Australian Government
Department of Industry, Innovation and Science

Australia-India Strategic Research Fund

Joint Research Centres

AISRF48454 - End of Project Report

Contents

Instructions

The end of project report is a contracted obligation for all Australia India Strategic Research Fund (AISRF) grant recipients. When completing this report, you should refer to the agreed details in your Grant Agreement, the information contained in the Grant Opportunity Guidelines and any advice or information provided by the department's grant management team.

The amount of detail you provide in this report should be commensurate with the project size, complexity and grant amount.

Any required evidence should be submitted with, or as attachments to this report.

The final payment cannot be made until the department assesses the project as complete in accordance with your Grant Agreement and accepts the end of project report.

Submit your completed report to aisrf@industry.gov.au no later than the due date in your Grant Agreement.

Grantee name	Sugar Research Australia Limited
Project title	Genetic control and genomic selection for important traits in sugarcane, and comparison of elite Indian and Australian germplasm.
Project number	AISRF48454
Primary Indian partner	ICAR Sugarcane Breeding Institute, Coimbatore
Reporting period	01/05/2016 to 01/05/2019

1. Project activities

a. Complete the following table, updating for all milestones shown in the Activity Schedule of your grant agreement.

No.	Milestone description (as per your Grant Agreement)	Agreed completion date	Actual /anticipated completion date	Milestone progress (per cent complete) by the project end date
1.	Two workshop meetings, one in India and another in Australia conducted and detailed experimental plan developed.	30/04/2017	30/08/2017	100%
2.	Plant trial in India established.	30/04/2017	30/08/2017	100%
3.	Commencement of identification of SNP markers associated with water stress response.	30/04/2018	30/04/2018	100%
4.	Commencement of discovery and development of SNP markers for commercially important traits: Screening test populations for SNP markers linked to cane yield, sugar content, water stress tolerance and resistance to red rot disease.	30/04/2018	30/04/2018	100%

No.	Milestone description (as per your Grant Agreement)	Agreed completion date	Actual /anticipated completion date	Milestone progress (per cent complete) by the project end date
5.	Completion of identification of SNP markers associated with water stress response.	30/01/2019	30/01/2019	100%
6.	Completion of discovery and development of SNP markers for commercially important traits: Screening test populations for SNP markers linked to cane yield, sugar content, water stress tolerance and resistance to red rot disease.	30/01/2019	30/01/2019	90%.
7.	Further development and validation of marker-trait association and genomic prediction with data collected from ratoon crop. Satisfactory submission of final report.	30/04/2019	30/04/2019	90%.

b. Briefly outline the project activities completed by the project end date. If applicable, comment on why all activities were not completed by the project end date.

Milestone 1. 100% complete.

Two workshop meetings, one in India and another in Australia conducted and detailed experimental plan developed.

Rationale and background to milestone:

Project scientists communicated regularly during the project via the internet and telephone. However, face-to-face meetings and visits to each other's breeding programs and research facilities are more effective for obtaining a detailed appreciation of potential constraints and understanding of details of materials and methods used or planned in the project (e.g. by inspecting field trials, looking at research methods in practice). The visits also provide an opportunity for the visitors to meet a wide cross section of staff on both sides, and to discuss and share views on detailed aspects of other related research and breeding programs.

Achievement:

Project workshops at both SBI and SRA were successfully conducted as planned. During the project, four scientists from the Australian project team visited SBI in India, and then later four staff from SBI visited SRA and CSIRO sites in Australia. During each workshop a combination of formal presentations, discussions, and field and laboratory visits were done. Project staff and senior managers at SBI and SRA met face to face and this clearly helped develop important technical and practical aspects of the project. In particular the technical aspects of high-throughput red rot screening were shared at the meetings, along with a cost and service evaluation of different SNP genotyping providers. Project scientists and breeders involved in visiting each country were also able to examine and share views on the commercial breeding program operations in each country.

Milestone 2. 100% complete.

Plant trial in India established.

Rationale and background to milestone:

In this project, an important aim was to compare genomic predictions for the key traits of cane yield, sugar content and red rot resistance between India and Australia. This entailed obtaining both DNA marker data (using the SNP marker array) and trait data in both countries. Appropriate data for cane yield and sugar content was collected from 2017 and this data was made available to the project. However, this was not the case in India and therefore data on cane yield and sugar content needed to be obtained for a set of clones that would also be screened with the same SNP array as already used in Australia.

Achievement:

This activity was completed on time despite funding delays in India. Approximately 500 clones were planted in a replicated field trial at SBI, India. Due to some concerns about the quality of the data subsequently obtained, a second similar field trial was again established in the following year.

Milestone 3. 100% complete.

Commencement of identification of SNP markers associated with water stress response.

Rationale and background to milestone:

Water stress is an important constraint to higher commercial sugarcane yields in many years in both Australia and India. In this project one aim was to identify markers that could potentially be used to help predict response of sugarcane clones to water stress. Two complementary approaches were used: firstly, to identify markers correlated with canopy conductance which plays a central role in determining water loss and hence development of water stress. Secondly, to identify genes near to these markers that have been identified as having functional roles in stress response and may therefore be hypothesised as having a causal role in affecting response to water stress in sugarcane. In milestone 3, work on the second approach was done. This information was then available to link with the marker data obtained later in the project.

Achievement:

Identification of SNP markers associated with water stress commenced with a literature search of published water stress related genes in sugarcane and related species. This data was later combined with the results of the canopy temperature genome-wide association study (GWAS) and tonnes cane per hectare (TCH) GWAS from the Kalamia field trial population (KAL16-32) to identify genome locations and associated genes that may modulate water use and drought tolerance in sugarcane.

Milestone 4. 100% complete.

Commencement of discovery and development of SNP markers for commercially important traits: Screening test populations for SNP markers linked to cane yield, sugar content, water stress tolerance and resistance to red rot disease.

Background and rationale to milestone:

As explained for milestone 2, an important aim in this project was to compare genomic predictions for the key traits of cane yield, sugar content and red rot resistance between

India and Australia. Cane yield and sugar content together determine total sugar yield and hence revenue obtained by sugarcane growers. Red rot is a major sugarcane disease and an important problem in the sugar industry in India, with resistance in new varieties regularly breaking down. At present, the disease is of lesser importance in Australia. It is of great interest to breeders to understand the genetic basis for resistance to red rot and understand why it is so important in India but not in Australia. This could lead to ways to better breed for durable resistance to the disease in India, and also potentially safeguard the Australian industry from future incursions to the disease.

The work toward these objectives firstly entailed obtaining both DNA marker data (using the SNP marker array) and trait data including some same genotypes in both countries. In Australia extensive data for cane yield and sugar content was collected from 2017 and this data was made available to the project. However, there was insufficient data available for red rot resistance and obtaining this was a major activity in the project in Australia. Some additional data on cane yield and sugar content was also obtained during the project to add to the extensive data already collected. All data collected on trait performance would then be combined with the SNP marker data to determine markers linked to trait performance and determine if marker data could predict trait performance.

Achievement:

The work towards the milestone was carried out as planned. A set of 315 clones were measured for cane yield, sugar content, canopy temperature and red rot resistance. All of these clones were also screened with DNA markers using the SNP chip.

Milestone 5. 100% complete.

Completion of identification of SNP markers associated with water stress response.

Rationale:

As explained for milestone 3, water stress is an important constraint to higher commercial sugarcane yields in Australia and India. One aim of the project was to identify markers correlated with canopy conductance, which is known to play a central role in determining rate of water loss, and hence development of water stress in sugarcane crops. These markers may have a useful role to play in selection for better response to water stress during selection in breeding programs.

Achievement:

The field trial (code named KAL16-32) was conducted in the Burdekin region in north Queensland and was used to obtain data. This field trial contained 315 clones in 4 row × 10m long plots. Canopy temperature and green leaf area (indicators of water stress response) of clones in the field trial were measured during a period of water stress.

Genome-wide association tests were performed between the SNP genotypes and the canopy measurements in the KAL16-32 population to identify SNP markers associated with canopy traits. Genes co-located with significantly associated SNPs were identified by searching publicly available sugarcane and sorghum genome databases.

Milestone 6. 90% complete.

Completion of discovery and development of SNP markers for commercially important traits: Screening test populations for SNP markers linked to cane yield, sugar content, water stress tolerance and resistance to red rot disease.

Rationale and background to milestone:

As indicated above a major objective of the project was to obtain genomic predictions of key traits for sugarcane breeding populations in Australia. This necessitated combining data on performance for the key traits of interest (cane yield, sugar content and red rot) with the DNA marker data, and identifying markers and combinations of markers that could explain the variation in the traits. The markers explaining the traits would be later compared with those identified in India. This would allow us to predict high performing parents in each country for the other and help target future exchange of parental material. The identification of combinations of markers predicting traits in each country could also facilitate effective marker assisted selection within commercial breeding programs in each country after the project.

Achievement:

All genotyping and phenotyping of the Australian population was completed in both the plant and ratoon crop cycles. Highly significantly-associated SNP markers for each trait were identified. Genomic selection methodology was applied to derive predictions of the traits using all marker data combined. The genomic location of the most important markers and co-located genes with previously reported functionality were also identified. This work used publicly available sugarcane genome databases and the high level of synteny between the sugarcane and sorghum genomes to deduce candidate genes that may be involved in regulating these traits.

The Indian populations have been phenotyped for all traits. We are currently awaiting data from the Indian populations in order to complete activities relating to the comparison of Indian and Australian germplasm.

Milestone 7. 90% complete.

Further development and validation of marker-trait association and genomic prediction with data collected from ratoon crop. Satisfactory submission of final report.

Rationale and background to milestone:

Collection of data in a further year (ratoon crop) was done to obtain measurements of cane yield and sugar content across another crop cycle. Genomic prediction is a data analysis method that combines all marker data to predict performance of a trait. Accuracy of prediction can be determined by using cross-validation methods. “Accuracy” is a term used in genomic prediction studies to refer to the correlation between the predicted performance of a set of genotypes (i.e. predicted performance for a trait based on using just the marker data), and the observed data for the trait.

Achievement:

All milestones related to Australian activities have been completed. Accuracy of genomic prediction for each trait was calculated using data from the KAL16-32 population. Recommendations for marker development outputs for the Australian breeding program were presented to the SRA plant breeding team. We are currently awaiting genotype data for the Indian populations in order to identify Indian marker-trait associations, compare them to Australian results, make recommendations to the Indian breeding programs, and make recommendations to both countries regarding potential variety exchange.

c. Briefly outline the extent of your collaboration with your Indian partners. How did you engage, and how often did you engage with them?

Australian and Indian researchers on this project collaborated closely to design and execute the project activities. Visits to Australia and India were made by scientists involved in the project in addition to the two workshops that involved all project members. In person visits were particularly useful for technical work such as field trial design and data analysis, and facilitated engagement by allowing research staff from the two institutes to meet each other in person. A detailed description of face-to-face meetings between the Indian and Australian project collaborators is given in Appendix 1.

In addition to face-to-face meetings, regular engagement between Australian and Indian scientist was through email, phone calls and WhatsApp. Frequency of engagement via these methods varied depending on the nature of current project activities, and increased during report writing, experiment design, and data analysis periods.

Collaboration between SBI and SRA was mutually beneficial, particularly through the exchange of technical expertise. SBI has extensive research expertise in red rot disease of sugarcane and they advised SRA on methods to rapidly screen clones for resistance to this

disease. SRA was able to share technical expertise regarding statistical analysis of marker trait associations in sugarcane populations, and field experiment design.

The collaboration was hindered by delays on the Indian side of the project, which meant that project activities in the two countries were not concurrent. SBI and SRA endeavoured to synchronise project activities as was initially planned during project design but funding delays in India meant that activities in India were delayed by approximately 12 months compared to Australian activities. Consequently, comparison of results between the two countries could not be made in time for the submission of this report. Both SRA and SBI intend to complete the comparison of Australian and Indian results following submission of this report from Australia, to capture the originally intended major mutual benefits sought from this project.

Outside of the aims of the research described here, the collaboration between SBI and SRA on this AISRF project was seen as a valuable catalyst to further a strategic partnership between the two sugarcane breeding institutes, with the intention to collaborate on future research projects for the mutual benefit of both the Indian and Australian sugar industries. A memorandum of understanding reflecting this initiative was developed by both institutes during the course of this project and is described in Appendix 2, pages 6 and 7.

d. Attach any agreed evidence required with this report to demonstrate progress or successful completion of your project. List the attached documents below against the relevant activity/ies.

Evidence for completion of Milestones 1 to 4 was previously provided in progress reports one and two.

Milestone 5. 100% complete.

Completion of identification of SNP markers associated with water stress response.

- Canopy temperature and green leaf area data was collected from the KAL16-32 population under water stress conditions in order to measure drought response phenotypes in the field. Drought response genes from sugarcane and other crop species were identified from peer-reviewed publications (Appendix 4).

Milestone 6. 90% complete.

Completion of discovery and development of SNP markers for commercially important traits: Screening test populations for SNP markers linked to cane yield, sugar content, water stress tolerance and resistance to red rot disease.

- Markers associated with canopy temperature were identified by GWAS and are discussed in Appendix 4.

- Remaining clones from the KAL16-32 population were screened for red rot resistance rating. Markers associated with red rot resistance trait were identified by GWAS and are discussed in Appendix 3.
- Markers associated with the yield traits TCH and CCS were identified by GWAS and are discussed in Appendix 5.

Genotyping of the Indian population was not completed by SBI in time for the submission of this report. Therefore, discovery of trait-associated SNP markers in the Indian germplasm, and comparison with the Australian results are not reported here. This occurred due to funding delays on the Indian side of the project which delayed the commencement of research activities at SBI by approximately 12 months. Additional delays were encountered when sending sugarcane genomic DNA to Thermo Fisher Scientific in the United States for SNP genotyping.

This issue was communicated to Department of Industry, Innovation and Science representatives, Dr Kris Browne and Dr Sarojini Mitchell, in person at the AISRF Grantees Forum in Brisbane on 21/09/2018. The delay was again communicated to DIIF Program Officer Vickii Saunders by phone on 15/03/2019.

Both SRA and SBI intend to complete the analysis of SBI germplasm and compare the results with those obtained in the SRA population, as this will capture the major benefits originally targeted in this project and inform potential germplasm exchange between the nations going forward. This will occur outside the project funding period in Australia, with costs incurred by SRA for the completion of this analysis provided in-kind.

Currently the SBI project team has collected phenotypic data for their population and have isolated genomic DNA for the population as well. They are currently awaiting the results of SNP profiling of these DNA samples, which will be carried out at Thermo Fisher laboratories in the United States. This genotyping laboratory typically has an eight week turn-around time for delivery of SNP data. Once genotype information is obtained for the SBI germplasm, the SRA project team will be able to complete the remaining activities in Milestones 6 and 7.

Milestone 7. 90% complete.

Further development and validation of marker-trait association and genomic prediction with data collected from ratoon crop. Satisfactory submission of final report.

- Genomic prediction accuracies for all traits were calculated and are included in Appendices 3, 4 and 5.
- Outputs for this work and recommendations for implementation of these outputs into the SRA breeding program were presented to the SRA plant breeding scientist at the

annual SRA Breeders Meeting in March 2019. The presentation is included in Appendix 6.

Milestone activities related to the comparison of Australian and Indian marker-trait associations for this milestone are incomplete as described for Milestone 6 above.

2. Project outcomes

a. Outline the project outcomes achieved by the project end date.

Comparison between Indian and Australian germplasm.

As indicated elsewhere, one of the most important outcomes planned and anticipated from this project will arise from comparison of common DNA marker data from germplasm phenotyped in Australia and that in India. At the time of writing this report, key data from India had not yet been obtained due to delays in India outside of the Australian team's control. When key data from India has been obtained (expected within 2-3 months) comparison of results between countries will have very important implications for ongoing cooperation. In particular, we will be (i) better able to predict breeding values of clones from one country for the other (which will improve effectiveness of mutually beneficial exchange of germplasm between breeding programs), and (ii) determine if some important genetic effects for key traits are present in one country but not the other (e.g. markers affecting resistance to red rot).

Outcomes from results from Australia.

Apart from outcomes expected from comparison of data from India and Australia, some significant outcomes from data collected in Australia alone have arisen with identification of SNP markers significantly associated with yield traits, water use, and red rot resistance, as described below.

Large marker effect for resistance to Red Rot disease.

Perhaps the most striking and readily adoptable outcome of this research project so far is the identification of a single large effect QTL affecting resistance to red rot pathogen in the Australian germplasm. While red rot disease does not have as significant economic impact in Australia as it does in India, it is a disease that causes production losses for Australian growers, particularly in the Mackay and Plane Creek growing regions. The identification of the red rot QTL in this project is the first time such information has been produced for Australian germplasm or elsewhere, and preliminary discussions with the SRA Plant Breeding Team has identified this as a useful trait for incorporation into future genomic selection initiatives in Australia.

Of particular interest when data from India is available, will be the comparison of marker effects for red rot resistance between the two breeding programs. For example, it will be of interest to determine if the large effect QTL revealed for the Australian germplasm is present in the Indian germplasm, and if it is, whether it has any effect. This knowledge could have important implications for ongoing breeding for red rot resistance in both countries. Red rot is a very economically significant disease in India and the results obtained here in Australia are likely to inform genomic selection strategies in the SBI breeding program as well.

Genomic predictions for cane yield and sugar content.

The genome wide associations studies produced by this research program successfully identified genetic markers significantly associated with economically important traits in sugarcane. Marker associations were identified for cane yield and sugar content and this information may help lead to genomic selection and prediction strategies to accelerate the rate of genetic gain in sugarcane varieties for the Australian Industry.

The most useful application of the cane yield and sugar content phenotype data and associated SNP genotypes reported here is to combine the data from this project with results obtained in other research projects to produce large reference populations that will collectively provide stronger genomic prediction accuracies for improving yield by genomic selection. Further investigation of the genes physically associated with the significant SNPs may also provide an improved understanding of the genetic control of yield in sugarcane. This line of work will remain ongoing within the Australian sugarcane-breeding program, in combination with other projects.

Markers related to stomatal conductance and response to water stress.

This project produced the first association study between water use phenotypes and genomic markers in sugarcane and so provides the first step in developing genomic selection strategies for breeding sugarcane varieties with specific water use characteristics. This may prove particularly useful for developing different optimum varieties for Australian growers depending on whether they farm in an irrigated or non-irrigated growing region. Information about the water use characteristic of sugarcane varieties will become increasingly important as rainfall becomes increasingly unpredictable and irrigation costs continue to rise.

Comparison of genotyping platforms.

At the start of this project a pilot study was done to confirm that the CSIRO-SRA-Syngenta Affymetrix SNP marker array chosen for the research was indeed the best marker platform to use. An alternative approach would be to use a “genotyping-by-sequencing” (GBS) method. GBS is not dependent on prior sequencing data, and therefore could in some

situations offer some advantages. For example, the SNP array would not be useful if screening germplasm that has ancestors not sampled in the sequencing used to generate data to identify SNPs chosen for the SNP array. It was decided to compare the SNP marker array with two commercially available GBS methods, namely DArTseq (provided by DArT Pty Ltd, based in Australia) and the service offered by Rapid Genomics (based in the USA). A set of 96 sugarcane clones was screened using all three methods. A much larger number of informative (polymorphic) markers were revealed by the SNP array, and it was concluded that this method was the most cost-effective. This result reinforced the view that this method was the best to use for both this project and others underway in SRA.

b. Do the achieved project outcomes align with those specified in the grant agreement? ☐ yes ☒ no

If no, explain why.

As described in sections 1 and 2 of this document, we have not yet been able to obtain data from the SBI germplasm. This has meant that at the time of preparing this final report we have not been able to complete project activities related to the comparison of Australian and Indian germplasm. However, all work from the Australian side for the joint project has been completed, and we understand that necessary work from the Indian side required to address this outcome is in hand and will be done shortly.

Both SRA and SBI are committed to the successful completion of these activities in the near future, because it is important to define if and how, ongoing mutually beneficial cooperation in sugarcane breeding between our industries should be directed. We anticipate that this will provide novel and important information regarding how the genetic control of different traits, especially red rot resistance, varies between the Indian and Australian germplasm.

The ultimate intended outcome of this project is the facilitation of germplasm exchange between Australia and India and this project will achieve this by creating strong scientific networks between SBI and SRA and by providing genomic prediction studies that will allow sugarcane breeders at both institutes to make informed recommendations for targeted germplasm exchange.

c. List and provide links or attach copies of any published reports and promotional material, relating to the project.

A report on the collaborative project and meetings between SBI and SRA staff was published in SRA's quarterly industry magazine CaneConnection, and is included in Appendix 2 (pages 6 and 7).

Project results were presented to the SRA annual breeders meeting on 19/03/2019. This was a meeting of all SRA plant breeders and variety officers, along with researchers from the University of Queensland and CSIRO who also work in the area of sugarcane breeding research. The purpose of the meeting was to discuss how outputs from this project and

others could directly benefit the Australian sugarcane industry through the SRA breeding program. The presentation for this project is attached in Appendix 6.

The presentation was well received, with particular interest in the application of red rot markers in the breeding program, and potential uptake of the rapid red rot screening method by SRA pathologists.

A manuscript for publication of project results in a peer-reviewed journal is currently being drafted.

d. Are there any planned events relating to the project that you are required to notify us about in accordance with your agreement? ☐ yes ☒ no

If yes, provide details of the event including date, time, purpose of the event and key stakeholders expected to attend.

[Insert text]

3. Project benefits

a. What benefits has the project achieved?

Red rot resistance marker development.

The identification of a single major effect QTL for red rot resistance in Australian germplasm by this project will likely lead to the inclusion of red rot resistance markers in genomic selection and prediction initiatives currently underway at SRA. Discussions with sugarcane plant breeding researchers in Australia have identified the red rot resistance markers reported here as suitable for inclusion in a low-cost 'breeder's SNP chip' platform that may be developed by the industry in the near future. Such a genotyping platform would allow plant breeders at SRA to affordably screen a large amount of germplasm for a smaller number of economically important SNP markers.

Technology sharing and network development between SRA and SBI.

This project provided an opportunity for SRA and SBI researchers to meet in person, exchange knowledge and ideas, and work closely together to deliver benefits to the sugar industry in both India and Australia. SRA and SBI share the common goal of providing high value sugarcane varieties to their respective industries and this project represents the first step in a mutually beneficial collaboration for the two institutes.

The project has generated (and still generating) a set of data which will enable important comparisons between germplasm within each breeding program, and help direct ongoing mutually beneficial cooperation after the project finishes. This is important because intelligent and directed use of parental germplasm from each country probably offers

important benefits to the other. There has been no exchange of sugarcane germplasm between India and Australia for many decades, and the results from this project may facilitate mutually beneficial exchange in the future.

This project also facilitated technology transfer between SRA and SBI. Most notably, SRA benefitted from the expertise of SBI researchers in the areas of red rot screening and knowledge of the red rot pathogen. In turn, SRA researchers were able to share their knowledge and skills in genomic selection and GWAS in sugarcane with their SBI counterparts. It is intended that this project will mark the start of continued collaborations between SRA and SBI to advance technical capacity in sugarcane breeding in Australia and India.

Environmental benefits of optimally adapted varieties.

The discovery of genetic markers associated with yield, water use, and red rot resistance in this project will contribute to the development of optimally adapted varieties for Australian and Indian growers. Optimally adapted varieties underpin productivity in all agricultural industries by providing optimum yields with minimal inputs.

The identification of genetic markers for red rot resistance will likely facilitate the removal of red rot susceptible germplasm from progeny in the SRA breeding program and help inform parental selection during crossing. By providing growers with varieties that are genetically resistant to fungal pathogens, growers are able to improve productivity without increased use of fungicides, resulting in an environmental benefit. This also creates a profitability benefit for the grower by reducing input costs.

Similarly, the markers associated with water use efficiency identified in this project may contribute to the development of sugarcane varieties that are optimally adapted for productivity in water-limited environments. Water resources are becoming more limited, rainfall is increasingly unpredictable, and costs for irrigation and electricity for pumping are rising steadily. Consequently, there are large opportunities for environmental and productivity benefits through variety development targeting optimum yields with minimal water inputs. Additional data collection will need to occur to produce more robust genomic predictions for water use traits before the preliminary data presented here can be capitalised on in genomic selection programs.

The yield traits TCH and CCS are the main drivers of productivity in the Australian sugar industry and the genomic predictions for these traits produce by this project will contribute to the larger sugarcane genomic selection initiatives currently underway at SRA, CSIRO, and UQ. The data collected in this project will be combined with other populations studied in other projects to provide stronger genomic prediction accuracies across a wider variety of environments and germplasms. Increased productivity and profitability allows for adoption of best practises by growers resulting in reduced inputs and waste.

b. What ongoing impact will the project have?

Collaboration between SBI and SRA.

SRA and SBI are the premier sugarcane breeding institutes for their respective countries and among the leading programs worldwide, and this project represents an unprecedented partnership between the two institutes. This collaboration has provided an opportunity for the development of professional networks between SRA and SBI and it is hoped that this will lead to future collaborations between the institutes. This project has highlighted the benefits of international collaboration between sugarcane researchers and has been mutually beneficial for both SBI and SRA, particularly through the exchange of technology and skill development for researchers.

Facilitation of future germplasm exchange between SBI and SRA.

We intend that this project will provide a foundation for future mutually beneficial and reciprocal germplasm exchange between SBI and SRA. Marker-trait association data collected within this project will help inform decision making around targeted germplasm exchange. Genomic predictions developed in part from data contributed by this project will allow breeding value of candidate clones in India for use in Australia to be predicted, and vice versa. In addition, QTL with large positive effects in one country but not present in the other could be targeted for exchange. Additional challenges related to the movement of biological material out of India will need to be addressed before germplasm exchange can take place, and it is hoped that the networks developed, and demonstration of potential benefits possible from the completed analysis of data in this collaborative project will help facilitate these discussions.

Strengthening of genomic selection initiatives in Australia.

The marker-trait association data generated by this project will directly contribute to the development of genomic selection initiatives in the Australian sugarcane industry. Modelling presented at the SRA Breeders Meeting in March 2019 suggests that deployment of genomic selection tools in the SRA breeding program can result in an increase in the rate of genetic gain to 2 % per annum. The population data collected in this project will be pooled with data from other projects in Australia to strengthen genomic prediction accuracies and provide robust markers for genomic selection.

c. Did the project result in any unexpected benefits? ☒ yes ☐ no

If yes, explain what and why.

At the conception of this project, red rot disease was considered a relatively low-priority trait for genomic selection initiatives in Australia, but a very high priority trait for genomic selection in India. This is due to differences in the economic value of this disease between the Australian and Indian sugar industries. SRA germplasm has a high proportion of red rot

resistant clones but red rot disease does occur in the Australian industry, and is a particular problem for cane growers in the Mackay and Plane Creek areas.

All SRA varieties are screened for red rot resistance phenotype in the field before release to the Australian industry using a method that takes approximately 14 months to complete, and only a limited number of clones can be screened by this method each year due to resource constraints.

During the course of this research project, SBI researchers shared their extensive experience in researching red rot disease of sugarcane with SRA researchers, including their method for high-throughput screening of red rot resistance in sugarcane. This was the first time this method had been trialled in Australia and their method was found to be fast, affordable and reliable. This method allows the screening of large numbers of clones in a controlled environment chamber, and produces red rot ratings in two weeks compared to 14 months in the field-based method. This method is now well established at SRA and will be used in another research project. SRA is currently looking to develop this rapid screening method to potentially include it as a routine component of the SRA disease-screening pipeline in Australia. This is a good example of a technology transfer outcome achieved in this project.

This method allowed SRA researchers in this project to screen over 300 Australian clones for red rot resistance within the three year project timeframe. This would not have been achievable using the SRA field-based method for red rot screening. The reliability of the SBI rapid screening method meant that disease phenotype data was able to be collected from these clones with a low amount of random error. This resulted in a highly significant GWAS result (more than four orders of magnitude more significant associations than for any other trait measured in the project).

This highly significant GWAS result, combined with the relative genetic simplicity of disease traits compared to other traits, means that red rot genetic markers are likely to be one of the first outputs of this project to be translated into real industry applications in Australia and potentially India.

d. Is there any other information you wish to provide about your project? ☐ yes ☒ no

If yes, provide details.

[Insert text]