ADVANCES AND CHALLENGES IN SUGARCANE BIOTECHNOLOY AND PLANT PATHOLOGY: A REVIEW OF THE IX PLANT PATHOLOGY WORKSHOP AND VI MOLECULAR BIOLOGY WORKSHOP

By

J.C. COMSTOCK[1], A. DOOKUN-SAUMTALLY[2], B. CROFT[3], A. D'HONT[4], F.F. GARCES OBANDO[5], E. MIRKOV[6], G.P. RAO[7], S. SAUMTALLY[2], G.M. SOUZA[8] and D. WATT[9]

[1]*USDA-ARS Sugarcane Field Station, 12990 Highway 441, Canal Point, Florida 33438, USA*
[2]*MSIRI, Réduit, Mauritius*
[3]*BSES, 90 Old Cove Rd, Woodford Qld 4514, Australia*
[4]*CIRAD, Avenue Agropolis, 34398 Montpellier Cedex 5, France*
[5]*CINCAE-FIADE, Elizalde 114 y Malecon, Casilla letra S, Guayaquil, Ecuador*
[6]*Texas A&M University Agricultural Experiment Station, Weslaco, Texas, USA*
[7]*Sugarcane Research Station, Kunraghat, Gorakhpur UP, India*
[8]*Instituto de Quimica, University of Sao Paulo, Sala 1208, Sao Paulo, Brazil*
[9]*SASRI, Mount Edgecombe, South Africa*
jack.comstock@ars.usda.gov
adookun@msiri.intnet.mu

KEYWORDS: **Diseases, Plant Resistance, Genetic Mapping, Molecular Characterisation, Transgenics.**

Abstract

FOR THE second time, the International Society of Sugar Cane Technologists (ISSCT) pathology and molecular biology workshops were jointly held, from 23–27 June 2008 in Cali, Colombia. The meeting was hosted by CENICAÑA and organised by Jorge I. Victoria and Jershon López-Gerena. The response of participants was positive with 44 delegates representing 15 countries attending. Thirty seven oral presentations and ten posters covering a wide range of topics including molecular characterisation of yeasts, insect pests and pathogens, genetic transformation of sugarcane, molecular markers, genetic mapping, pathogen variability, disease diagnosis, plant resistance and disease epidemiology among others were presented. The workshop also provided the opportunity to listen to three plenary talks on biofuel production, transgenics and nutritional improvements in food crops through genomics. A special session was devoted to orange rust, a newly introduced disease in Florida and in Central America. Following the technical sessions, site visits were organised during two days to sugar mills, commercial fields, plots with transgenic sugarcane, and laboratories at CENICAÑA. The experience of having joint-section meetings proved very useful with excellent interaction among participants.

Introduction

The ISSCT IX Pathology Workshop and VI Molecular Biology Workshop were organised jointly in 2008. The workshops were hosted by the Colombian Sugarcane Research Centre (CENICAÑA) from 23–27 June 2008 at the Radisson Royal Hotel in Cali, Colombia. It was organised by Drs Jorge I. Victoria and Jershon López-Gerena. The Workshops were well attended by 44 participants, with 39 of them coming from overseas – Argentina (4), Australia (4), Brazil (3), Ecuador (1), France (3), Guadeloupe (2), Guatemala (2), India (2), Mauritius (2), Nicaragua (2), Panama (1), South Africa (2), USA (9), Venezuela (1) and Zimbabwe (1) – and 5 from Colombia.

Apart from three plenary talks on biofuel production in Colombia, transgenics and the role of genomics to improve nutrition in food crops, 37 verbal and 10 poster presentations were made during 11 sessions. The topics covered during the workshop were diverse. Site visits were organised during two days to sugar mills, commercial fields, plots with transgenic sugarcane, and laboratories at CENICAÑA.

Molecular characterisation of yeasts, insect pests and pathogens

In Colombia, ethanol production within the sugar industry is rapidly expanding, and is being driven primarily by price regulation and tax incentives from government. Although production is based on technology imported from India, efforts are being made on several fronts to adapt the technology to suit local conditions. Research focused on the isolation of wild yeast strains that have the potential to out-perform commercial yeasts. Biochemical and molecular characterisation of 18 isolates revealed that 10 of them were *Saccharomyces* and were capable of fermentative respiration to produce ethanol. All of the ethanol-producing isolates could tolerate ethanol concentrations of 12% (v/v) and were at least as efficient as commercial strains.

The Colombian sugar industry has a long and proud history of successful biocontrol of sugarcane pests and the insect vectors of pathogens. A strategy was reported to reduce the negative impact of the yellow sugarcane aphid (*Sipha flava*), which reportedly reduces sugar yield (tonnes sucrose/ha) by up to 52%. Currently, the effects of this pest are minimised by insecticide application, host plant resistance and natural predation. Attempts at biocontrol have been made through the introduction of commercially reared North American lacewings (*Chrysoperla* spp.), but release results were erratic and difficult to interpret. Consequently, researchers at CENICAÑA are searching for local lacewings that may serve as more effective biocontrol agents of the aphid. Molecular technologies were used for the analysis of the lacewing phylogeny and 11 chrysopid morphotypes have been found. These findings will serve as the foundation for the development of a biocontrol mechanism against the yellow sugarcane aphid.

A molecular and morphological diversity study based on the sequence of the mitochondrial cytochrome oxidase gene, *COII*, from 108 borer specimens collected along the Cauca Valley, in Colombia, was carried out in 2005 to determine possible new races of the three borer species in the region: *Diatraea saccharalis*, *D. indigenella*, and *Blastobasis gramineae* that may explain recent borer population increases in the region. *D. saccharalis* was found to be the main species behind the outbreak, and there were no new races that explained the recent borer outbreak, according to genetic differentiation indices based on PCR-RFLP and sequence of a *COII* gene fragment. Changes in climate or agricultural practices may explain the outbreak. A survey in 2006 indicated that the borer population has decreased after control practices were further implemented.

Genetically modified sugarcane

In Argentina, regulatory framework governing the commercial release of genetically modified (GM) crops encompasses both food safety and environmental issues. Concern exists over the potential of GM crops becoming weeds or crossing with wild species that have the potential to become weeds. As *Saccharum spontaneum* exists as naturalised populations in Argentina, consideration of the potential for transgene spread from GM *Saccharum* spp. hybrid crops is essential. The low temperatures (10–12ºC) experienced in Argentina in the period prior to anther opening (June and July) were believed sufficient to suppress male fertility. However, it was revealed that, during June to August 2006, fertile sugarcane pollen was detectable in the northern regions of the Argentinean industry (between S 23°16’ and S 24°50’), although prevalence decreased southwards, such that no fertile pollen was detected between S 26°30’ and S 27º55’. The unexpectedly high pollen fertility encountered in the northern regions was ascribed to unusually warm winter conditions. It is important to note that final interpretation of these observations and the impact that they may have on the assessment of the risk of transgene spread in Argentina will require assessment of pollen longevity, distance of dispersal and, ultimately, seed viability.

Many institutes involved in GM sugarcane research are seeking ways to simplify and speed-up the transformation process, as well as to reduce somaclonal variation that sometimes results from tissue culture. Efforts to reduce time in culture, viz. through imposition of a 1–2 week post-bombardment callus induction period where selection was restricted to the regeneration phase, resulted in plants with chimaeric phenotypes. Researchers at Chacra Experimental Agricola Station, in Argentina, proposed that insufficient selective growth of transgenic cells in the absence of a callus selection phase yields heterogenic masses of both transformed cells that develop into chimaeric embryos, which regenerate under non-stringent geneticin selection protocols. That group aims to further refine minimal culture and selection requirements, which will reduce or eliminate chimaeras.

In Brazil an attempt was made to evaluate stress-inducible production of proline in transgenic sugarcane. Researchers expressed into sugarcane the heterologous P5CS gene (for proline biosynthesis) from the drought resistant bean, *Vigna angustifolia*, under the control of the synthetic stress-induced AIPC promoter. A series of transgenic events with 1–4 insertions was generated and, upon drought stress, the proline content was on average 2.5 times higher than in the controls, and this led to good drought tolerance. It was determined that the mode of action was not due to osmotic adjustment but, instead, related to a component of oxidative defence system.

In Australia, *Agrobacterium*-mediated and biolistic methods for transformation of sugarcane were compared. Several parameters were tested in transient assays to optimise *Agrobacterium*-mediated transformation of embryogenic callus of the variety Q117. *Agrobacterium* strains LBA4404 and AGL1, and a pCambia vector with GUS as the reporter gene under the control of the CaMV 35S promoter were used. Vacuum infiltration worked well for transient expression. Further optimisation was done with AGL1 and it was found that dilution of the *Agrobacterium* cultures to an O.D. of 0.4 was best as was a 4-day co-cultivation period on EM3 medium. However, no transgenic plant was regenerated, and constructs using the maize Ubi 1 promoter rather than the CaMV35S promoter were produced and generated over 200 plants. Most of the plants had only 1 or 2 insertion events. In a comparison between *Agrobacterium* and biolistic methods for expression levels, the biolistic approach led to much higher expression levels, but there was no correlation with copy number.

Molecular markers and genetic mapping

Microsatellite primers were used to DNA fingerprint varieties in Colombia and in USA, and DNA databases are being built. The intended use of these databases includes identification of mislabelled parental clones, as molecular descriptors for newly released varieties determine genetic relatedness of elite clones, assessing the quality of crosses, and identifying F1 hybrids from crosses with wild germplasm.

In South Africa, progress was reported to identify the key control steps in sucrose accumulation in sugarcane. Early work focused on changes in gene expression, biochemistry, and physiology occurring along internode maturation in one or a few varieties with different sucrose accumulation capacities. Gene expression studies moved to focus on key metabolic pathways identified by subtractive DNA libraries and boutique arrays. A small set of candidates was identified, and some of them studied on transgenic plants grown in the field. Currently, physiological evidence points to source-sink communication as crucial to sucrose metabolism, where feedback inhibition between sucrose concentration in the culm and leaf photosynthesis limits further accumulation of sucrose. New candidate genes will be tested via simple and stacked transgenic approaches to attempt unlocking the key to sucrose accumulation.

Also in South Africa, the potential of combining two relatively new PCR-based marker systems, Targeted Region Amplified Polymorphism (TRAP) and Motif-Directed Profiling (MDP) into a high-throughput hybrid system to generate polymorphic markers around targeted candidate gene sequences for smut resistance, was explored.

In Colombia, QTLs for sugar content and biomass components were identified in a population of 300 individuals from a cross between a high sugar content cultivar and a low sucrose cultivar.

In Mauritius, efforts were deployed to detect QTLs for yellow spot disease resistance. The foundation of the study was a bi-parental cross between a resistant and a susceptible parent, which generated 227 progeny with a segregation pattern for yellow spot infection suggestive of monogenic dominant inheritance (3:1). A genetic map of variety M 134/75 was constructed using 764 single-dose polymorphisms assigned to 102 linkage groups, each of which contained at least two markers in coupling. QTL analysis by means of QTLCARTOGRAPHER v1.17d and MAPMAKER/QTL v1.1 identified a major QTL located on Linkage Group 87, flanked by an AFLP and SSR marker.

Work from CIRAD in France provided evidence of a major dominant gene *Bru1*, conferring brown rust resistance, identifed in cultivar R570 to confer resistance to eight isolates from Brazil, Colombia, Zimbabwe, USA (Florida), Réunion and Guadeloupe. The target haplotype map encompasses 15 markers that co-segregate with *Bru1* and markers, and the physical map encompassing 16 BAC clones was discussed. The markers surrounding *Bru1* in R570 were surveyed in nearly 400 international sugarcane cultivars and were also phenotyped for rust resistance in Réunion and Guadeloupe islands and found that *Bru1* was present in most of the resistant cultivars. Only 7% of them did not display the Bru1 haplotype, and thus they represent alternative sources of resistance to the rust pathogen. The PCR marker in perfect linkage disequilibrium with *Bru1* can also be used as a diagnostic for the presence of *Bru1* in experimental sugarcane cultivars.

Preliminary results regarding tagging alleles involved in *X. albilineans* leaf infection resistance were reported by Hoarau and collaborators from CIRAD, Guadeloupe. The authors used a large unstructured population of 198 sugarcane clones that was recorded for severity of leaf symptoms, and 700 polymorphic AFLP markers. A set of six markers explained 31% of the total phenotypic variation in necrotic leaf symptom intensity. This first insight into *X. albilineans* leaf colonisation resistance needs to be continued with additional markers to further tag sugarcane alleles involved in this resistance.

Leaf scald disease

Results of a proteomics approach to study sugarcane's reaction to infection by *Xanthomonas albilineans* were presented by researchers from Lousiana State University, USA. They used a differential protein expression analysis based on 2-dimensional electrophoresis using one resistant (Ho 95-988) and one susceptible (CP 89-846) sugarcane variety and compared protein profiles from infected and non-infected plants. Proteins that were differentially up and down-regulated in the susceptible and resistant varieties were found.

Leaf surface colonisation and stalk infection by *Xanthomonas albilineans* of sugarcane was determined in varieties grown under high rainfall conditions in Guadeloupe. The *X. albilineans* colonisation of sugarcane leaf surface after aerial spread of the pathogen varied according to the host cultivar. The stalks of two (out of 8) sugarcane varieties that exhibited the highest leaf surface populations were also the most infected by *X. albilineans*. Additionally, severity of leaf necrotic symptoms was correlated with intensity of leaf colonisation. It was also concluded that resistance of sugarcane to leaf scald appears to be controlled by several mechanisms, from leaf surface colonisation to stalk colonisation. It was noted that only a few reports of aerial spread of *X. albilineans* have been reported in Florida, USA, Guadeloupe and Mauritius and that possible recovery from stalk infection from one crop cycle to another could occur. The importance of high temperature on leaf scald symptom progress and severity was discussed

Viruses

The first large-scale survey of the causal agent of sugarcane mosaic in Argentina and neighbouring regions was made. This survey was undertaken to determine the mosaic virus

population present in Argentina and to improve control of mosaic with transgenic plants. Five hundred and twenty two plants showing mosaic symptoms were analysed by RT-PCR, and leaves were sampled from 111 sites and 106 sugarcane varieties. The majority (95%) of samples from Argentina were infected by *Sugarcane mosaic virus* (SCMV). *Sorghum mosaic virus* (SrMV) was found in only 1.5% of the samples. SCMV was present in the 35 samples from Bolivia and Uruguay. Both SCMV and SrMV were detected in symptomatic plants from Paraguay, but only a few samples originated from this country. Some samples (4.4%) from Argentina tested negative for SCMV and SrMV and the virus present in these samples remains to be determined.

Mike Grisham described the virus strains causing sugarcane mosaic symptoms in Louisiana and Florida, USA. No SCMV was found in Louisiana and no SrMV in Florida. In Louisiana, strains of SrMV present were: SrMV-I, 66%, SrMV-H, 14% and SrMV-M 6%. In 7% of samples, RFLP analysis indicated that the strain was different from strains H, I and M. Furthermore, an unknown strain was present in 10% of samples showing mosaic symptoms, suggesting the presence of another virus causing mosaic in Louisiana. In Florida, only SCMV-E was observed in symptomatic samples. No *Sugarcane streak mosaic virus* (SCSMV) was detected in samples from both States. The results of this study showed that there has been a shift in the strain profile in Louisiana since 1990–1995, when SrMV-H was most abundant (90%), followed by SrMV-I (10%) and SrMV-M (3–5%). The difference in the strain distribution of Florida and Louisiana could not be explained. It was felt that there is a need to investigate the genetic diversity of SCMV internationally.

In Mauritius, a sensitive detection technique for *Sugarcane yellow leaf virus* (SCYLV) using real-time fluorescent Taqman ® RT-PCR assay was developed. This was found to be 100x more sensitive than conventional RT-PCR. This method allowed the simultaneous detection of the virus and an internal sugarcane positive control. The internal positive control increases the reliability of the test by eliminating false negatives. Also, genetic diversity studies using a two-step RT-PCR showed the presence of the REU genotype of the virus, predominantly, as well as CUB and BRA-PER genotypes in the Mauritian sugarcane germplasm collection. Mixed infection of REU with either CUB or BRA-PER genotype was also present.

Also in Mauritius an island-wide survey for the presence of SCLYV in 22 commercial cultivars revealed that 58.8% of the over 3000 samples were infected with the virus. The incidence of infection ranged from zero in variety M 1176/77 to 100% in variety R 579. Severe symptoms were observed in varieties M 695/69, M 52/78, M 387/85, M 1186/86, M 1400/86, M 2004/88, M 703/89, M 2593/92, R 570, R 573, and R 575, but did not correlate closely with the presence of the virus. The presence of the aphid vector, *Melanaphis sacchari* was low and the spread of the virus was thought to be primarily by seed cane.

The incidence of SCYLV was compared in the two geographically close islands of Guadeloupe and Martinique. Infection was lower in Guadeloupe, although the vector population and cultivated varieties were the same. In Guadeloupe, the REU genotype predominated over BRA-PER. In Martinique, BRA-PER was more important and sometimes with mixed infection of REU. The differences observed between the two islands suggest the occurrence of local effects and interactions.

In Ecuador, from 2001 to 2005, the incidence of SCYLV increased dramatically. Yield trials using disease-free plants obtained via meristem culture had 20% more cane production and 36% more tonnes sucrose per hectare (TSH) than infected plants. Plants treated with insecticides increased yields compared to untreated plants. The best method of control was a combination of using virus-free plants derived from meristem culture along with systemic insecticides.

Studies at CIRAD indicated that, of the four different genotypes of SCYLV, diagnosis of the CUB genotype was the most difficult with the available primers. New primers were developed that allowed detection of all isolates of CUB genotype. The distribution of CUB isolates is being investigated using the newly developed primers.

Evidence was presented by research carried out in Australia that the causal agent of Ramu stunt disease is a virus. Viral preparations from infected leaves showed a 36-kDA protein to be consistently detected and isometric viral particles were observed from the infected cultivar Ragnar. Sequences of RNA with homology to viral RNA-dependent RNA polymerase have been cloned. A test that can detect a 1 kb RT-PCR product in leaf RNA extracts and the insect vector has been developed for the disease.

Phytoplasmas

In India, nucleotide sequence analysis of the 16SrRNA gene and the 16S/23S rDNA established that sugarcane grassy shoot (SCGS) phytoplasma is closely related to that of sugarcane white leaf (SCWL) disease. The two sugarcane phytoplasmas share a 97.5–98.8% homology with respect to their 16S rDNA sequences. SCGS phytoplasma was also found to belong to the rice yellow dwarf phytoplasma group. In contrast, sorghum grassy shoot phytoplasma was more distantly related to SCGS. Nested PCR was required to reliably detect SCGS. Resistance to the disease was found to be present among cultivated varieties.

The occurrence of sugarcane yellows phytoplasma (SCYP) associated with yellow leaf syndrome (YLS) exhibiting symptoms of sugarcane leaf yellows and yellowing of midribs was also reported in India. A phytoplasma characteristic ~0.840 kb rDNA PCR product was amplified from DNAs of all infected sugarcane leaf samples but not in healthy sugarcane plants tested using phytoplasma universal primer pairs P1/P7 and fU3/rU5. RFLP analysis of PCR products with *Hae* III and *Hha I* endonuclease generated fragment profiles that were identical for all the samples. The 16S rRNA sequence of the Indian SCYP isolate (EU170474) showed the closest identity (99%) with that of SCYP isolate in Cuba identified in *Macroptilium lathyroides* (AY725233) and other grasses like *Cynodon dactylon* (AB052871), *Conyza canadensis* (AY 725231) and *Sorghum halapense* (AY 725232), which belong to 16SrXII (Stolbur group). This was the first report of 16SrXII group phytoplasma affecting sugarcane in India.

Smut

With the introduction of sugarcane smut (*Ustilago scitaminea*) into Queensland in Australia in 2006, a smut-screening program started there, as it was clear that the disease could not be eradicated. The proportion of smut-resistant clones increased from 0.4% in 2000 to 52% in 2007.

Spore traps were used to detect sugarcane smut spores in areas prior to the visual detection of the disease. Initially, smut spores were identified by visual inspection of the collection tapes. Because of dirt particles and other spores, visual confirmation was slow and difficult. A DNA extraction and PCR-based assay method was developed that allowed easy confirmation of the presence of smut spores.

In several sugarcane growing areas, smut was identified on the tape samples prior to the actual visual observation of smut whips in the same areas. The confirmation of the aerial spread of smut into areas where smut had not been observed helped to influence growers to shift to smut-resistant varieties.

Although smut spores are a major method of spread of smut over long distances, their survival is influenced by temperature and moisture. Studies showed that spores germinated under temperatures ranging from 12 to 36°C. Under moist conditions, smut spores survived only for short time periods (2–3 months) in the soil, sugarcane trash and in the laboratory. However, survival of smut spores under dry conditions is greatly extended. Smut spores will survive for up to 6 months on machinery and on cotton clothing, and these mechanisms could, in theory, spread the pathogen.

Rusts

The epidemiology of brown rust (*Puccinia melanocephala*) in Louisiana was discussed with major emphasis on yield losses, resistance and fungicidal control. The magnitude of demonstrated losses strongly suggested that the application of fungicides be explored. Strobilurin fungicides were found more effective than triazole fungicides in reducing rust severity and yield losses. However,

combinations of these two fungicide types were superior. Two applications of fungicides can provide better economic benefits against rust incidence and infection severity. However, further research is required for the time and mode of application of fungicides against rust infection for maximum economic benefit, and research is in progress. Until now, host resistance is the most desirable control method of brown rust in Louisiana, but adaptability of the pathogen and problems in regular replacement of commercial sugarcane varieties in sugarcane are the major hurdles.

In Colombia, brown rust severity has increased on resistant varieties (CC 85-92, CC 84-75, CC 93-3895, CC 92-2804 and CC 94-5827) during the last 2 years. No molecular variation in the rust pathogen was observed using ITS 1F/ ITS4 primers and restriction enzymes (*ALU I* and *Hinf I*). More genomic regions in the rust pathogen are being evaluated. The reason for the increased severity of rust symptoms is unknown. Based on microscopic evaluation, only the brown rust pathogen was present. Based on the differences in rust symptom expression, it is assumed that a new race may be present.

Until 2007, orange rust (*Puccinia kuehnii*) had been observed only in Australia, Philippines, Indonesia and Papua New Guinea. In Australia it was considered as a minor disease until an epidemic occurred in 2000 and caused millions of Australian dollar losses to the sugar industry there. Then, in 2007, orange rust was confirmed in Florida (USA), Costa Rica, Guatemala, Nicaragua and Panama. In Guatemala, the presence of sugarcane orange rust (*Puccinia kuehnii*) was detected in September 2007. The disease was found to be widespread on CP 72-2086 with low severity of symptoms.

Concerns were expressed over the appearance of the disease in the American continent, and ways and means to counteract the disease were discussed including the replacement of susceptible commercial varieties and the identification of resistant parents for crosses.

New techniques

The usefulness of tools applied in precision agriculture to plant pathology was explained by the group of researchers from Louisiana, USA. The influence of environmental conditions and cultural practices on the incidence of brown rust was investigated. Infection was found to be positively correlated with soil properties, particularly the levels of phosphorus and sulfur. It was deduced that excess fertiliser applications could bring about a higher rust incidence and thereby negatively affect sucrose and cane yields. Remote sensing using a fibre optic spectrometer was utilised to determine leaf infection by SCMV or SrMV. Analysis of mild and severe SCMV leaf reflectance measurements were correctly classified in 75 and 68% of the cases, respectively. Leaves infected by SCYLV were correctly identified 77% of the time.

Conclusion

The workshop was very successful and the quality of work presented by participants was high. It is evident that a number of important and significant advances have been made recently both in the field of sugarcane pathology and biotechnology since the last workshops. The ISSCT sponsored workshops have played a major role in advancing the knowledge, cooperation and technology of sugarcane scientists. The attendees of the Workshop thank Drs Victoria and López-Gerena and CENICAÑA for hosting this excellent Workshop.

LES AVANCÉES ET LES DÉFIS EN BIOTECHNOLOGIE ET PATHOLOGIE DE LA CANNE À SUCRE: UNE REVUE DU IX ATELIER DE PATHOLOGIE ET DU VI ATELIER DE BIOLOGIE MOLÉCULAIRE

Par

J.C. COMSTOCK[1], A. DOOKUN-SAUMTALLY[2], B. CROFT[3], A. D'HONT[4], F.F. GARCES OBANDO[5], E. MIRKOV[6], G.P. RAO[7], S. SAUMTALLY[2], G.M. SOUZA[8] et D. WATT[9]

[1]*USDA-ARS Sugarcane Field Station, 12990 Highway 441, Canal Point, Florida 33438, États Unis*
[2]*MSIRI, Réduit, Maurice*
[3]*BSES, 90 Old Cove Rd, Woodford Qld 4514, Australie*
[4]*CIRAD, Avenue Agropolis, 34398 Montpellier Cedex 5, France*
[5]*CINCAE-FIADE, Elizalde 114 y Malecon, Casilla letra S, Guayaquil, Équateur*
[6]*Texas A&M University Agricultural Experiment Station, Weslaco, Texas, États Unis*
[7]*Sugarcane Research Station, Kunraghat, Gorakhpur UP, Inde*
[8]*Instituto de Quimica, University of Sao Paulo, Sala 1208, Sao Paulo, Brésil*
[9]*SASRI, Mount Edgecombe, Afrique du Sud*
jack.comstock@ars.usda.gov
adookun@msiri.intnet.mu

MOTS-CLÉS: **Maladies, Résistance des Plantes, Cartographie Génétique, Caractérisation Moléculaire, Transgénique.**

Résumé

LES ATELIERS de travail de Pathologie et de Biologie Moléculaire de l'International Society of Sugar Cane Technologists (ISSCT) ont été tenus conjointement pour la deuxième fois du 23-27 juin 2008 à Cali, Colombie. La réunion a été parrainée par le CENICAÑA et organisée par Jorge I. Victoria et Jershon López-Gerena. La participation fut très positive avec la présence de 44 délégués de 15 pays. Trente-sept présentations orales et dix posters, couvrant un large éventail de sujets, tels que la caractérisation moléculaire des levures, les ravageurs et les pathogènes, la transformation génétique de la canne, les marqueurs moléculaires, la cartographie génétique, la variabilité des pathogènes, le diagnostic des maladies, la résistance de la plante et l'épidémiologie des maladies ont été abordés. Trois discours sur la production des biocarburants, la transgénèse et le génomique de l'amélioration nutritionnelle des cultures vivrières furent prononcés pendant les sessions plénières. Une session spéciale a été consacrée à la rouille orangée, une maladie nouvellement apparue en Floride et en Amérique Centrale. Pendant deux jours, les participants eurent aussi l'occasion de visiter des sucreries, des champs industriels, des parcelles de canne transgéniques ainsi que les laboratoires de CENICAÑA. Cette réunion conjointe s'est avérée fructueuse et elle a donné lieu à une excellente interaction entre les participants.

AVANCES Y RETOS EN LA BIOTECNOLOGÍA Y PATOLOGÍA DE LA CAÑA DE AZÚCAR: UNA REVISIÓN DEL TALLER IX DE PATOLOGÍA Y VI DE BIOLOGÍA MOLECULAR

J.C. COMSTOCK[1], A. DOOKUN-SAUMTALLY[2], B. CROFT[3], A. D'HONT[4], F.F. GARCES OBANDO[5], E. MIRKOV[6], G.P. RAO[7], S. SAUMTALLY[2], GT.M. SOUZA[8] y D. WATT[9]

[1]*USDA-ARS Sugarcane Field Station, 12990 Highway 441, Canal Point, Florida 33438, USA*
[2]*MSIRI, Réduit, Mauritius*
[3]*BSES, 90 Old Cove Rd, Woodford Qld 4514, Australia*
[4]*CIRAD, Avenue Agropolis, 34398 Montpellier Cedex 5, France*
[5]*CINCAE-FIADE, Elizalde 114 y Malecon, Casilla letra S, Guayaquil, Ecuador*
[6]*Texas A&M University Agricultural Experiment Station, Weslaco, Texas, USA*
[7]*Sugarcane Research Station, Kunraghat, Gorakhpur UP, India*
[8]*Instituto de Quimica, University of Sao Paulo, Sala 1208, Sao Paulo, Brazil*
[9]*SASRI, Mount Edgecombe, South Africa*
jack.comstock@ars.usda.gov.
adookun@msiri.intnet.mu

PALABRAS CLAVES: **Enfermedades, Resistencia, Mapeo Genético, Caracterización Molecular, Transgénicos.**

Resumen

POR SEGUNDA vez, la Sociedad Internacional de Tecnólogos de la Caña de Azúcar (ISSCT) se celebraron conjuntamente los talleres de Patología y de Biología Molecular, entre el 23–27 junio de 2008 en Cali, Colombia. La reunión fue organizada por CENICAÑA bajo la dirección de Jorge I. Victoria y Jershon López-Gerena. La respuesta de los participantes fue positiva, con 44 delegados en representación de 15 países asistentes. Treinta y siete presentaciones orales y diez carteles que cubrieron una amplia gama de temas, se presentaron, incluyendo la caracterización molecular de levaduras, insectos plagas y patógenos, la transformación genética de la caña de azúcar, marcadores moleculares, mapeo genético, la variabilidad del patógeno, el diagnóstico de enfermedades, resistencia de las plantas y la epidemiología de la enfermedad, entre otros. El taller también brindó la oportunidad de escuchar tres conferencias plenarias sobre la producción de biocombustibles, los transgénicos y las mejoras nutricionales en los cultivos de alimentos a través de la genómica. Una sesión especial fue dedicada a la roya de naranja, una enfermedad de reciente introducción en la Florida y en América Central. Tras las sesiones técnicas, se organizaron visitas durante dos días en los ingenios azucareros, los campos comerciales, terrenos con caña de azúcar transgénica, y los laboratorios de Cenicaña. La experiencia de tener reuniones y sesiones conjuntas nuevamente demostró ser muy útil por la excelente interacción entre los participantes.