined and standardized for key traits by month 24. *Status: **completed 2016.***

Activity 1.2 Phenotype the genetically diverse potato panel for 7 traits.
Milestone: Diversity panel phenotyped for 7 traits across sites by month 36. *Status: **ongoing**.*

Other than virus resistance in China, field evaluations for all other traits have been completed, and the field books are being processed for uploading in CIP's dataverse for open access by the end of 2018.

Activity 1.3. Genotype the genetically diverse potato panel by genotyping by sequencing (GBS)
Milestone: GBS data of the diversity panel ready by month 24. *Status: **completed 2015**.*

Activity 1.4. Marker-trait associations: associate genotype and phenotype data in genome-wide association study (GWAS). *Status: **ongoing***
Unfortunately, the vast majority of the analytical tools for involving genomic and genetics analysis have been developed for diploid species and do not enable the analysis of more genetically complex autotetraploid species such as potato. However, recently two important tools have become available enabling single nucleotide polymorphism (SNP) calling for tetraploid species from sequencing data (Freebayes) and analyzing genome-wide association utilizing polyploid data (GWASpoly). We are currently developing a pipeline for calling SNPs considering gene dosage. Dosage information is expected to improve the likelihood of finding significant marker-trait associations for quantitative traits. We will develop a full report by the end of the project.

Work Package 2: Capacity building

Output 2: New tools and capacities to evaluate traits and link genotypes with phenotypes available and used by national agricultural research systems (NARS) of China and Ethiopia
Milestone: Training of young researchers from target countries in automatic phenotyping and modern data management, leading to PhD thesis on validation of phenotypic parameter derived from automatic phenotyping in agro-environments. *Status: **ongoing***

Besides his research work, Mr. Gedif Mulugeta (1) presented his progress seminar at MPI; (2) attended a 1-day course on good scientific practice at MPI; and (3) participated in the

Plant Phenotyping Forum at Tartu, Estonia.

Activity 2.1. Convene a workshop on modern genomics for crop improvement and phenotyping for NARS researchers
*Status: **completed 2015.***

Activity 2.2. Develop tutorials for the use of the online database
*Status: **completed 2015.***

Work Package 3: Next-generation selection strategy

Output 3: Next-generation selection systems for directing and scaling out genetic gain defined with network of NARS and end-users

Activity 3.1. Compile stakeholder and expert knowledge and observations on local (subregional) potato productivity; crop rotation; and pest, soil, and water risk and management practices
Milestone: Key informant survey results of baseline data for risk assessment and sustainable productivity gains available by month 24. *Status: **completed 2016.***

Milestone: Site characterization data and interrelation with phenotypic data documented by month 30. *Status: **ongoing***

The multilocation phenotypic data from WP1 can be utilized as such for conducting stability analysis for the traits measured and connecting the phenotypic data with the Climate & Soil Similarity Tool (see 2nd progress report). This will further facilitate the understanding of genotype x environment interaction patterns.

Activity 3.2. Conduct gender-integrated, multistakeholder participatory varietal selection (PVS) and consumer preference studies in Ethiopia
Milestone: Seed for participatory trials available by month 12. *Status: **completed 2015.***
Milestone: Detailed report on multistakeholder PVS and consumer preference studies with gender focus ready by month 30. *Status: **completed 2017.***

A gender-mainstreamed PVS method was used to evaluate potato genotypes at Adet Agricultural Research Center experimental station in Amhara, Ethiopia. The goal was to document the farmers' trait preferences and to identify potato genotypes with potential for variety release. Women and men farmers had different trait preferences between each other, and their preferences were also different from those of the breeders. The results confirm that the perspectives of both genders need to be integrated into breeding programs to ensure that the clones released meet their needs. For example, out of five important genotypes, preferences of male and female farmers agreed for only the top two selected by the breeders. And although both men and women were interested in marketable traits, women had additional requirements, particularly relating to processing. See full report in annex (PVS report.docx).

Activity 3.3. Establish and compare models for genome-estimated breeding values for their predictive accuracy in potato based on Output 1. *Status: ongoing*

During the last reporting period, we found that all genomic selection (GS) methods tested had good enough predictive accuracies for late blight (LB) resistance even though the marker dosage information was not considered. This may indicate that for traits with large

effects, such as LB resistance, the dosage may not be as pivotal as it is for more quantitatively inherited traits. Yield, yield components, bulking-based maturity, and drought tolerance will likely benefit from including the marker dosage in the model. We are currently developing a pipeline for calling SNPs considering the dosage. Once this is carried out, we will identify these GS models that best predict traits related to drought tolerance, virus resistance, and bulking. This work is ongoing, and we expect to finalize the work by the end of the project.

Activity 3.4. Apply multi-trait selection index using data generated in WP1. *Status: ongoing*.
Multi-trait index selection is expected to provide breeders with an efficient way to make simultaneous progress in improving several traits of interest. In potato for example, breeders select for over 40 traits. The relative weight assigned to the traits is based on the target environment and the market requirements, and may also include economic weights although these are difficult to determine objectively in most breeding programs. We are currently working on our multi-environment phenotypic data to characterize sites in a milestone in activity 3.1 to identify the most important target traits for each environment. We will then apply multi-trait indices for the determined target environments. Additionally, we will compare phenotypic index selection and molecular eigen index selection using the SNP data from activity 3.3. This work is ongoing.

Activity 3.5. Develop and apply performance prediction tools to support variety recommendation. *Status: ongoing*.
Milestone: A PhD thesis on predictive models for genome-estimated breeding values for potato ready by the end of the project (with complementary funds). *Status: **Not done**.*
Although a PhD thesis was not undertaken, this milestone relates to activity 3.3. We will use the best predictive model for each trait from activity 3.3 or the multi-trait selection index to select clones for each target environment. These clones will later need to go into testing in target environments alongside those selected from phenotypic selection so as to compare the performance of clones from both selection methods. The testing will, however, not be undertaken within the current life span of the project. This analysis is ongoing as it depends upon completion of activity 3.3.

Milestone: Stability analyses of LB resistance published by month 36. *Status: **ongoing**.* The field books with LB resistance evaluations from Yunnan 2015, Yunnan 2016, Holeta 2016, Holeta 2017, and Oxapampa 2014 were utilized to determine the stability of LB resistance of the CIP elite potato genotypes. Based on the principal component analysis of the mean rAUDPC (relative area under the disease progress curve) of 25 potato genotypes evaluated in all experiments, the best ranking genotypes are CIP393077.54, CIP392634.49, and CIP393371.58; very high levels of LB resistance were found in all experiments. All three genotypes belong to the B3 population that has been bred for LB resistance. More detailed analysis using mixed models is ongoing and will be drafted as a manuscript intended for publication in a peer-reviewed science journal by the end of 2018.

Milestone: Cross-locational meta-analysis of virus resistance published by month 36. *Status: **ongoing**.* Virus resistance experiments were conducted in Peru and Yunnan, China. The field trials at each location need to be conducted in three consecutive years to allow for sufficient virus load accumulation in the plants. The experiment in Peru has been finalized, but the trial in China is still pending the final evaluation in April 2018. The cross-locational evaluation of resistance will be conducted after the trial is finalized.

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General Achievements and Problems encountered
The main achievement of the project to date has been the establishment and coordinated phenotyping of a large set of elite bred genotypes by all project participants and sharing of the respective raw data. The main challenge, on the other hand, was that even though protocols were shared and the materials agreed upon, not all genotypes were evaluated in all environments, and different field designs were used. In retrospect, it would have been good to include yearly progress meetings in the project to improve communication among partners. The NARS partners have selected promising potato genotypes for further testing and have learned new evaluation methods. The EIAR partner identified five LB-resistant CIP genotypes with better performance than their preferred cultivar 'Belete'. This partner will include them and 14 other promising genotypes in a further intensive selection process involving farmers. They also identified early-maturing CIP genotypes with excellent yield of 50 t/ha (2017 EIAR Report.pdf). The Gansu and Heilongjiang partners have also identified promising materials suitable for their climate conditions. In addition, they found the CIP protocols helpful and appreciated the opportunity for international collaboration (Gansu progress report.pdf, Heilongjiang progress report.pdf). They also suggested improvements to some of the trait measurements undertaken, which provides CIP with helpful feedback for its next projects. In the project-planning phase, a PhD thesis on predictive models for genome-estimated breeding values for potato was envisaged with complementary funding; however, this PhD project never materialized due to lack of funding. Thus, relying on commitments without proper costing of the activities can be risky. The drought trial conducted in Peru in 2017 caught the interest of a local university (Pontificia Universidad Catolica del Peru), which collected tuber samples from the trial for a metabolomics study. The same experiment was also utilized to collect image data with the help of a flying unmanned vehicle (drone), with complementary funding from other sources. The image analysis, coupled with the phenotypic evaluations, is expected to guide the development of high throughput phenotyping protocols for drought tolerance evaluation in potato. These spill-over experiments illustrate the purpose of the TON panel. The panel, besides its coordinated evaluation for breeding purposes, is providing opportunities for specialists to develop improved phenotyping procedures that may improve the precision of selection in future generations of potato-breeding programs.

IDO Contribution
Smallholder farmers in Ethiopia (22 women, 23 men) took part in the PVS field trials. Five NARS organizations (project partners) have accessed the tools and technologies from CIP.

Conclusions for the following Reporting Period
Several important activities in outputs 1 and 3 required for finalizing the online database with phenotypic and genotypic data, peer reviewed publications, and manual on next-generation breeding schemes are currently under execution. Nevertheless, we expect to be able to finalize all activities by the end of 2018. Through the introduction of the new germplasm and the new methods, we have already significantly contributed to the project goal and purpose, through the effective collaboration and engagement with five NARS organizations. Our collaborators have already selected suitable potato genotypes for their crossing programs and genotypes for further evaluations in farmer participatory trials. They have also benefited from the CIP protocols; CIP in turn has gained valuable information on the performance of the potato genotypes in multi-location trials and learned about the traits preferred by female and male farmers in Ethiopia. Although part of the output 2 activities have already been completed, the training of the PhD student (Gedif Mulugeta) continues at MPIMP, Germany. Genotypes and phenotypes from some of the project's stress exposure trials—mainly exposure to drought—have attracted the interest and investment of additional

institutions. They have begun to collect data and samples for their research, which will likely further scientific knowledge for informed trait discovery and improvement in ongoing and future projects.

Publications, Papers, and Reports

- PVS_report.pdf
- 2017 activity report by EIAR.pdf
- Gedif 2017 progress report.pdf
- Heilongjiang Annual Progress Report.pdf
- Gansu-Annual Progress Report.pdf

Summary

Most of the trait evaluations have been completed, and the phenotypic data are available in the field books, which will be made open access by the end of the project. These data will be utilized to identify early maturing, climate-resilient potato genotypes resistant to LB and tolerant to drought. The genotypic data are currently being processed with modern tools suitable for autotetraploid potato, to maximize the information on the marker alleles for quantitative traits. Once finalized, the genotypic and phenotypic data will be utilized to identify genome-wide associations, to test genomic selection models and improve selection indices. These results will be an excellent source of new information for CIP's breeding program to develop a next-generation breeding strategy, which will be validated in future projects with NARS and other partners. The NARS partners have committed to the project's activities and successfully utilized CIP protocols and tools for trait evaluations. They have also identified germplasm for their breeding programs or for other future research projects. The PhD research taking place at MPIMP in Germany is progressing well. It is contributing to the capacity development of a young Ethiopian researcher and to the development of new phenotyping methods for drought tolerance evaluation in potato. Valuable information on farmers' trait preferences was obtained from a gender-focused PVS trial in Ethiopia.