Attachment 1

TERMS OF REFERENCE FOR REVIEW TEAM

Mid-term Review of Project

CIM/2014/081 – Mitigating the effects of stripe rust on wheat production in South Asia and eastern Africa

1. Background to the Review

The project effectively started in February 2017 (inception meeting in Dubai) which is 6 months behind the original plan. It is due to finish in June 2020 but will be extended to December 2020 or preferably to June 2021. The Mid Term Review is overdue. However, experimental activities in the first half of the project were dedicated to building populations, for phenotyping in the second period, so it is timely to review the available materials and adapt the plans for obtaining the scientific results expected by the end of the project. The first half of the project also invested in training.

2. Reviewers

The review will be undertaken by the Crops Program Research Program Manager Eric Huttner

3. Process for the Review

The review will be conducted on 16-19th October during the annual meeting of the project in Kulumsa (Ethiopia).

4. Template for the Review Report

As follows.

REVIEW REPORT

Project ID:	CIM-2014-081
Project title:	Mitigating the effects of stripe rust on wheat production in south Asia and eastern Africa
Project Leaders:	
Commissioned organisation:	University of Sydney, Prof Robert Park
In country:	Ethiopian Institute of Agricultural Research, Dr Mohammed Yussuf Pakistan Agricultural Research Council, Dr Shahzad Asad Nepal Agricultural Research Council, Dr Suraj Baidya Indian Institute of Wheat and Barley Research, Dr Subhash Bhardwaj
Reviewer:	Eric Huttner, ACIAR
Dates of review:	16-19th October 2019

1. Methodology/approach adopted for review

Review project document, annual reports.
Attend the annual meeting and review the presentations made at the meeting.
Visit field trials in Ethiopia.
Consult project participants and stakeholders as required.

2. Background

The project is a contribution to the ongoing management of wheat yellow rust (YR) in 4 countries where wheat is an essential component of food security: Pakistan, Nepal and India in south Asia (SA) and Ethiopia in eastern Africa (EA). Yellow rust is a fast-evolving, ongoing threat to wheat production in ACIAR target regions of SA and EA, and in Australia. Keeping the wheat crop protected through the deployment of effective resistance genes is a key contribution. New YR races originate in SA, therefore surveillance and testing in that region is of benefit to the global wheat crop. Research investment has not been commensurate to the threat recently because of the affordability of fungicides in recent times and their use to control the disease.
The project is focused on finding robust and long-lasting genes for resistance to YR, through four objectives:

1. Characterize resistance to YR in wheat germplasm in partner countries
2. Validate minor gene combinations for resistance to YR and refinement of markers
3. Surveillance of the YR causing pathogen *Puccinia striiformis*
4. Build partner capacity in rust pathology and genetics through training

The project strategy is to generate or select a range of diverse material, test them in multiple locations for YR phenotype and genetically map the resistance genes identified in the process. The project is building and deploying various types of populations for this purpose: diversity panels, breeding lines and landraces from the partner countries, and a Nested Association Mapping Population based on parents relevant to the partner countries. It is also building a unique set of near isogenic lines containing combinations of minor resistance genes to identify races of the pathogen and dissect the effect of these resistance genes and their combinations.

3. Review Executive Summary and Recommendations

Ongoing relevance

Statements from the team leaders from all countries confirmed the ongoing importance of the disease for their countries and the relevance of the project. The strategy of identifying, characterising and deploying minor Adult Plant Resistance (APR) genes remains sound and has good potential for impact over time when improved varieties are released. All partner countries appreciated the training undertaken in the project.
India's strategy to manage wheat rust is based on surveillance and deployment of resistance genes, with stable resistant varieties containing multiple APR minor genes: this is aligned well with the project objectives.
The project is complementing Ethiopia's efforts in managing wheat rusts, in the context of pathogen movement. Characterising the germplasm available for breeding will be useful.
Nepal currently uses very low diversity of germplasm in cultivated wheat. The evolution of new pathotypes is an ongoing challenge to wheat production, therefore germplasm diversification allowed by the project will be useful.
Yellow rust is an ongoing threat to Pakistan wheat production, as shown by the high degree of susceptibility of the wheat cultivars currently grown in Pakistan, and the development of new pathotypes of the YR causing pathogen. Outbreaks of the disease in 2019 in Pakistan caused major concerns.
The Avocet NILs developed to characterise the pathogen isolates for their virulence will be a long-lasting legacy of the project, useful to researchers and breeders in all partner countries and globally.

Operation of the research partnership

Following retirement of Dr Bekele Hundie, communication of project team with management of the Ethiopian Institute of Agricultural Research (EIAR) became excessively informal. EIAR requests that procedures be followed. The current Ethiopian leader Dr Adam Bekele was unable to attend the meeting but EIAR staff representing the project provided excellent input into the review. The contribution of retired Dr Bekele Hundie to the review was also critical.
The team will need to solve the obstacle of sending the populations to partner countries, created when the phytosanitary certificate requires irrelevant information. This is more of a problem when a declaration of freedom for a disease not present in Australia (e.g. Karnal Bunt) is required. In this case it is not reasonable to require from the shipper testing for "freedom from disease". Requiring unnecessary testing and assurance of freedom will delay or prevent the material to be sent for testing. If this issue cannot be solved, there is a serious risk that the project outputs will not be obtained in full by the end of the project.
Training has been a successful activity of the project. The partners have suggested that future training include more data analysis and statistics. This is a common request in many projects and points to a structural skill shortage for data analysis in partner teams. The Australian team should ensure that all opportunities are used in the project to expand the skills of partners from data collection to complex data analysis. Opportunities to do so will become increasingly available as more genotypic data are generated for the populations within the project.

Progress of the research activities

The detection and mapping of existing and new genes in the various populations is progressing well. The populations have been built and characterised professionally. Wheat germplasm and four key populations are becoming available:

- Association mapping (Genome Wide Association Studies, on the Core Set including 250 partner lines, selected from the initial large set),
- Additional germplasm characterised for rust resistance (300 wheat lines and 94 synthetics),

- Bi-parental mapping (12 Double Haploid families),
- Nested Association Mapping (about 1000 lines out of potentially 2750),
- Near Isogenic Lines (NILs) in Avocet + APR genes for field assessment of pathogen virulence on minor gene resistance.

The phenotyping of the Core Set lines has been done very well by partners with support from the Australian team, but a large part of the rest of the technical work has been performed by the Australian team due to availability of characterised pathogen isolates in particular. In the next 18 months, the partner teams will take on a major role of data collection but should be also key contributors to data analysis and drawing the conclusions.

The key results from the project will depend on successfully testing the wealth of germplasm built by the team. The precision and accuracy of the phenotyping in multi-location trials will be key to the scientific impact of the project, as well as the ability of the project to deliver useful breeding lines to the breeding programs by the end of the project. At this stage of the project, it is on track to deliver new knowledge (resistance genes and their performance), molecular markers, wheat lines (the NILs) to continue pathogen surveillance, and wheat lines for breeding. The project is also on track to deliver more research outputs than initially planned: populations are larger, more populations are being screened and additional phenotypes are being scored. However, success will require addressing the logistical challenges of managing effectively thousands of lines, trials and data points in the 4 countries and at multiple sites. It is hard to see how this could be achieved without a shared data management system.
The team agreed at the Kulumsa meeting on a plan for distribution of seeds from the various populations and for setting up the multiple trials required, but the plan needs to be firmed up and articulated into its specific components for each population.
The collection of data and their analysis to allow conclusions to be reached (about resistance genes, their mapping, markers, choice of breeding parents, etc.) will require the project to continue until June 2021.
Annual report of 2020 should present how well trials have progressed. Ideally, estimating error rates in phenotyping would allow experimental procedures and designs to be improved.

Data capture, storage and management

A data management strategy is missing from the current mode of operation: this represents a serious risk to the delivery by the project of outputs usable by the widest possible community of next-users. A suitable system should be put into place in the next year. The system would allow:

- the management of all the lines produced by the project (unambiguous identification and naming, pedigree, seed stocks, etc.)
- the management of the trials (with experimental design and barcoding)
- the collection of phenotypic data (with electronic data capture if appropriate)
- the sharing of all data (with access control if desired or necessary)
- building the skills of project participants so that they contribute to data analysis
- accessibility to data and ongoing data collection, reporting, and analysis after project ends.

Several options are available for the data management system. The review notes that the Breeding Management System (BMS) is being adopted by breeding programs of Ethiopia and India and is being used by University of Sydney Plant Breeding Institute: it may be the easiest system to implement. The project may have to allocate resources to the deployment of a data management system.
The annual report of 2020 should present progress made in adopting a data management system, and the challenges encountered. The report should also contain a plan for ensuring the availability of the system after the end of the project. Ideally, the partners would be able to support their own

use of the system as they continue the research and breeding activities. The plan should identify which specific resources (if any) would be needed for the ongoing support of a shared electronic data repository.

Opportunities for further impact

The project research activities can – if successfully completed- deliver in parallel:

- knowledge (genes, markers) of use to researchers and breeders,
- material (characterised lines) which can be used by breeders as parents (donors of resistance) or as varieties (although unlikely), and
- material (experimental lines) useful to researchers for analysing pathotypes.

The Australian team (at PBI) has acquired Leaf Rust and Stem Rust data for the material tested, in addition to the Yellow Rust. The expanded data could become useful to partners later and needs to be shared: this would be best done through the shared data management system.

The Core Set collection of 250 lines should be screened for Wheat Blast resistance, since most of the lines are expected to not have the 2NS translocation (which complicates the detection of new resistance genes). Under ACIAR project CIM-2016-219, the Core Set could be sent to the Bangladesh phenotyping platform in Jashore.

The impact pathway, from project results and materials to future impacts, needs to be thought through in the remaining period of the project. The annual report of 2020 should present a plan for impact, including what the project has to do in the final year and what the partners and their next users need to do to ensure impact is not delayed or blocked.

Recommendations

To Country partners

- Review and rationalise the phytosanitary requirements to exchange germplasm, so that they match the actual biosecurity risks and needs of the country.

To Project team

- Implement a data management system to ensure the wealth and diversity of data acquired by the multiple teams involved in the project are captured, stored and made usable to all researchers during and after the project.
- Design a plan for post-project data management and report in the next annual report(s).
- Formalise the procedures to communicate with the EIAR project team, ensuring management is kept fully engaged and informed.
- Prepare a strategy for the end-of-project dissemination of results and material, especially the Avocet NILs for typing pathotypes, so that the scientific impact of the project can be scaled out beyond project partners, and beyond project period
- Present in the annual report of 2020 the plans for end-of-project (Data, Material, Impact Pathway).

To ACIAR

- Extend the project to June 2021.
- Facilitate the testing of Core Set for Wheat Blast in ACIAR project CIM-2016-219.

4. Project outputs

Determine and comment on how well the project has achieved the outputs and milestones against each of the objectives. Reviewers should refer to Sections 3 and 4 of the Project Document for a more complete discussion of objectives, outputs, activities and methodologies.

The overall aim of the project is to systematically reduce vulnerability to YR of wheat in SA and EA, by establishing, equipping and mobilising a collaborative network of key cereal improvement centres and a knowledge base in SA and EA that will enable ongoing research and development. We anticipate significant spill-over benefits to Australia by increased preparedness for potential future incursions of YR, by identifying markers linked to effective resistance genes that can be used in pre-emptive breeding and via the development of rapid diagnostic tests to profile pathogen isolates.

Objective 1: To characterize resistance to YR in wheat germplasm in partner countries

No.	Activity	Outputs/ milestones	What has been achieved?	Comments
1.1	Identification of the most important genomic regions associated with YR resistance in wheat germplasm grown in SA and EA.	At least 100g of seed of each Core Set genotype (up to 250) is available for use. Rust resistance gene postulation based on seedling phenotypic and marker screens at PBI. All major resistance genes (stripe, stem and leaf rust) identified in the Core Set, along with APR for which diagnostic markers exist (*Sr2*, *Yr18*/*Lr34*/*Sr57*, *Yr29*/*Lr46*/*Sr58*, *Yr46*/*Lr67*/*Sr55*). **Yr2, mo12**	Germplasm screening for rust resistance, Germplasm enhancement. A set of 3,000 diverse wheat genotypes was rust tested at PBI in 2018. A subset of 300 selected lines will be tested again under field conditions during crop season 2019. **Completion date - Dec 2018.**	**In progress.** 3,000 lines set screened at PBI and 250 lines **core set** selected for Adult Plant Resistance testing. The **core set** comprising 50 lines per partner country: 250 lines grown by partners and scored for the 3 rusts in Australia & Ethiopia and for stripe rust resistance in other three partner countries. **Additional** set: 300 lines chosen from the 3,000 initial set. **Additional set**: 94 synthetic lines Genotyping done.

		Field screening of Core Set genotypes and control genotypes in Australia (PBI), Mexico (Toluca, CIMMYT), Morocco (Marchouch, ICARDA), Ethiopia (Kulumsa and Sinana), India (Karnal, ICAR - IIWBR), Nepal (Khumaltar and Bhairahawa, NARC), and Pakistan (Peshawar, Pirsabak, PARC). Response of each genotype to stripe rust is recorded using the modified Cobb scale. **Yr2, mo 12, annually recurring in Yrs3 and 4.**	Core Set of 250 lines was field tested at PBI, WA (Australia), and across the number of field sites in all partner countries (SA and EA) in 2018. Full set will be screened again in 2019 in all countries. Single plants per line have been selected harvested in the greenhouse and sown in the field to generate further seed for greenhouse and field testing. Later on, single plant increased seed can be distributed among the partner countries as well, and pure stock will be maintained at PBI. **Completion date - Dec 2018.**	The 250 Core Set lines have been tested in the greenhouse at PBI with multiple different pathotypes of stripe rust to determine what **seedling resistance genes** are present The Core Set has been tested in the field in 17 different environments (locations x year of testing) in Australia, India, Nepal, Pakistan, Ethiopia and Kenya. The Core Set has been genotyped for the resistance genes *Yr18*, *Yr36*, and *Yr46* and genotyped using the 90K iselect SNP chip. Data obtained but not analysed yet. Additional set of 300 lines screened in Australia and sent to Ethiopia, so will be screened there as well. Additional set of 300 lines genotyped for the resistance genes *Yr18*, *Yr36*, and *Yr46*. Set of 94 Synthetic wheat lines have been tested in the greenhouse at PBI with multiple different pathotypes of stripe rust to postulate the seedling resistance genes. Synthetic lines were also subjected genotyping using APR linked markers; *Yr18*, *Yr36*, and *Yr46*.

1.2	Genetic characterization of YR resistance in wheat genotypes from SA and EA using up to 8 RIL populations developed within the project based on the results from Activity 1.1.	Seed of F_7 RIL populations available for multilocational testing. **Yr2, mo12** RIL populations phenotyped (seedling greenhouse in Australia with at least 3 stripe rust pathotypes and adult plant field in Australia (PBI), Mexico (Toluca, CIMMYT), Morocco (Marchouch, ICARDA), Ethiopia (Kulumsa and Sinana), India (Karnal, ICAR-IIWBR), Nepal (Khumaltar and Bhairahawa, NARC), and Pakistan (Peshawar, Pirsabak, PARC).		Project has produced 12 Double Haploid populations instead of 8 RIL. 200 lines per cross, which would involve partners testing some 2,000 lines. The 12 resistant (APR, stable resistance) parents are from the Core Set and comprise 3 synthetic wheats, two cultivars from EA, and two from SA. All were crossed with Avocet S (stripe rust susceptible). Synthetics: AUS30521, AUS34169, AUS34198 Australia: Braewood, Carinya, EGA Stampede, Monad East Africa: Kenya: Kenya Kudu, Kingbird South Asia: Danphe, Munal#1 Seed of the DH lines will be available in March 2020, seed increase in Australia, and for distribution to all partner countries for field testing during the second half of 2020.
1.3	Development of markers linked to new resistances.	Markers developed for the most important genes identified from the mapping work undertaken in Activity 1.2. **Yr4, mo12** All markers developed applied to the core set to genotype each entry to allow genotyping for the genes with which they are linked.	Core Set lines phenotyping, Genotyping for GWAS and for the presence of stripe rust resistance APR genes linked markers. DNA from a single plant selected from each of the 250 Core Set lines have been extracted and sent to Agriculture Victoria Research for 90Kiselect SNP chip genotyping. Multi location field data collected in different seasons and generated 90Kiselect SNP chip data will be used to preform GWAS to identify reliable sources of APR. All the Core Set lines were also genotyped at PBI using molecular markers for the APR genes *Yr18*, *Yr29*, *Yr36* and *Yr46*. **Completion date - May 2019.**	OK. Preliminary Genome Wide Association Study analysis presented for the Core Set. 33,000 usable markers. Based on the 17 environments phenotyped for YR, found 100 + markers with LOD>4. More to come but hopeful. For the 12 DH populations: genotypic data will be obtained by end of 2020, but phenotypes only from Australia (1 location). Not sure that markers can be found by end of the project, but information generated should at least provide more detail on the inheritance of resistance in each parent.

Objective 2: Validation of minor genes and refinement of markers

No.	Activity	Outputs/ milestones	What has been achieved?	Comments
2.1	Generation of a Nested Association Mapping (NAM) (F_4) population based on elite minor gene donors and 4 reference cultivars selected to represent EA and SA.	At least 100g of seed of 900 F_4 NAM population lines. **Yr2, mo12**	Selections for agronomical traits, Development of F2s. More than 200 BC1F2 plants were raised from each of the 41 crosses of NAM population. Tall, lodged and too short BC1F2 plants were discarded and rest of the progeny was harvested individually to get BC1F3 seed. **Completion date - Dec 2018.**	OK Genotyping to be done in 2020. 6 donors (Australia, sources of R genes) and 11 cultivars. BC1F4 stage reached. 40 crosses, 2750 BC1F5 lines need to be trimmed further, before genotyping: about 2,000 lines. Cost 65 AUD per line: would be good to reduce numbers while preserving genetic diversity. Plan to test in south Asia first half of 2020 and east Africa second half of 2020.
2.2	Field phenotyping of the NAM population	Phenotypic stripe rust data (modified Cobb scale) from field testing in Australia and adult plant field in Australia (PBI), Mexico (Toluca, CIMMYT), Morocco (Marchouch, ICARDA), Ethiopia (Kulumsa and Sinana), India (Karnal, ICAR -IIWBR), Nepal (Khumaltar and Bhairahawa, NARC), and Pakistan (Peshawar, Pirsabak, PARC). **Yr3, mo12**	Over the summer generation of NAM population, Development of BC1F3. More than 4500 BC1F3 plants were raised in the Controlled Environment Rooms (CERs) and a single head per line was harvested for BC1F4 seed. Many lines turned sterile under CERs and didn't produce seed, still we were able to harvest 2750 single heads. **Completion date - May 2019**	OK. Interesting observation of low fertility (seed set) under controlled environment, **rarely mentioned by the proponents of speed breeding**. Caused by interaction between maturity time and LED lights. Plants may have been too crowded. NAM: 900 to 1000 lines targeted for testing. The population is bigger therefore more testing could be done but resources are limited.

2.3	Selection by project partners of locally adapted lines with combinations of minor rust resistance genes.	F_5 seed harvested from best performing lines. **Yr3, mo12**	Next generation of NAM population seed distribution, Development of BC1F5 seed. In June 2019, BC1F4 seeds threshed from 2750 single heads were sown as short rows to get BC1F5 seed. Further selections will be made to reduce the NAM population size below 2000 and by the end of this year BC1F5 seed will be distributed for multilocation rust screening. **Completion date - June 2019.**	OK The phenotyping of the NAM lines will also be an opportunity for selection by breeders for using as donors of resistance in breeding crosses.
2.4	GBS genotyping of the NAM population and mapping of resistance based on phenotypic data from Activity 2.2.	Marker trait associations refined, and robust markers identified.		Not due yet, too early. Genotyping planned in early 2020

Objective 3: To undertake stripe rust pathogen surveillance to assess variation

No.	Activity	Outputs/ milestones	What has been achieved?	Comments
3.1	Provide training in rust surveillance, including sample collection, preservation and processing.	Personnel in each partner country trained in protocols for collecting and preserving rust samples; each collecting rust samples off wheat and barberry annually and preserving isolates for future pre-breeding efforts. **Yr2, mo12**	Stripe rust causing pathogen survey, Pst surveillance. Stripe rust samples were collected across the field sites from all participating countries. These rust samples were to be analysed locally by our collaborators, with key laboratories at Shimla (India), Murree (Pakistan) and Kulumsa (Ethiopia). **Completion date – March, April 2019.**	Strength of Shimla, Murree and Kulumsa research facilities to conduct the analysis effectively. Sound practices are in place for collecting rust isolates from the field, race analysis, and storage. Nepalese scientists are provided with technical backstopping by the ICAR-IIWBR Regional Station at Shimla, having sent 18 samples of stripe rust for race analysis over the 2017-19 period. Data of the initial NILs (which contain major genes, not the minor genes targeted by this project) presented from Ethiopia.

3.2	Rust identification and race analysis, in-country with technical backstopping from India and Denmark.	Rusted barberry samples identified to species, race analysis undertaken either in-country or in India and/or Denmark on all isolates that are identified as *P. striiformis*. **Yrs2, 3, and 4, mo12**		Sample were collected on barberry in India, Nepal and Pakistan In India and Nepal, they do not infect wheat. Not on critical path for other objectives. Can be done later, or maybe restricted to Pakistan samples where diversity seemed very high (higher than others).
3.3	SSR genetic fingerprinting (at PBI) of isolates of *Pst* collected annually in participating countries.	DNA fingerprinting of all isolates completed at PBI, initial assessments made of genetic diversity using standard population genetic approaches. **Yrs2, 3, and 4, mo12**		Obsolete: now use whole genome sequencing.
3.4	Development of new diagnostic tools for *P. striiformis* based on either bar-coded GBS or DArT-seq, or transcriptome sequencing of infected host tissue, to allow assessments of the degree of genetic diversity and mechanisms driving pathogen evolution.	SNP- based assessment of variation within the stripe rust pathogen of wheat. **Yr4, mo12**		Haplo-phased sequence for pathogen is now available. 25 isolates have been sequenced. One large deletion was found in a single isolate, this is being investigated further to determine if it is associated with a virulence change. In field diagnostics: possible collaboration with UK, MARPLE technology based on 242 diagnostic genes, transcriptome Nanopore sequencing, Dr Diana Saunders for analysing Ethiopian samples. But not quite a field diagnostic yet: still requires a lab and is costly.

3.5	Development of a set of near isogenic lines to complement the current Avocet series, to allow precise assessments to be made, both in the field and greenhouse, of pathogen virulence for minor resistance genes.	Six BC_3F_4 lines near isogenic to Avocet +Yr18: Avocet +Yr18 +YrCk1, Avocet +Yr18 +YrCk2, Avocet +Yr18 +Yr16, Avocet +Yr18 +*Yr36*, Avocet +Yr18 +*Yr46*, Avocet +Yr18 +*Yr49*. **Yr2, mo12**	Backcrossing NILs carrying minor genes for stripe rust resistance. Backcrossing is in progress and by the end of this 2019 BC6F1 seed will be generated. This year BC5F1s have been planted in the greenhouse to generate further generations. By the end of 2020, BC5F4 seed will be distributed among the partner countries for multilocation field rust testing. **Completion date - Dec. 2019.** Markers Assisted Selection (MAS) of BC5F1s. Selection of minor genes using available markers. Through MAS, the BC5F1 generation was produced and progeny are currently being raised in the greenhouse for further selection and backcrossing. **Completion date - Jan 2019.**	Logic of the work: characterise minor genes in a fixed background Avocet +Yr18. Done as near isogenic lines in multiple countries: should be able to detect race specific effects and combination effects using minor genes. The major genes NILs already exist. This is critical to establish whether the variations in resistance observed with APR genes in any particular location is caused by environment or pathogen virulence. All catalogued genes have been BC into AvocetS: now putting the minor genes, one by one. Can determine the race virulence profile in greenhouse on seedlings, and the APR gene performance in infected fields. Detect shifts in virulence. BC6F4 (and BC5F5). Resource will be available for field testing in 12 months. Done with 7 genes initially. Field testing done in Australia. Tested in greenhouse at seedling stage: all susceptible, which is as expected: No seedling R in this material so APR genes can be fully characterised. Aim to get single, double and triple gene combinations, based on Yr18, Yr29 and Yr46. **Now initiated work with 14 other genes: this is additional to the project plan. This project to deliver Avocet – *Yr18* NILs carrying *YrCk1, YrCk2, Yr16, Yr36* and *YrHereward*.** The stocks will allow to build more complex combinations of APR genes by crossing selected NILs with 2 genes.

		Preliminary field testing of the stripe rust response of the six NILs at Australia (PBI), Mexico (Toluca, CIMMYT), Morocco (Marchouch, ICARDA), Ethiopia (Kulumsa and Sinana), India (Karnal, ICAR - IIWBR), Nepal (Khumaltar and Bhairahawa, NARC), and Pakistan (Peshawar, Pirsabak, PARC) using BC_3F_4 generation lines. Yr3, mo 12	Rust screening of BC5F1s Selection of minor genes through rust screening. BC5F1 generation produced through greenhouse rust screening of adult plants. Plants are growing in the greenhouse for further selection and backcrossing and selfing. **Completion date - Feb 2019.**	BC5F5 seed will be delivered by the end of Dec. 2019 for field testing in the partner countries, and BC6F4 seed will be delivered by the end of 2021. In progress (see above). The lines will be a resource used by the collaborators for many years to come: as was the case for the previous (Dr Colin Wellings) project. **Lines will be the output: delivered by the project, but data will not be acquired during the project.**

Objective 4: Train key personnel from participating countries in rust pathology and genetics

No.	Activity	Outputs/ milestones	What has been achieved?	Comments
4.1	Training at PBI for 5 months for up to 8 young scientists.	Training for four young scientists completed. **Yr1, mo12**	Two cohorts, training. Despite our continuous efforts, training was delayed two times in 2018 because of visa and organization approvals. **Completion date - July and Nov. 2018 (not started)**	**OK**

4.2	Training for six young scientists completed.	**Yr2, mo12**	Single group of six trainees, training. A five-month training in rust pathology and genetics was conducted at PBI from 1st Feb. to 30th June 2019. Six trainees including Mr Dawit Asnake Tigabu and Mr Tamene Mideksa Sarbesa (Ethiopia), Dr Satish Kumar and Dr Pramod Prasad (India) and Mr Prem Bahadur Magar and Mr Shiwarttan Kumar Gupt (Nepal) successfully completed their training and have returned to their parent countries. Ms Aline Casassola, a student from Brazil, also joined this training to complete her internship. Remaining two scientists Dr Muhammad Fayyaz and Mr Muhammad Sufyan from Pakistan Agricultural Research Council, Pakistan are expected to start their training in July 2019. Students were trained in rust survey, host-pathogen interactions, molecular studies including DNA extractions and running microsatellite and KASP markers and in conducting preliminary genetic analyses of rust resistance in wheat segregating and DH populations. Lectures on host pathogen interaction including pathology and genetics, on EndNote software, photography, and work safety were delivered. Trainees presented their research work at ACIAR Office in Canberra. Trainees also had the opportunity to visit War Memorial, Australian Parliament House and CSIRO. Trainees have successfully submitted their final reports at the end of training on **30th June 2019**	OK good adaptation of the original plan, reflecting logistical difficulties. Training was broader than plant pathology and genetics, included Project Management, Occupational Health and Safety, working together as a team. Further improvement to training suggested by trainees for future: data analysis and software, statistics. This is a very common request.

Objective 5: Project management

No.	Activity	Outputs/ milestones	What has been achieved?	Comments
5.1	Annual reports	Report detailing progress for each year of the project prepared and submitted to ACIAR. Yrs1, 2, and 3, mo12	An annual meeting is planned for 17-18 October 2019, at the Kulumsa Agricultural Research Centre, Ethiopia. Air tickets and lodging of delegates from partner countries will be arranged well in time. **Completion date - Oct 2019.**	**OK**
5.3	Annual project meetings	Meetings with presentations from all partners, minuted with actions for the coming 12 months. Meeting in Year 2 can be held in conjunction with mid-term review, and in Year 4, final review. Yr1 mo2, Yr2 mo8, Yr3 mo2, Yr4 mo8	Mid-term review meeting has been planned in conjunction with the annual meeting on 17-18 October 2019, at Kulumsa. **Completion date - Oct 2019.**	**OK**

5. Project Evaluation

In completing the following table, the reviewers are requested to synthesise the information listed in the Project Outputs table (Section 4); quantitative evidence from reviews, reports, etc.; as well as qualitative information from interviews, case studies and the like. The first four questions (Group A) relate to the specific outcomes of the project. The next six (Group B) concern best practice and longer-term impact. The final two (Group C) are specifically for ACIAR's learning processes. Be sure to include where appropriate information to support the recommendations that are listed in the Executive Summary.

Scoring not needed at Mid Term Review

The scoring for Groups A and B is defined as follows:

Satisfactory		**Less than satisfactory**	
6	**Exceptional quality** Equal to or greater than 90%. Beyond normal project expectations; an example of a project team delivering significantly more than anticipated at the time of project design.	**3**	**Adequate quality** 50-64%. Some areas of core expectations probably not achieved, although factors, external or outside of the control of the project team, may have been responsible.
5	**High quality** 80-89% performance. Overall very good work, with virtually all outputs achieved, although possibly some minor gaps that could have been closed. Strong, positive cooperation across the entire project team.	**2**	**Less than adequate quality** Project did not deliver on several areas of core expectations. Reviewers consider that, given the circumstances of the project, outputs and outcomes should have been at a higher level.
4	**Good quality** 65-79%. Performance quite good. Project team has delivered on the majority of the activities, with valid justifications for those not achieved.	**1**	**Poor quality** Unacceptable performance, even after consideration of all mitigating factors.

A – Specific outcomes of the project		
A1 – Skills and knowledge change	***Guidance:*** *Evaluate the extent to which the project is increasing knowledge and skills of researchers in partner countries, through their participation in the project and the training elements.*	
	Results Statement: **Well organised and delivered training program: a key deliverable of the project.**	**Score:**
A2 – Institutional and group practice change	***Guidance:***	
	Results Statement: **Not seen yet. Adoption of an electronic data management system would be such a change.**	**Score:**

A3 – Communication / extension / dissemination processes and strategies	***Guidance:*** *Are the communication and extension activities and strategies appropriate?*	
	Results Statement: Not much done yet in the project. Plan for impact pathway towards the end of project to be designed.	**Score:**
A4 – Publications, scientific outputs	***Guidance:*** *Assess the scientific, technical and extension outputs in terms of their number, quality, distribution and potential contribution to other scientific projects or activities.*	
	Results Statement: Not yet but likely to be substantial. Quality to be assured.	**Score:**
B – Best practice and longer-term impact		
B5 – Appropriateness / Relevance	***Guidance:*** *Is this project still relevant? Is it an appropriate contribution for Australia to be making at this point in time?*	
	Results Statement: **Yes, no question about this.**	**Score:**
B6 Effectiveness	***Guidance:*** *Are we achieving the results that we expected at this point in time?*	
	Results Statement: **At this point in time yes, but the most important work is yet to be done.**	**Score:**
B7 Efficiency	***Guidance:*** *Is the investment making appropriate use of time and resources to achieve outcomes? Is this project value for money?*	
	Results Statement: **OK so far.**	**Score:**
B8 – M & E	***Guidance:*** *Assess the extent to which there is a robust monitoring and evaluation system providing useful information which is being used for learning and accountability. Assess the extent to which this information is used.*	
	Results Statement:	**Score:**

	Only for project activities. Not very rigorous in the absence of data management system. No estimate of error rate.	
B9 – Legacy / Sustainability	***Guidance:*** *Assess the extent to which benefits are likely to endure after the project ceases.*	
	Results Statement: Improved varieties using genes discovered in the project are likely to have enduring benefits. But not there yet.	**Score:**
B10 – Gender equity	***Guidance****: Is the investment making a difference to gender equality and empowering women and girls?*	
	Results Statement: No	**Score:**
C – ACIAR Learning		
C11 – Lessons learnt	***Guidance:*** *The intention is to capture experiences and learning which are not dealt with elsewhere in the review and which should be brought to the attention of ACIAR. It could cover, for instance, difficulties with capacity building, complex or changing institutional arrangements that impact of delivery of outcomes, personnel arrangements, difficulties in managing projects remotely, poorly developed financial administration structures, infrastructure inadequacies inhibiting project implementation, risk management and impacts of uncontrollable events, etc.*	
	Results Statement: **As in many other similar projects, the difficulty of exchanging germplasm.**	
C12 – Follow-up	***Guidance:*** *Advise ACIAR on what, if any, additional or follow-up activities and support are desirable to ensure that maximum benefit is derived from the expenditure to date.*	
	Results Statement: **To be discussed towards May 2020 based on interim results.**	