Pushing the frontiers of sugarcane improvement: a summary of the joint ISSCT 11th Germplasm and Breeding and 8th Molecular Biology workshops

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Abstract The 11th Germplasm and Breeding and 8th Molecular Biology joint Workshop was held in Saint-Gilles in Réunion Island from 1-5 June 2015 and hosted by eRcane. The theme of the Workshop was Pushing the frontiers of sugarcane improvement. It attracted 74 participants from 16 countries. There were 48 oral presentations, with half classed in the germlaspm and breeding section, and half classed in the molecular biology section. However, in many cases the distinction was not clear. There were also eight and seven posters for these sections, respectively. There were six discussion sessions: Germlaspm/introgression; Genome analysis; Breeding I; Physiology; Molecular genetics; Breeding II; Molecular biology/transgenics. A master class in statistical analysis of field-trial data, and a business session meeting for both sections combined were also held. Visits were made to eRcane breeding stations where participants gained an overview of the entire local selection scheme, including smut-resistance trials. Most delegates were in favour of holding future breeding and molecular biology workshops together, since there are many topics of common interest.

Key words Germlaspm, genome analysis, physiology, molecular genetics, breeding, molecular biology

INTRODUCTION

The 11th Germplasm and Breeding and 8th Molecular Biology joint Workshop was held in Saint-Gilles in Réunion Island from 1-5 June 2015 and hosted by eRcane. The local organizing committee consisted of Audrey Thong-Chane (eRcane), Laurent Barau (eRcane) and Jean-Yves Hoarau (eRcane/CIRAD). The workshop was attended by 74 delegates from 16 countries (Table 1). The theme of the workshop was Pushing the frontiers of sugarcane improvement.

Table 1. Country of origin and number of attendees of the 11th ISSCT Germplasm and Breeding and 8th Molecular Biology workshop.

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There were 48 oral presentations, with half classed in the germlaspm and breeding section, and half classed in the molecular biology section. However, there is a general trend for merging of molecular biology and breeding and germlaspm methods, and so in many cases the distinction was not clear. There were also eight and seven posters for these sections, respectively. Poster authors presented their work through short five-slide presentations. There were six discussion
OPENING

An informal welcome with a cocktail was held on the Sunday evening prior to the main technical program. The opening started Monday morning with a welcome from the local organizing committee, followed by a welcome from ISSCT by Jean Claude Autrey, who gave an overview of ISSCT. Bernard Siegmund, director of eRcane, gave an overview of the Réunion sugarcane industry and research and development based in Réunion. Phil Jackson for the Germplasm and Breeding committee section and Angélique D’Hont for the Molecular Biology committee section also gave brief introductions.

Emerging concerns among sugarcane industries worldwide about limited progress in productivity improvement in sugarcane, especially in comparison with some other crops, was mentioned. Opportunities opening up with new technologies such as DNA markers were highlighted and workshop participants were challenged to think of new ways to approach sugarcane improvement.

The program was arranged in six sessions: Germplasm/introgression; Genome analysis; Breeding I; Physiology; Molecular genetics; Breeding II; Molecular biology/transgenics.

GERMPLASM AND INTROGRESSION BREEDING

This session had 11 presentations from both the Germplasm and Breeding and the Molecular Biology sections and was chaired by Anna Hale and Phil Jackson.

Interest in enlarging the genetic diversity of cultivars through hybridization with wild species and genera was covered from a range of perspectives. This included improving sugarcane using wild relatives for various production systems based on energy and total biomass production. Interestingly, almost half of the presentations in this session reported on attempts to exploit the genus *Erianthus*. It seems that there is a renewal of interest for exploiting this genus. However, some participants expressed a view that there was too much emphasis or optimism put on using *Erianthus*, and more focus on *S. spontaneum* should occur.

Progenies from intergeneric crosses from *Erianthus* have now been routinely characterized with molecular markers and molecular cytogenetics, and this allows genuine hybrids to be identified, and chromosome composition and transmission between generations can also be studied. The main difficulty remains the lack of fertility of the F1 intergeneric hybrids. Based on the knowledge of the workshop participants, it seems that out of many attempts worldwide, only a very small number (3-5) verified and fertile F1 intergeneric hybrids have been obtained (in China and India). Different teams are exploiting various back-crosses from these hybrids, but so far there has been no commercially released cultivars to the knowledge of the workshop participants. BC4 progeny have been obtained and characterized: they contained very few chromosomes from *Erianthus* and sometimes chromosomes with an *Erianthus* segment and a *Saccharum* segment, attesting recombination or translocation between chromosomes from the two genera. The added agronomic value of introgressed *Erianthus* chromosomes still have to be demonstrated.

Interest in better exploiting the species *S. spontaneum* that displays a very large phenotypic variability and its relative ease in crossing with *S. officinarum* and cultivated material compared to *Erianthus* was stressed. It seems quite a number of programs have produced promising clones derived from recent introgression of *S. spontaneum*, and good results were presented, especially in cooler areas such as Japan and Louisiana. However, introgression of *S. spontaneum* is long-term and difficult particularly because of the adverse effects on sugar content. The potential role of DNA markers in identifying positive and negative parts of the introduced *S. spontaneum* genome was discussed.

GENOME ANALYSIS

This session had four presentations from the Molecular Biology section and was chaired by Angélique D’Hont.

The two first presentations reported on an international initiative to produce a sugarcane reference genome sequence based on the cultivar R570. Because sugarcane has probably the most complex genome of any crop plant with a complete set of homeologous chromosomes predicted to range from 10 to 12 copies, and a high level of heterozygosity, the assembly of the whole genome through the current shotgun approach would be very challenging. An alternative sequencing strategy
Based on the fact sugarcane displays a high level of microsynteny conservation and collinearity between sugarcane hom(ologous) chromosomes and with sorghum was reported. Based on a comparison with sorghum, a core set of 5,000 BACs that corresponds to the minimum set of BACs to be sequenced to obtain the best coverage of the gene-rich part of the sugarcane chromosomes was identified. Through international collaboration between CIRAD in France, CSIRO and QAAFI in Australia, SASRI in South Africa and the International Consortium for Sugarcane Biotechnology half of these BAC have already been sequenced.

In contrast Australian delegates reported on the production of whole genome shotgun (WGS) sequences from cultivar R570 and its use to attempt to assemble the genome and to identify SNP markers. CSIRO (Australia), in collaboration with Syngenta, reported on the development and test of a single nucleotide polymorphism chip based on the Affymetrix Axiom technology as a way to produce high-throughput markers. SNPs were selected using categories designed to maximize low-dose (single/double) markers that are the one exploitable for genetic mapping. Due to the difficulty in identifying low-dose SNP markers, a two-step approach was taken with the first chip containing 345 k SNPs. Then a subset of 70 k high-quality informative markers was selected for the production of a smaller SNP chip that will be more cost effective. Preliminary data for the screening of an association mapping population of 480 individuals across the 345 k SNP chip were presented.

SRA in Australia reported on the use of molecular cytogenetics to better understand the organization of the sugarcane genome. Progress on the use of molecular hybridization of BAC (= chromosome segment) on chromosomes (BAC-FISH) to determine the number of homologous chromosomes by chromosome categories was reported and seems very promising.

**BREEDING PART I**

The first breeding-focused session (chaired by Hermann Hoffmann) contained several presentations looking at a range of practical methodologies to either speed up or improve accuracy of data collection from selection trials. Because getting data from selection trials comprises the major effort in most breeding programs, it is important to try and improve routine methodologies. The use of near-infrared spectroscopy for analysis of cane samples in the eRcane program was presented (Roussel et al.), and delegates later viewed this methodology during the field tour. Presentations were also given on using soil-conductivity scanning methods to reduce error variation in field trials (work done by Wei et al., Australia), and use of software for crossing (Uchino et al.).

**PHYSIOLOGY**

Four presentations were made in this section chaired by Jershon Lopez: two focused on molecular methods, and two on whole-plant and crop-level physiology. Although there has been much work over many years on developing a better physiological understanding of sugarcane and its response to the environment, there are views that this has not translated very much into practical improvements in sugarcane breeding. Nevertheless, many people remain hopeful that physiological research will provide direction and opportunities for more targeted genetic improvement in future.

The two molecular presentations focused on using gene-expression analysis to characterize sugarcane responses to different stresses. The use of next-generation sequencing to analyse gene expression patterns is presenting new ways of understanding genotype by environment interactions. However, the technology is clearly immature with rapid progress being made. At this stage it is not clear what the best pathways and research approaches will be to deliver practical improvements to breeding programs. Different ways to analyse and look at the vast volumes of data that may be collected were presented.

The two whole-crop level presentations (from Australia) focused on responses of different genotypes to water stress. Despite water stress having a major impact on reducing yield, experiments have shown a high genetic correlation between performance under well-watered and water-stress conditions. It seems highly vigorous genotypes are favoured under a range of different water levels. Further, stomatal conductance (which is strongly related to photosynthesis rate) has been shown to be related to yield. Use of thermal imaging from unmanned aerial vehicles (drones) is being used in other crops to screen for conductance (which is negatively correlated with leaf temperature). This may offer a way to screen for vigorous and high yielding clones in early stages of selection when the plants are young and before severe interplant competition occurs that affects measurements of yield.
MOLECULAR GENETICS

This session, chaired by Jean Christophe Glaszmann, had eight presentations from the Molecular Biology section and a keynote presentation.

The keynote talk was given by Mark Sorrells from Cornell University Department of Plant Breeding and Genetics on ‘Genomic selection in plants: A new tool for crop improvement’ with emphasis on application of genomic selection to wheat breeding.

It is interesting to note that as for other crops sugarcane geneticists are moving from QTL detection study to Genome Wide Association Studies (GWAS) and Genomic Selection (GS) that should allow a more direct link with breeding programs. Some of this direction is being driven by the ability to screen genotypes relatively cheaply with massive numbers (50,000 or more) of DNA markers at the same time, using SNP chips or Genotyping by Sequencing (GBS) methods. Methods of data analysis are under rapid development at present, with applications in many different crop and animal species.

The Mauritian team reported on QTL analysis for resistance to yellow spot disease. Five presentations from teams from Australia, Argentina, Brazil, France and USA reported on attempt to use GWAS to analyze the genetic determinism of various characters. Two presentations from Australia and France were on experimental assessment of genomic selection in sugarcane.

BREEDING PART II

Six presentations, chaired by Nils Berding, covered a range of topics from breeding programs from different parts of the world. Two presentations focused on the breeding program in Réunion, where a theme was the contrasting types of environments being targeted in this program. There has been some success in directing the breeding program to target development of specifically adapted cultivars by using parents and selection systems focused on different sub-environments within the island. These environments vary from rainfed places with less than 1000 mm per year on the western part of the island up to very high rainfall zones (>3000 mm) on the eastern side. This theme was also addressed during the field trip in the workshop. Delegates also heard how the eRcane breeding program is supplying seeds from crossing (fuzz) to 10 selection stations in a range of countries in Africa, with the first cultivar released from this effort expected in 2016. Research and efforts to fine-tune the large crossing program of eRcane (supplying around 150,000 seedlings per year) were described.

A presentation was given about aspects of the huge Brazil sugarcane industry, focusing mainly on the highly successful RIDEISA breeding program (producing ‘RB’ named varieties and currently supplying about 64% of the Brazil sugarcane production), and how efforts in breeding programs could be redirected to produce sugarcane suited to bio-energy production involving production of biofuels from fibre as well as sugar.

It is worth noting that several years ago there seemed to be more interest in use of sugarcane fibre for production of biofuel, but now there is less interest, presumably because of the reduced oil price.

Efforts to develop varieties with high sugar content very early in the harvesting season in Mauritius were presented (Badalo et al.). This is being driven by an industry need to reduce costs and run sugar mills for a longer proportion of the year. It seems likely that new clones with higher early sugar content will arise from this program in coming years. The importance of foreign germplasm in breeding programs was emphasized in a presentation by Orozco et al. The high success of CP clones as parents was mentioned by several delegates, and this an interesting point. The use of family selection, and methods of data analysis used in selecting for the destructive borer Eldana saccharina in South Africa were also featured.

MOLECULAR BIOLOGY AND TRANSGENICS

Chaired by Erik Mirkov, this session had five presentations.

A presentation from Australia reported on test with the ShSUT1 transporter gene with the aim of increasing the amount of sucrose stored. Brazil reported preliminary result on Setaria viridis that suggest that a Multidrug and Toxic Compound Extrusion Family (MATE) gene isolated from Sorghum bicolor may have potential to increase aluminium tolerance in
sugarcane. A Colombian team reported on the expression of glutamine synthetase in the context of ammonium and nitrate assimilation confirming that sugarcane capture nitrogen in the roots assimilating both nitrate and ammonium efficiently.

A team from Argentina highlighted the usefulness of UPOV traits together with molecular markers for early selection of transgenic events that closely resemble their parental genotypes. In the context of improving knowledge to support risk assessment for deployment of GM sugarcane varieties, a presentation was made by an Australian team on new findings on physiology of sugarcane seed and seedlings and their ability to overcome the constraints to survival in and around sugarcane fields.

**DISCUSSION SESSIONS**

**Use of wild germplasm and introgression breeding (chaired by Anna Hale and Phil Jackson)**

The difficulty and risk in undertaking introgression breeding, and the potential role of DNA markers to assist with sorting out positive and negative genome components during selection and backcrossing, and the potential value in international cooperation and exchange in introgression breeding and development of parents were discussed.

There was discussion about the status of international germplasm collections. It was noted that an additional ISSCT sanctioned germplasm collection was being established based in Brazil, hosted by Institute of Campinas (IAC) of the São Paulo Agribusiness Technology Agency, a research entity of the Department of Agriculture and Supplies of the state of São Paulo, Brazil.

As with previous workshops, some concerns were expressed at accessing germplasm from the Indian collection, as well as a hope that we could have better communication and participation by Indian breeders in international meetings, for mutual benefits.

**Can we agree on an international set of SSR for sugarcane variety identification? (chaired by George Piperidis)**

A survey was conducted prior to the workshop to collect information on the number of labs using SSRs for variety identification, and the primers that are being used for this purpose. With the advent of new improved platforms for revealing SSR markers and advanced software for allele identification, it was considered an opportune time to follow up on previous investigations.

The response to the survey was very positive, with 11 laboratories from seven countries providing the information requested. Summary details of the survey were presented at the workshop. A total of 46 gSSRs (five labs) and 10 EST-derived SSRs (six labs) were reported. It was clear from the discussion session that there is a strong interest in developing a standard set of primers for sugarcane variety identification. The most commonly used SSRs, CV29, CV37, CV38, mSSCIR14, mSSCIR19, SMC119CG, SMC36BUQ, SMC278CS, and SMC222CG were proposed as a standard set of primers for further investigation.

It was also suggested during the discussion that the DNA fingerprints of major varieties could be stored in the Variety Notes database on the ISSCT website for future reference.

**Molecular-marker system and application (chaired by Karen Aitken)**

Because sugarcane has a very large genome due to its high polyploidy, a very high number of markers is required to cover the entire genome for genetic analysis. The most informative markers for genetic mapping are single-dose markers (present on only one of the 10-12 homeologous chromosomes) but they are relatively rare. Hence, the genetic maps obtained so far are all partial due to insufficient number of single-dose markers.

Various technologies are being tested to try to increase the coverage of the genome with markers for genetics studies. The Australian group are testing DArT and SNP markers (the latter in partnership with Syngenta), while CIRAD and Mauritius are testing Genotyping by Sequencing (GBS and RADseq) and USDA is testing capture sequence. The promising use of genomic selection methods (which was the topic of focus of our invited speaker) was discussed. This has a possibility of changing sugarcane breeding in the future, possibly through rapid recurrent selection of clones based on breeding value.
Germplasm exchange (chaired by Goolam Badaloo)

It is well recognized by breeders around the world that germplasm exchange is highly beneficial, and in fact all breeding programs are based on introduction and exchange of basic or improved clones. However, different breeding programs currently place different emphases on exchange, with some programs vigorously seeking access to elite cultivars from other countries through regular exchanges, while others do not put a high priority on this. It seems in general that exchange of clones from different countries has impacted in many cases more strongly through the use of the introductions as parents rather than direct releases as cultivars. This presumably reflects the fact that at least some local selection is needed to address some specific local issues or environmental factors. In Australia, SRA breeders highlighted that about 50% of all cultivars released in recent decades are derived from parents that are foreign cultivars. The VISACANE initiative by CIRAD (presented by Guinet-Brial) seems to be providing a great service which may be increasingly used in the future. This service provides quarantine and ‘clean up’ of clones, which requires specialist and high-level pathology and molecular skills, which many programs and companies lack. It was suggested that perhaps in the near future, or even currently, molecular techniques could replace visual observations and greatly reduce quarantine times for exchange. The scope to exchange true seeds was discussed – however, there is still some uncertainties about whether viral diseases may be passed through seeds, and some investigations into this are being conducted (USA).

The desire to better understand what causes apparently large genotype by country interactions (i.e. why some varieties are outstanding in one country but extremely poor in another that has apparently similar climate and diseases) was raised, as this issue has long puzzled many breeders. This may be an interesting topic for international cooperative research.

FIELD TRIP

Delegates visited breeding activities conducted by eRcane that breeds and selects sugarcane varieties for the industry of Réunion Island (25,000 ha, 2 mills). The local industry encompasses numerous different agro-climatic zones (from leeward to windward coasts, from sea level up to highlands). In the morning participants went on a field visit to two experimental stations located in contrasted environments: at Vue-Belle station (West zone, 700 m altitude, thermal stress, water deficit), an overview of the entire local selection scheme was presented (operational organization and selection practices) from seedling stage to final regional trials. At Etang-Salé station (South dry coastal area with drip irrigation), the visit focused on smut resistance selection trials conducted in close collaboration with the CIRAD Phytopathology Unit, and on agronomic practices within selection fields. In the afternoon participants visited facilities and central laboratories of the eRcane headquarters (La Bretagne, North). Facilities and practical organization of breeding and seed sowing campaigns (glasshouses, flower lab and germination chamber) were presented. The routine potential of eRcane is 150,000 seedlings per year obtained with about 2,500 sexual combinations. A relatively small breeding team operates safely all breeding and sowing tasks within a short period of time (3 months) thanks to the use of an efficient tracking barcode system dedicated to the entire production pipeline (from the collection of flowers in the fields up to seedlings trays ready to be transplanted in five different regional nurseries). A laboratory equipped with a semi-automatic near infra-red spectroscopy (NIRS) device (a Brucker Matrix-F and linked CPS conveyor) dedicated to fresh cane analysis allowed routine assessment of the cane quality at a much higher work rate than the previous conventional method (two operators working 3 days a week during 5 months and handling a total of 10,000 analyses). Delegates visited also the green chemistry laboratory of eRcane and its bio-refinery pilot unit dedicated to the valorization of molecules of economic interest within sugarcane by-products.

FINAL DISCUSSION

Chairied by Phil Jackson and Angélique D’Hont, a range of topics were raised and discussed, including:

- The potential for an international partnership and sharing in introgression and parental improvement programs. Louisiana team witnesses to the production of recent promising results with *S. spontaneum* introgression work for commercial production adapted to its typical cold weather conditions.

- The need for sugarcane breeding programs to think about new approaches, since it seems the general breeding schemes used for the last 40-50 years are not giving large improvements to yield and sugar content (although maintaining disease resistance). In this context the potential for breeding schemes like reciprocal recurrent selection that can capture and enhance non-additive genetic effects could be of value. It was noted that a few specific crosses in sugarcane breeding programs can deliver many good cultivars – emphasizing the importance of combinations of genes in delivering high genetic value.
The potential for genomic selection methods to assist in achieving genetic gains. The interesting developments in other crops and animals was noted, and some groups are progressing in this area in sugarcane.

The possibility to better sharing data, particularly DNA marker data, across programs, for mutual benefits.

Some ways in which ISSCT could assist with international communication (covered below).

BUSINESS SESSION

A session jointly covering both the Germplasm and Breeding, and Molecular Biology sections was held. During this discussion, it was suggested for the next workshop to have fewer presentations but longer. It was also suggested that perhaps more review-type presentations could be done, particularly reviews of molecular technologies and that presentations should accommodate that it was a joint meeting with breeders and molecular biologists. Most delegates were in favour of holding the breeding and molecular biology workshops together, since there are many topics of common interest and it is well recognized that in genetic improvement the line between breeding and molecular biology is increasingly overlapping.

It was proposed to scan all the ‘breeding newsletters’ and make them publicly available since they contain very interesting information but are not easily accessible.

The initiative to put ‘Variety Notes’ online was discussed. ‘Variety Notes’ is based on the concept (originally developed by Rossi Machado, Brazil) who produced a book that documented all the major sugarcane cultivars from around the world. Data on current cultivars is being collated (currently data from >40 countries has been collated) and has been placed on a website (http://www.sugarcanevariety.org) linked to the ISSCT homepage. It is planned that this site will continue to be developed in coming years, be collectively maintained by members of the Germplasm and Breeding section of ISSCT (with inputs from sugarcane breeders around the world) and provide information helping support international exchange of varieties.

It was suggested that the Germplasm and Breeding section could play a more active role in standardizing some protocols (e.g. naming varieties, methodology) and that a website could help communicate and facilitate this.

It was propose to again have a joint meeting breeding/germplasm and molecular biology for the next workshop. Two countries propose to host the meeting: Japan and Fiji.

ACKNOWLEDGEMENTS

The joint ISSCT 11th Germplasm and Breeding Section workshop and the 8th Molecular Biology workshop was hosted by eRcane. We thank all those staff involved in organizing this event, particularly Camille Viot, and the technician teams assisting with the visits of Vue-Belle, Etang-Salé and La Bretagne stations.

Repousser les frontières de l'amélioration variétale: un résumé de l'atelier conjoint de l'ISSCT entre le 11ème atelier germoplasme et amélioration variétale et le 8ème atelier de Biologie Moléculaire

Résumé. L’atelier conjoint de l’ISSCT entre le 11ème atelier germoplasme et amélioration variétale et le 8ème atelier de Biologie Moléculaire, organisé par eRcane, s’est tenu à Saint-Gilles, l’Île de la Réunion, du 1 au 5 juin 2015. Le thème de l’atelier était Repousser les frontières de l'amélioration variétale. Elle a attiré 74 participants de 16 pays. Il y a eu 48 présentations orales, avec la moitié tombant dans la section germoplasme et amélioration variétale, et l’autre moitié dans la section de biologie moléculaire. Cependant, dans bien des cas, la distinction n'était pas claire. Il y avait aussi huit et sept affiches pour ces deux sections, respectivement. Il y avait six séances de discussion: le germoplasme/introgession; analyse du génome; amélioration génétique I; physiologie; génétique moléculaire; amélioration génétique II; biologie moléculaire/transgénomique. Une session de formation niveau Masters traitant l’analyse statistique des données, et une session d'affaires pour les deux sections regroupées ont également eu lieu. Des visites ont été effectuées aux stations de sélection d’eRcane où les participants ont eu un aperçu de l'ensemble des travaux de sélection menés par eRcane, y compris les essais de résistance au charbon. La plupart des délégués sont d’avis, qu’à l’avenir, des ateliers conjoints germoplasme et amélioration variétale et biologie moléculaire devraient avoir lieu en raison des sujets d’intérêt communs.

Mots-clés: Germoplasme, analyse du génome, physiologie, génétique moléculaire, amélioration variétale, biologie moléculaire

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Expansiendo las fronteras del mejoramiento de la caña de azúcar: un resumen de los talleres conjuntos de la ISSCT 11avo de germoplasma y mejoramiento y octavo de Biología Molecular

Resumen. El taller conjunto onceavo de Germoplasma y Mejoramiento y octavo de Biología Molecular se llevó a cabo en Saint-Gilles en la isla Reunión del 1 al 5 de junio de 2015 y fueron organizados por eRcane. El tema del taller fue expandiendo las fronteras del mejoramiento de la caña de azúcar. Atrajo a 74 participantes de 16 países. Hubo 48 presentaciones orales, con la mitad clasificadas en la sección de Germoplasma y Mejoramiento, y la otra mitad clasificadas en la sección de Biología Molecular. Sin embargo, en muchos casos, la distinción no era clara. También hubo ocho y siete posters para estas secciones, respectivamente. Hubieron seis sesiones de discusión: Germoplasma/introgresión; análisis del genoma; mejoramiento I; Fisiología; Genética molecular; mejoramiento II; Biología molecular/transgénicos. También se llevó a cabo una clase magistral del análisis estadístico de datos de ensayos de campo, y una reunión para ambas secciones combinadas. Se hicieron visitas a las estaciones de mejoramiento de eRcane en los que los participantes obtuvieron una visión general de todo el sistema de selección local, incluidos los ensayos de resistencia al carbón. La mayoría de los delegados estuvieron a favor de la celebración de futuros talleres de mejoramiento y biología molecular en conjunto, ya que hay muchos temas de interés común.

Palabras clave: Germoplasma, análisis del genoma, fisiología, genética molecular, mejoramiento, biología molecular