AVRDC
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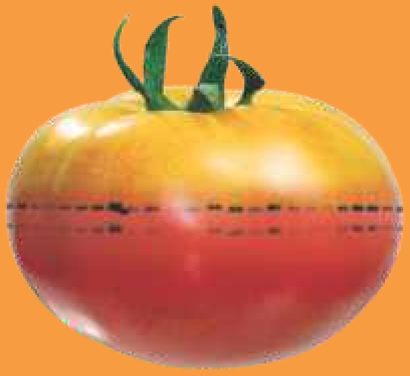
APAARI

Asia-Pacific Symposium on Molecular Breeding

1–3 October 2013
Shanhua, Tainan, Taiwan



Editors

Roland Schafleitner
Jawahir L. Karihaloo

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1-3 October 2013

EDITORS
Roland Schafleitner
Head of Molecular Genetics, AVRDC – The World Vegetable Center

Jawahir L. Karihaloo
Coordinator, Asia-Pacific Consortium on Agricultural Biotechnology (APCoAB),
Asia-Pacific Association of Agricultural Research Institutions (APAARI)

ORGANIZERS
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Prosperity for the poor and health for all

AVRDC - The World Vegetable Center is the leading international nonprofit research and development institute committed to alleviating poverty and malnutrition in the developing world through the increased production and consumption of nutritious and health-promoting vegetables.

AVRDC - The World Vegetable Center
P.O. Box 42
Shanhua, Tainan 74199
TAIWAN
Tel : +886 6 583 7801
Fax : +886 6 583 0009
Email : info@worldveg.org
Web : avrdc.org

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Asia-Pacific Association of Agricultural Research Institutions (APAARI)
4th Floor, FAO RAP Annex Building
202/1 Larn Luang Road
Pomprab Sattrupai District
Bangkok 10100
THAILAND

Tel : + 66 2 282 2918
Fax : + 66 2 282 2919

C/o ICRISAT
National Agricultural Science Center Complex
Dev Prakash Shastri Marg
New Delhi-110012
INDIA

Tel: +91 11 32472305, +91 11 65437870
Fax: +91 11 25843243

Web : www.apaari.org   www.apcoab.org

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FOREWORD

Molecular breeding has emerged to be a powerful tool for genetic improvement of crops and livestock. Tangible outcomes of molecular breeding programs implemented by public sector institutions, international research centres and the private sector have now become available to farmers in some Asia-Pacific countries. Pearl millet 'HHB 67 Improved' with resistance to downy mildew and rice varieties with submergence tolerance and bacterial blight resistance are molecular breeding successes that have found favour with farmers. Several research programs on the application of molecular and other genomic tools for crop and animal breeding are in operation in the Asia-Pacific region. However, a lack of laboratory infrastructure and screening facilities as well as adequately trained human resources constrain the adoption of molecular breeding in developing countries across the region.

Nevertheless, a number of national agricultural research systems and international institutions have made significant advances in the field of molecular breeding and use of genomic tools. Efforts must be made to develop linkages and initiate collaborative programs to share expertise, knowledge and benefits of the technology across the region. APAARI and AVRDC – The World Vegetable Center have been engaged in assisting Asia-Pacific countries to utilize new tools and techniques for agricultural development and farmers' benefit. We are happy that the APAARI-AVRDC-COA Asia-Pacific Symposium on Molecular Breeding held at AVRDC headquarters on 1-3 October 2013 brought together more than 60 scientists from 11 countries to discuss priorities and collaborations in crop and animal molecular breeding. It is also satisfying that interactions among the participants resulted in important proposals for regional research networks to share resources and expertise on crop and animal improvement. We hope this initiative will be carried forward, and that the networks will evolve into lasting partnerships to ensure food and nutrition security in the Asia-Pacific region.

J.D.H. Keating

Dyno Keatinge
Director General
AVRDC – The World Vegetable Center

Raj Paroda
Executive Secretary
APAARI

Acronyms and Abbreviations

APAARI	Asia-Pacific Association of Agricultural Research Institutions
ASR	Asian soybean rust
AVRDC	AVRDC-The World Vegetable Center
BAC	bacterial artificial chromosome
BIL	backcross introgression line
BLB	bacterial leaf blight
CAPs	cleaved amplified polymorphic sequences
CLRRI	Cuu Long Delta Rice Research Institute, Vietnam
cM	centimorgan
CMDV	Center for Marker Discovery and Validation, Malaysia
COA	Taiwan Council of Agriculture
DARES	District Agricultural Research and Extension Station
EST	expressed sequence tags
GBNV	*Groundnut bud necrosis virus*
GS	genomic selection
IBAPs	intron-based amplicon polymorphisms
IIHR	Indian Institute of Horticultural Research
IIVR	Indian Institute of Vegetable Research
IPM	integrated pest management
ITS	internal transcribed spacer
JIRCAS	Japan International Research Center for Agricultural Sciences
MARDI	Malaysian Agricultural Research and Development Institute
MAS	marker-assisted selection
MB	molecular breeding
MPOB	Malaysian Palm Oil Board
MYMV	*Mungbean yellow mosaic virus*
NGS	next-generation sequencing
NILs	near-isogenic lines
NTU	National Taiwan University

PCAARRD	Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development
PCR	polymerase chain reaction
PNG	Papua New Guinea
QTLs	quantitative trait loci
RAD	restriction site associated DNA
RAPD	random amplified polymorphic DNA
RDA	Rural Development Administration, Korea
RFLP	restriction fragment length polymorphisms
RIL	recombinant inbred line
SCAR	sequenced characterized amplified region
SNP	single nucleotide polymorphisms
SSR	simple sequence repeat
TARI	Taiwan Agricultural Research Institute
TLRI	Taiwan Livestock Research Institute
ToLCV	*Tomato leaf curl virus*
TSS	Taiwan Seed Improvement and Propagation Station
WBVN	*Watermelon bud necrosis virus*

Asia-Pacific Symposium on Molecular Breeding

AVRDC – The World Vegetable Center
Shanhua, Tainan, Taiwan
1-3 October 2013

The application of marker-assisted selection in plant and animal breeding is called molecular breeding. Molecular breeding has proven capacity to make plant and animal breeding more efficient. Using molecular markers for selection in breeding makes the production of new crop and animal varieties faster and more cost effective. Breeding virus-resistant tomato, flood tolerant rice, or high quality poultry can be achieved more efficiently by using molecular markers for selection, instead of relying on phenotypic selection alone. During the last 15 years, the private sector has strongly benefitted from this technique, but adoption of molecular breeding in the public sector is still limited, and in most of the developing countries it is hardly used.

Ensuring food security for a fast growing population and enhancing competitiveness of agricultural production requires the use of modern technologies such as molecular breeding. The rapid development of DNA technologies, particularly next generation sequencing, and the ever-decreasing costs of marker technologies opens up new opportunities for molecular breeding.

The Asia-Pacific Symposium on Molecular Breeding aimed to promote marker-assisted selection in crop and animal breeding in the region to enhance food security and income generation along the whole agricultural value chain. The event brought together more than 60 scientists involved with plant and animal breeding from 11 Asia-Pacific countries. The symposium program was divided into three parts: the first part provided a technical update on marker-assisted selection in breeding and on genotyping innovations; the second part reported on the status and the progress of molecular breeding in the countries represented in the symposium; and the final part comprised a networking session designed to build bridges between the research institutions in the region to enhance collaboration in marker-assisted selection for improvement of priority crop and animals.

Symposium Proceedings

INAUGURAL SESSION

The inaugural session was chaired by Dr. Yin Fu Chang, Deputy Director General of Administration, AVRDC – The World Vegetable Center, Taiwan.

The symposium was opened by Mr. Sing-Hwa Hu, Deputy Minister, Council of Agriculture, Taiwan. He welcomed the symposium participants and emphasized the importance of innovative technologies in plant breeding to ensure food security and competitiveness of the Asia-Pacific seed sector. He gave examples of the successful use of marker-assisted selection in crop and animal breeding and expressed his hope that the symposium would contribute to overcoming bottlenecks in the adoption of molecular breeding techniques in the Asia-Pacific region.

In his welcome address, Dr. Jawahir Karihaloo, Asia-Pacific Association of Agricultural Research Institutions (APAARI) thanked the present Director General of the Department of International Affairs of the Council of Agriculture of Taiwan, Dr. Kuei-son Sheu and the former Director General, Dr. Su-san Chang for their continuous support to joint APAARI-COA activities, and Ms. Tracy Tarng for helping to organize these joint events. He mentioned that all APAARI member countries invited were represented, and that the symposium was unique in the sense that animal and plant breeders, together with molecular biologists, were exchanging knowledge and experience in marker-assisted breeding.

Dr. Yin-fu Chang welcomed all participants of the symposium at AVRDC. After a short introduction to the history of marker-assisted selection, he highlighted the involvement of AVRDC scientists in the use of marker-assisted breeding of tomato, which resulted in the release of virus-resistant varieties in Asia starting about 10 years ago.

Dr. Roland Schafleitner, Head of Molecular Genetics at AVRDC, welcomed the symposium attendants and gave a brief introduction to the symposium, highlighting the importance of collaboration in research.

TECHNICAL SESSION I : MOLECULAR BREEDING

Integrating molecular approaches with conventional breeding to accelerate crop improvement

D.S. Brar
School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana (Punjab), India

During the last few decades, major advances have been made in increasing productivity of various crops, particularly cereals where yield has increased 2-3 fold, which has ushered in the Green Revolution. This was achieved primarily through the application of principles of Mendelian genetics and conventional plant breeding. However, we need to increase crop productivity to meet the demand of ever increasing population. This is even more challenging given the continual threat to crops by several diseases, insects and many abiotic stresses (drought, floods, salinity, cold, heat, etc.) particularly in the context of global climate change. The major challenge at present is how to overcome these constraints which limit crop productivity and sustainability. The other concern is how to produce more agricultural output in an eco-friendly way with lesser chemicals, water, land and labor. This will call for adoption of practices that lead to an 'evergreen' revolution - improved crop productivity and sustainability without associated ecological harm and environmental degradation.

Recent advances in cellular and molecular biology and genomics have provided new opportunities to develop improved germplasm with new genetic properties, accelerate breeding programs and to understand the complex function of genes governing agronomic traits. Some of the recent developments in crop biotechnology include: (i) dense molecular maps and availability of new generation of markers such as SNPs, facilitating mapping of genes, fingerprinting and precise characterization of crop germplasm and specialized genetic stocks (NIL's, RIL's, introgression lines etc), pathogen populations and determining purity of commercial hybrids; (ii) many important genes/QTLs governing abiotic and biotic stresses have been tagged with molecular markers; (iii) MAS practiced to accelerate crop breeding programs for tolerance to biotic and abiotic stresses and improved quality traits; (iv) accelerated pyramiding of genes/QTL's, for enhanced tolerance to stresses; (v) map-based cloning of important genes which facilitate gene-based MAS and allele mining of the germplasm/breeding lines; (vi) broadening gene pool of crops through transfer of novel genes from wild relatives; (vii) availability of new genetic resources for functional genomics; (viii) high-throughput methods/materials (SNP chips) for MAS and gene chips for gene discovery and gene expression analysis; (ix) use of markers in background selection and accelerated transfer of transgenes into elite breeding lines; and (x) genome sequence data in large number of crop plants for future research in forward and reverse genetics. In addition, genome wide selection, sequence based MAS and next-generation sequencing offer new opportunities to accelerate crop breeding.

Molecular approaches and new genomic tools offer new opportunities for transfer and pyramiding of genes/QTL's for tolerance to biotic/abiotic stresses including newly cloned yield related genes and develop high-yielding designer crops with value-added traits. Integration of molecular approaches with conventional breeding is emphasized to accelerate crop improvement programs and to further increase productivity and sustainability of crops.

Discussion points:

QTLs for yield: Major genes (e.g. for grain size, grain number, tiller number etc.) can be identified and pyramided to improve yield. But additionally there are hundreds of genes involved with yield. QTL regions are quite large and not precise. Candidate gene identification improves the use of QTLs in breeding.

Phenotyping efforts for detecting yield QTLs is challenging and needs exact description of the most important yield traits.

The production of rice hybrids requires markers for cytoplasmic male sterility and restorer genes. Several of these genes are known and are tracked by markers.▪▪

Genomic Selection in Animal Breeding

M.-C. Wu[1], D.-Y. Lin[1], R.-B. Liaw[1] and H.-L. Chang[2]
[1] Livestock Research Institute, Council of Agriculture, Taiwan
[2] Department of Animal Science, National Ping Tung University of Science and Technology, Taiwan

Molecular information of genetic marker assisted selection (MAS) can increase the selection accuracy of economical traits and subsequently the selection response in animal breeding programs. From dairy cattle to pig, the rates of genetic improvement could increase from 30 to 70% and production traits can be improved more effectively. In Taiwan, animal genomics research and quantitative genetics are applied to accelerate genetic marker assisted selection for economic traits of food animals with favorable genes. Animal genetic resources comprising 77 breeds and strains (19 native, 38 imported, and 20 selected) serve as a gene- bank for the study of genetic diversity. Taiwan dairy cattle, pig, goat, deer, duck, geese and chicken with trait performance records and genotyping information are being promoted for export to southeast Asia due to their adaptation to hot, humid weather. Recently, the traits with less-defined marker associations have been tracked by genomic selection (GS) tools and dense set DNA information across the entire genome has been developed. This gives GS a profound advantage over traditional animal breeding and MAS to permit application of genomics for improving the health and performance of farm animals, especially for meat, milk and egg production in tropics. Clearly, low cost diagnostics based on MAS and/or GS information will be the next wave of development for livestock and poultry farming at farmer scale. In Taiwan, genomic breeding stocks based on their high economic value to industry are registered at www.angrin.tlri.gov.tw with their pedigree and DNA barcode. The successful breeding program via genomic information mainly depends on the extent of DNA information, an accurate and reliable recording system, and the efficiency in integrating both. In conclusion, genomic information is becoming increasingly important for quality improvement of meat, milk and egg, and has applications for breeder farms and the animal industry. ▪▪

TECHNICAL SESSION II : TECHNOLOGICAL ADVANCES IN MOLECULAR MARKER TECHNOLOGIES

Whole genome sequencing and marker development for marker-assisted breeding and genomic selection

B. Chang
Yourgene Bioscience, Taiwan

Next Generation sequencing (NGS) technologies are rapidly transforming genetic research and applications in all major life science field. Marker-assisted selection (MAS) is a process whereby a marker (genetic, biochemical or morphological) is used for indirect selection of desired traits. An overview of current status of NGS technologies was presented along with a summary of the steps required to build a reference genome sequence, discover mutations, and localize the candidate genetic markers responsible for the mutant phenotype.

Challenges in bioinformatics for NGS data and sequence variant analysis

C.-Y. Chen
National Taiwan University, Taiwan

This talk introduced the role of next generation sequencing (NGS) in accelerating genomics studies. Basic concepts and challenges about NGS applications from the bioinformatics point of view were briefly explained, including *de novo* genome assembly, genome re-sequencing, whole transcriptome sequencing, splicing form detection, expression quantification, and sequence variant analysis between individuals or strains. Several examples using non-model organisms exemplified how different types of NGS data can be integrated and exploited to associate the genetic sequence variances with the phenotypes of interest. Limitations and pitfalls of current bioinformatics tools on NGS data analysis were addressed. Future directions for collaboration between wet and dry labs to tackle such challenges were discussed.

Simultaneous discovery and genotyping of single nucleotide polymorphisms using Restriction site Associated DNA (RAD) sequencing

R. Schafleitner
AVRDC — The World Vegetable Center, Shanhua, Tainan, Taiwan

Lack of polymorphic markers has been a constraint for molecular breeding for a long time, especially for less researched crops. The exponential reduction in cost for DNA sequencing and improved bioinformatics tools has made it much easier to obtain sufficient molecular markers for any application. Genotyping by sequencing in connection with appropriate complexity reduction methods of genomic DNA can yield thousands of polymorphic markers for tens to hundreds of genotypes at moderate cost. Restriction site Associated DNA (RAD) sequencing became one of the most popular genotyping by sequencing methods. It applies restriction enzyme digestion of genomic DNA as a reliable means for genome complexity reduction and is based on acquiring sequence information adjacent to a set of particular restriction enzyme recognition sites. The method does not need prior DNA sequence information and thus is particularly useful for getting large numbers of polymorphic markers for non-model organisms. It is a powerful tool for genetic mapping and analysis of quantitative trait loci, as well as genetic diversity and phylogeography analysis. The introduction of barcoding for sequencing reads allows sequencing of pooled samples at low costs. Barcoded RAD tags derived from dozens of individuals thus can be sequenced in a cost-effective manner, which points to another advantage of RAD sequencing: marker discovery and genotyping can be accomplished simultaneously. AVRDC is currently testing RAD sequencing on mungbean and tomato to obtain a sufficient number of polymorphic markers for mapping populations derived from cultivated lines. While the sequencing work is outsourced to DNA sequencing companies, the analysis of the RAD sequencing raw data is accomplished by using a bioinformatics pipeline based on the open-source software STACKS. For genotyping laboratories working on a number of different crops with limited genomic resources, RAD sequencing is a useful method to obtain a critical quantity of markers in a cost-efficient manner.

Discussion points:

How to choose the appropriate genotyping method for different crops with different levels of genetic diversity?

Application of innovative genotyping methods in bulked segregant analysis.

Can gene-based markers improve the resolution of genetic diversity analysis? Neutral markers might be better for analysis of genetic diversity than gene-based markers. ▪▪

The SNP genotyping platform at NTU

C.-W. Tung
Department of Agronomy, National Taiwan University (NTU), Taiwan

The advent of inexpensive, high-throughput genotyping has changed the field of crop genetics and breeding significantly in recent years. Genotyping is no longer an experimental bottleneck, and large, diverse populations have now been assembled to take full advantage of the increased genotyping capacity. Among the various forms of DNA-based markers, single nucleotide polymorphisms (SNPs) are the most abundant in the plant genome. Because of the ease of discovery, validation and data mining, SNPs have become popular markers in assisting molecular breeding and crop genomics research. In this presentation, the speaker introduced two SNP genotyping platforms established recently in the Department of Agronomy at National Taiwan University, “Genotyping by Sequencing, GBS” and “Fluidigm EP1 system”, and discussed their applications and potential use for collaboration in the agricultural research.

Discussion points:

Correlation between genetic distances (centimorgan) and physical distance (mega bases) in rice. On cM corresponds to about 200 kb.

Choice of SNP markers for diversity analysis in rice: markers diagnostic for different rice species.

Nucleotide exchanges are preferred as SNPs in plants, while indels are preferred in animals. Indels are more important to indicate phenotypes.

Choice of restriction enzymes in GBS: Methylation-sensitive enzymes are more appropriate for species with large genomes. Enzymes are most often used where commercially available adapter sequences are available. ▪▪

TECHNICAL SESSION III: COUNTRY REPORTS

Current status of molecular breeding in vegetable crops

A.T. Sadashiva[1], K.V. Ravishankar[1], M. K. Reddy[1], R. V. Gowda[1], K. M. Reddy[1], T. S. Aghora[1], H.C. Prasanna[2], T.H. Singh[1], M. Pitchaimuthu[1], E.S. Rao[1], R. P. Kumar[1], G. Christopher[1] and T.K. Krithika[1]
[1]Indian Institute of Horticultural Research, Hessaraghatta Lake Post, Bengaluru-89, INDIA
[2]Indian Institute of Vegetable Research, Varanasi, INDIA

India ranks second in area (7.57 million hectares) and production (105.79 million metric tonnes) of vegetables, next to China (FAO, 2013). However, low productivity (14 t/ha) partly due to occurrence of various biotic and abiotic stresses, has been a concern for breeders. Breeding efforts have resulted in the release of several disease resistant varieties/F1 hybrids in the past few decades. Recent advances in molecular markers technology and marker-assisted selection (MAS) have helped to speed up breeding procedures.

In tomato, public domain molecular markers linked to *Tomato leaf curl virus* (ToLCV), bacterial wilt, late blight and root knot nematode resistance have been validated at the Indian Institute of Horticultural Research (IIHR) and are being used for pyramiding and stacking of resistance genes. New sources of resistance to ToLCV, *Groundnut bud necrosis virus* (GBNV), high temperature and drought have also been identified and mapping populations have been generated to identify molecular markers. At Indian Institute Vegetable Research (IIVR), marker-assisted pyramiding of *Solanum habrochaites* (Ty-2) and *Solanum chilense* (Ty-3) has been accomplished. The pyramided line VRT-6-1-4 showed better performance over all other lines in agronomic evaluation trials conducted over two seasons.

Allele specific primers associated with pvr1 in chili were used to identify potyvirus resistant lines. Candidate gene analysis of Fom-1 and Fom-2 genes in melon for lines resistant to a local race of Fusarium wilt revealed that the local race is different from those reported earlier (Races 0, 1 and 2), and Fom-1 and Fom-2 based resistance cannot be deployed in India. RIL and backcross introgression line (BIL) populations were developed in watermelon using wild species *Citrullus lanatus* var. *citroides* (resistant to Fusarium wilt) and *Citrullus colocynthis* (resistant to WBNV) for mapping of these resistance traits. Bulk segregant analysis was employed to identify a random amplified polymorphic DNA (RAPD) marker linked to *Mung bean yellow mosaic virus* (MYMV) resistance in French bean (*Phaseolus vulgaris* L.).

Allele mining for Acyltransferase gene linked to pungency in an array of chilli germplasm revealed several SNPs linked to the trait.

In chili, two cytoplasmic male sterility specific sequence characterized amplified region

(SCAR) markers, CoxII and Atp6, were validated in an array of genotypes. Mitochondria specific markers linked to petaloid male sterility in carrot were identified. In Okra, two RAPD markers were found to be tightly linked to genic male sterility. Candidate gene analysis for sex expression in melon resulted in the development of high frequency female lines.

Molecular markers were developed for hybrid purity testing of F1 hybrids in brinjal and onion.

Discussion points:

Commercialization of hybrids and parents through the private sector, seed supply to farmers by IIHR.

Status of RAPD markers for horticultural crops; RAPDs are still used at IIHR to rapidly tag traits.

Molecular and conventional breeding must go hand in hand.

Pyramiding resistance genes increases durability of resistance.

Search of new genes in wild species must be continued.

Heterosis breeding in vegetables. ▪▪

Application of DNA markers to plant breeding and researches in JIRCAS

N. Yamanaka, D. H. Xu, M. Obara, Y. Fukuta
Japan International Research Center for Agricultural Sciences (JIRCAS), 1-1, Ohwashi, Tsukuba, Ibaraki, 305-8686, Japan

About 30 years have been passed since DNA marker was first advocated as a tool for applied plant breeding. Now, marker-assisted selection (MAS) using various DNA markers has successfully been adopted in breeding a wide range of plant species. In this presentation, some latest examples of MAS application in breeding and other researches in JIRCAS were introduced.

Asian soybean rust (ASR) caused by *Phakopsora pachyrhizi*, is one of the most serious economic threats to soybean growers in South America. A highly resistant soybean line pyramided with three ASR resistance genes has been developed and used as donor parent for line breeding programs there. Since ASR populations in South America are highly virulent and divergent, and reactions of known ASR resistance genes are similar, MAS was necessary to accurately and efficiently screen the backcrossed progenies carrying three resistance genes. Salt-affected soil is another big problem for soybean cultivation around the world. DNA markers have been used to identify and fine-map a major quantitative trait locus (QTL) for alkaline salt tolerance. The precise mapping of this QTL by DNA markers helped to isolate the candidate gene and to introduce it into soybean cultivars.

In rice, DNA markers were utilized to fine-map a major QTL for seedling root length and to introduce it into cultivars for enhancing rice yield. Development of multiline variety for rice blast resistance is also being conducting by using DNA markers, and nine isogenic lines carrying different blast resistance genes respectively have been released. DNA markers helped to detect and remove an undesirable gene tightly linked with target gene of donor parent in isogenic line.

These examples indicate that DNA marker and MAS are no more 'assistant' technologies rather they have become 'essential' technologies in plant genetics and breeding.

Discussion points:

> Grain, yield and height characteristics in near isogenic lines in rice carrying different disease resistance genes for multiline varieties.
>
> Nitrogen fixation in salt tolerant soybean lines requires further investigation.
>
> Role of JIRCAS as a research and funding organization in Asia.
>
> Markers can help to overcome linkage drag. ▪▪

Genome-wide marker development and its application in Korea

J. S. Kim
Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Agency (RDA), 150 Suin-ro, Suwon, 441-707, Korea

After the first model plant genome *Arabidopsis* and rice were sequenced, crop genome sequencing has dramatically changed with the availability of new technologies. The availability of NGS and whole reference genome sequences for major crops such as rice, soybean and maize provide a platform for understanding existing genetic diversity, associating gene(s) with phenotypes and exploiting natural genetic diversity to help develop superior genotypes. MAS is used to select parental genotypes in breeding programs, eliminate linkage drag in back-crossing and select for traits that are difficult to measure using phenotypic assays. MAS is especially useful for early selection of a trait in breeding programs. The Rural Development Agency (RDA) has used a molecular marker set with BPH18 and disease resistance fragments in rice and several crops.

Crop improvement has been described as an 'art', and to some extent this is still the case. Recovering a desirable phenotype unambiguously and quickly requires the 'art' to be supplement with technology such that yield gains are predictable and adaptable to challenging environments. At RDA the metabolic pathway genes for crotenoid biosynthetic, phenylpropanoid, flowering, and circadian rhythm are being studied in many crops. The molecular information will be of use to breeders by relating a molecular marker set to a particular breeding objective.

Brassica genus includes many important vegetables like *B. rapa* (Chinese cabbage, pak choi, and turnip) and *B. oleracea* (broccoli, cabbage and cauliflower), and oilseed crops (*Brassica napus, B. rapa, B. juncea* and *B. carinata*), which collectively provide 12% of the world's edible vegetable oils. The *B. rapa* Genome Sequencing Project Consortium reported the annotation and analysis of the draft genome sequence of *B. rapa* accession Chiifu-401-42, a Chinese cabbage. Anchoring of genome assembly to the *B. rapa* genome linkage includes two publically available *B. rapa* genome sequences (JWF3p and VCS_DH, http:// www.brassica-rapa.org) generating from RDA. Genome-wide variable genetic markers are developed from expressed sequence tags (ESTs), tandem repeat sequences, and bacterial artificial chromosome (BAC) sequences. A variable set marker includes restriction fragment length polymorphisms (RFLPs), simple sequence repeats (SSRs), cleaved amplified polymorphic sequences (CAPs) and Intron-based amplicon polymorphisms (IBAPs) respectively. Launching a Chinese cabbage design for Kimchi, could produce the same cultivars in four seasons in the near future.

Discussion points:

How to handle "gene-rich" regions in molecular breeding?

Research priorities at RDA. ▪▪

Status of marker assisted selection (MAS) in Malaysia

N. Abdullah, U. K. Abu Bakar
Biotechnology Research Centre, Malaysian Agricultural Research Development Institute (MARDI), Malaysia

Agriculture biotechnology received strong government support when the Economic Transformation Program was announced during the Tenth Malaysian Plan (2011-2015). Seed industry development was among the national key economic areas listed under this program. Championed by the Ministry of Agriculture, this program is mandated to review production methods for high-quality seeds and identification of economically important genetic materials using Marker Assisted Selection (MAS) technology.

Recent development on MAS has opened up new possibilities to identify and utilize genomic variation towards genetic improvement of crops. Conventional plant breeding has made remarkable progress in crop improvement. However, it is time-consuming and highly depended on plant phenotype and environmental conditions. The exploitation of MAS in plant breeding can further assist breeders in achieving tangible impact on crop improvement through the application of DNA based markers. MAS technology enables plants to be selected at juvenile stage from an early generation and thus plants with undesirable gene combinations can be eliminated. Subsequently, the number of lines that need to be tested will be reduced and time taken in completing a breeding program shortened.

In Malaysia, application of molecular markers for agriculture improvement is quite limited owing to high cost of analysis and the requirement of high-throughput genotyping equipment. However, the Malaysian Agricultural Research and Development Institute (MARDI) has been in the forefront of MAS technology with the establishment of Center for Marker Discovery and Validation (CMDV) in 2011. The CMDV laboratory is located in the Biotechnology Research Center, MARDI and equipped with high-throughput genotyping platforms such as Sequenom, Illumina, ABI 3730, Licor and robotic equipment such as liquid handler and nano dispenser. CMDV is actively involved in providing services such as high-throughput DNA extraction, SNP-and SSR-based genotyping, DNA fingerprinting and seed purity testing for both government agencies and the private sector.

In MARDI, MAS is currently being applied in rice breeding, mainly in assisting backcrossing to incorporate genes controlling aromatic trait, blast disease and brown plant hopper resistance into commercial varieties.

Besides MARDI, the Malaysian Palm Oil Board (MPOB), private companies such as Sime Darby Berhad and Genting Plantation Berhad have also invested in MAS technology with the aim to study the genetic variability of the germplasm and increase oil yield. MPOB successfully identified yield related gene (Shell gene) in oil palm and also discovered a mutation in this gene that enabled breeders to select only high yielding plants through the application of MAS technology.

The establishment of CMDV has opened up new opportunities to local scientists and breeders in utilizing molecular markers in their research and breeding programs. It is hoped that this new technology will enhance Malaysian agriculture in line with the CMDV role as the main enabler to enhance Malaysia seed industry development through application of molecular markers.

Discussion points:

Training program at MARDI.

Major pineapple diseases in Malaysia.

Marker for separation of flesh and seed in rambutan.

Molecular marker assisted breeding on food crops: an opportunity in Nepal

R. B. Amgai
Nepal Agricultural Research Council, Kathmandu, Nepal

Nepal is an agriculture dependent country. It is utilizing Green Revolution technologies and germplasm to boost crop production. However, the application of modern technologies for varietal development is in infancy. Use of the molecular markers for food crop research has only recently been initiated. Genetic diversity study of Nepalese germplasm collections of cereal crops (rice, wheat, maize, barley, finger millet, proso-millet, foxtail millet and finger millet); pseudo-cereals (buckwheat), underutilized crop (amaranth); vegetable crop (chayote); and spices (large cardamom and turmeric) have been completed using molecular markers. RAPD and SSR markers were used for this purpose. Similarly, molecular markers are being used for screening of the biotic and abiotic stress tolerance characteristics in rice, wheat and barley. Microsatellite markers are being used to screen blast and bacterial late blight (BLB) resistance, drought and flash-flood tolerance in rice; rust resistance, drought and heat tolerance in wheat; and rust, net blotch and leaf stripe resistance, and malting quality in barley. However, MAS has not yet been incorporated in regular plant breeding programs. Owing to the cost and case specificity of the molecular marker technology, Nepal is considering use of the markers for forward selection purposes.

Discussion points:

Virulence pathotype of rice blast in Nepal needs to be characterized. ▪▪

Molecular detection of adult plant rusts resistance genes in Pakistani bread wheats

M. Qamar[1,2], D. Ahmad [2], M. Iqbal [3]
[1]Wheat Program, National Agricultural Research Centre (NARC), Islamabad, Pakistan, [2]Department of Plant Breeding and Mol. Genetics, Faculty of Agriculture, University of AJK, Rawlakot , Pakistan, [3] Plant Biotechnology Program, National Agricultural Research Centre (NARC), Islamabad, Pakistan

Stripe and leaf rusts are the major constraints to bread wheat production in Pakistan. Molecular markers were used to investigate the presence of leaf rust and stripe rust resistance (gene complex Lr34/Yr18) and stem rust resistance (gene Sr2) in 52 Pakistani bread wheat cultivars/lines. Polymerase chain reaction (PCR) amplification of DNA fragments using DNA marker csLV-34 showed that 13 of the studied cultivars/lines, namely '03FJ26', 'NR 337', 'NR 339' 'NR 347', 'NR 350', 'Manthar', 'Margalla 99', 'Iqbal 2000', 'Saleem 2000', 'Wafaq 2001', 'Marwat 2001', 'Pirsabak 2004' and 'Fareed 2006' carry leaf rust and stripe rust resistance genes Lr34/Yr18. Stem rust resistance gene Sr2 was observed in 36 Pakistani spring wheat cultivars/lines using stm560.3tgag marker. The slow rusting gene Sr2 needs to be combined with additional stem rust resistance genes to establish durable resistance against Ug99 in modern wheat cultivars. Low frequency of Lr34/Yr18 was found in Pakistani wheats. This gene complex needs to be incorporated into newly developed Pakistani wheats for durable rust resistance.

Discussion points:

The extent of danger of Ug99 for wheat cultivation in Pakistan. ▪▪

Molecular breeding initiatives in Papua New Guinea and the Pacific

T. Shigaki
Papua New Guinea National Agricultural Research Institute, Kana Aburu Haus, Sir Alkan Tololo Research Centre, P. O. Box 4415, Lae 411, Morobe Province, Papua New Guinea

Crop and livestock breeding programs in Papua New Guinea (PNG) and other Pacific countries are often implemented as part of donor-funded projects and they are delimited by the project duration, typically 3-5 years. However, development of desired varieties takes much longer. State-funded agricultural institutes are not able to support long-term breeding programs due to insufficient government funding and lack of capacity. Molecular breeding including MAS and genetic engineering has a potential to reduce the time to develop desired varieties. Although no molecular breeding project is currently in progress in PNG, National Agricultural Research Institute (NARI) and other agricultural institutes appreciate the need to modernize their crop and livestock breeding. In June, 2013, a new facility, Dr. Ghodake National Biotechnology Centre, started its operation to accelerate such efforts. This facility will be capable of DNA fingerprinting, DNA barcoding, and molecular cloning. At present, mutation breeding of sweet potato and aibika (slippery cabbage) is under way. Desired lines can be selected using molecular methods, depending on the availability of markers. In-house development of molecular markers is not realistic at present in PNG and other Pacific countries. Besides, capacity in practical molecular biology techniques is very basic at best. Therefore, international collaboration is necessary to initiate molecular breeding programs.

Discussion points:

Aibika (slippery cabbage, *Abelmoschus manihot*) markers are available to be tested for diversity analysis.

These are legal and social issues for undertaking international programs for diversity screening of important species in PNG. ▪▪

Current status and prospects of crop molecular breeding in the Philippines

P. S. Faylon, J. E. Eusebio, E. A. Anit, A. M. O. Retuta
Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development (PCAARRD)-DOST, Los Baños, Laguna, Philippines

The Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development (PCAARRD), a sectoral council of the Philippines Department of Science and Technology (DOST) focuses on developing and providing science and technology based interventions and modern technology to meet the needs and expectations of the agriculture, aquatic and natural resources sectors. PCAARRD has always supported the development and utilization of modern technology through research and development funding and provision of enabling policies and pronouncements coupled with facility enhancement and manpower development.

The crafting of the roadmap on biotechnology and genomics (2012-2018), which includes molecular breeding (MB) or marker-assisted selection (MAS), was spearheaded by DOST with inputs from the Department of Agriculture (DA). There are several areas where MAS and related activities such as gene discovery and development of molecular markers, can be utilized for crop improvement. These include development of diagnostic kits, genetic mapping, germplasm evaluation and preservation, map-based gene discovery, characterization of economically important traits, pest and disease resistance and improved quality of produce and products.

The use of MB for crop research in the Philippines is not new. Several studies had already been conducted specially on gene discovery and the development of genetic or molecular markers associated with economically important traits of priority crops such as rice, coconut, corn and mango. The presentation discussed the current MB and MB-related activities of PCAARRD on abaca functional genomics, sugarcane and coconut genomics, genetic markers for 'Carabao' mango and rubber DNA fingerprinting as well as the 2012-2018 roadmap for crop genomics.

Discussion points:

Clonal and rootstock variation in mango.

Proportion of food and fiber production research in the PCAARRD program.

Status of coconut mite research.

Next-generation eco-tilling platform. ▪▪

R&D initiatives and extent of application of MAS in livestock and poultry production in the Philippines

A. R. M. Parungao
Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development (PCAARRD)-DOST, Los Baños, Laguna, Philippines

The Philippine agriculture sector shared about 13.2% of the total PhP 10.6 trillion domestic incomes in 2012. In the same year, the livestock and poultry (LP) industry which ranks second to crops (56%) contributed 27% of the total value in agriculture. Hogs, buffalo, cattle, goat, chicken and duck are among the livestock and poultry commodities being bred and produced in high volumes and considered as commodities of high economic importance in the country. Among these, the hog and the chicken contribute the highest in terms of volume of production, 46% and 32%, respectively. Backyard raisers dominate the livestock and poultry industry averaging more than 85%.

The Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development of the Department of Science and Technology (PCAARRD-DOST), as the lead agency for research and development for the sector recognizes the importance of the advancements in biotechnology, particularly MAS, in attaining its goals and objectives. Moreover, DOST crafted the National Biotech and Genomics Roadmap which serves as a technological platform to revolutionize R&D in health, agriculture and biodiversity for socio-economic development.

Livestock and poultry traits that are most likely to benefit with MAS are disease resistance, carcass quality, reproductive efficiency and yield, milk production and maternal ability, growth, birth weight and calving ease. In the Philippines, molecular breeding has been applied to buffalo and hog. Genetic characterization of other livestock and poultry species is currently being initiated. Gene markers for economically important traits are being developed in dairy buffalo and hogs. For instance, gene markers are used in the breeding program for dairy buffalo to improve milk yield, milk fat and total milk solids. Moreover, gene markers are also used to screen genetic defects in breeding herds. For hog breeding, gene markers are used in selecting for litter size, growth rate and meat quality. Gene markers are also used by the hog industry in selecting for disease resistance and screening genetic defects.

Application of MAS by Philippines industry offers huge opportunities for development. Partnerships between and among countries in the Asia-Pacific region are critical in achieving significant increments in livestock and poultry productivity and production efficiency that would lead to food security and improvement in the quality of life.

Discussion points:

> What are the next steps after characterizing local animal breeds? The next step should be the establishment of cross-breeding programs using MAS. ▪▪

QTL mapping and marker-assisted selection for bacterial wilt resistance in tomato

F.-I. Ho, P. Hanson, J.-F. Wang
AVRDC — The World Vegetable Center, 60 Yi-Min Liao, Shanhua, Tainan, Taiwan

Bacterial wilt caused by *Ralstonia solanacearum* is one of the most devastating diseases of tomato. Tomato cultivar 'Hawaii 7996' has been shown to have stable resistance against different strains of the pathogen under different environments. In order to locate QTLs associated with stable resistance, 188 RILs derived from 'Hawaii 7996' and 'West Virginia 700' were developed. The population was evaluated against phylotype I and phylotype II strains at seedling stage or in the field in Indonesia, Philippines, Taiwan, Thailand, and Reunion. Two major QTLs were identified to be associated with stable resistance, Bwr-12 on chromosome 12 controlled 17.9 to 56.1% of total resistance variation, and Bwr-6 on chromosome 6 explained 11.5 to 22.2% of the phenotypic variation. Bwr-12, delimited by SSR markers SLM12-2 and SLM12-10, is important for resistance to phylotype I strains. Two populations of near-isogenic lines (NILs) CLN3125A-23 and CLN3125L were evaluated to confirm the usefulness of SLM12-2 and SLM12-10 for marker-assisted selection. The NILs group with the resistance allele on Bwr-12 wilted less than those with the susceptible allele 27.9% and 24.2% individually. Research on fine-map Bwr-6 is continuing. Markers of Bwr-12 and Bwr-6 used for assisted selection should increase the efficiency to pyramiding resistant QTLs and to select novel sources for bacterial wilt resistance.

Discussion points:

> Is the level of resistance of QTL BW12 sufficiently high? BW12 does not provide immunity, but reduces disease susceptibility and is a useful component of an integrated crop management approach. For some regions such as Kerala (India), additional BW resistance genes are required.
>
> Variability of resistance in different environments. ▪▪

Molecular breeding of crop plants in Thailand — Cassava improvement for high starch content by DNA-marker selection: I. Genetic linkage map

B. Ruangwised, O Boonseng, A. M. K. Trividhayakorn, S. Tungpassornruang
Department of Agriculture, Thailand

Genetic linkage maps of cassava were constructed based on simple sequence repeat (SSR) and expressed sequence tag (EST-SSR) markers using two mapping populations created by reciprocal crosses, set A (Hanatee Hauy x Bong 60) and set B (Hauy Bong 60 x Hanatee). The genetic map of population set A was constructed using 317 SSR markers distribute on 29 linkage groups and the map spanned 1,481.42 cM with the average marker interval of 6.27 cM. Although the maps did not completely cover the whole genome of cassava, yet with the average marker interval of less than 10 cM and coverage of more than 80% of the genome, they were efficient and suitable for QTL analysis. Several QTLs underlying economically and agronomically important traits were identified. Considering the percentage of phenotypic variation explain (%PVE) of greater than 10%, most of the identified QTLs were major QTLs. Interestingly, several QTLs were identified on the same regions of the two sets of mapping populations.

Discussion points:

Yield of early maturing cassava varieties. The varieties are high yielding.

How to manage export of premium rice (branding)? Changing variety name is a disadvantage on the market. ▪▪

The achievements of marker-assisted selection in rice breeding at Cuu Long Delta Rice Research Institute (CLRRI), Vietnam

Nguyen Thuy Kieu Tien
Department of Plant Genetics and Breeding, Cuu Long Delta Rice Research Institute (CLRRI), Vietnam

The Mekong delta is the biggest granary of Vietnam. It produces more than 50% of rice in the country. The Cuu Long Delta Rice Research Institute was founded in January 1977 at the heart of the Delta. Main research themes have been plant genetics and breeding, plant biotechnology, plant protection, entomology, soil science, soil fertility management, microbiology, water management, post harvest technology, farm machinery, farming system models, and social and agricultural economics. Rice breeding using MAS has been applied at CLRRI from 1996. Some significant achievements are: 1) Rice breeding for PBH resistance: wild rice varieties have been considered as genetic sources of PBH resistance, linked to markers RM457F-R, RM270, RM260; 2) Rice breeding for Blast disease: wild rice varieties and local rice varieties have been considered as genetic sources of resistance, linked to: RM136; 3) Rice breeding for salt tolerant: local rice varieties have been considered as genetic sources of resistance, linked to markers C560-C747, R3156, C563, C1454, C397, R1684, RM223, RM315, OSR1; 4) Rice breeding for drought tolerance: local rice varieties have been considered as genetic sources of disease resistance, linked to marker RM201; 5) Rice breeding for low amylose content: local rice varieties have been considered as genetic sources of Wx genes, linked to markers RM42, RM276; 6) Rice breeding for aroma: local rice varieties have been considered as genetic sources of aroma, linked to markers RM223 and RG28F-R.

TECHNICAL SESSION IV : WORKSHOP ON REGIONAL COOPERATION IN MOLECULAR BREEDING

On the last day of the symposium, a workshop was held to engage the representatives of the APAARI member countries in an exercise to identify priorities, gaps and strengths in molecular breeding in their respective countries and to design first steps towards the establishment of a Molecular Breeding Network. Such a network could connect people, build bridges between the research institutions in the region, and pave the path for research collaborations in the region. The workshop was split into two parts:

1) Discussion on identifying needs and priorities: Country-wise response with respect to priority crops and traits, gaps in human resources, infrastructure and germplasm.

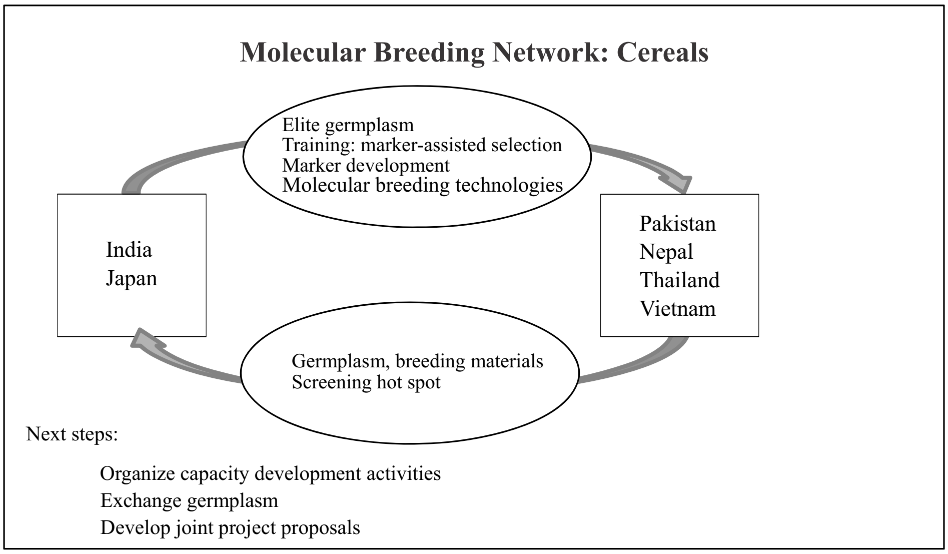
   Facilitator : Dr. Jawahir Karihaloo, APAARI.

2) Identification of network partners - Group work: Draft plan how to close the research gaps. Facilitator: Dr. Roland Schafleitner, AVRDC.

The results of the workshop are summarized in Table 1 and Figure 1-3

Table 1: Analysis of gaps and strength in molecular breeding among the represented APAARI countries

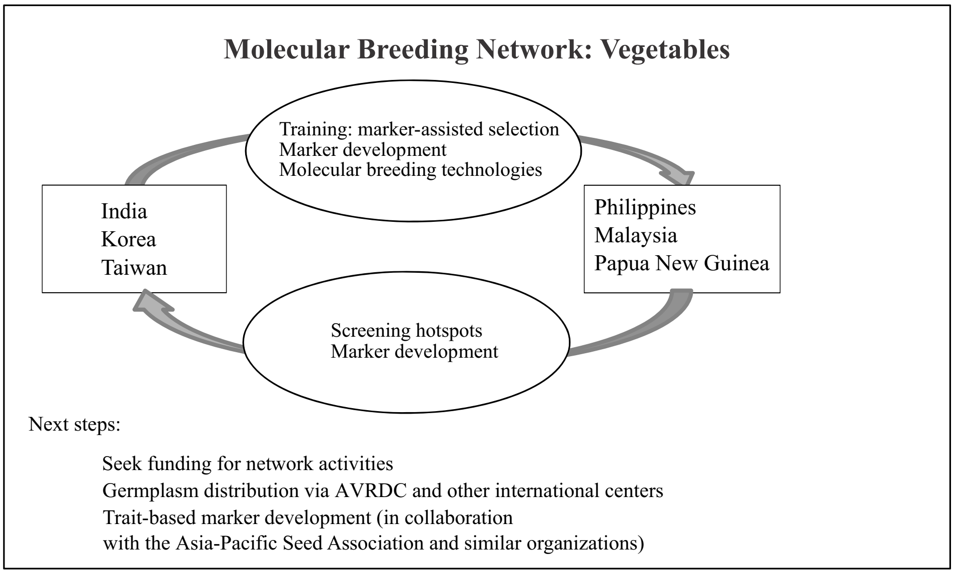
Country	Priority organisms	Strength	Gaps
India	Rice, banana, tomato, eggplant, chili pepper	Improved germplasm available Hybrids available for trials Strong capacity in MAS	Source germplasm for some resistance traits (e.g. Tospovirus, bacterial wilt (for some environments), chili anthracnose, chili leaf curl virus
Japan	Rice, soybean, wheat	Strong MAS capacity Resistance sources available	Access to testing environments
Korea	Rice, chili pepper	Genomic resources Stress tolerance sources	Trial sites in different agro ecologies
Malaysia	Rice, pineapple, banana, coconut, tomato	Germplasm (e.g. direct sowing rice varieties)	Manpower, capacity in bioinformatics
Nepal	Rice, tomato, citrus, cardamom	Phenotyping capacity and environments Local germplasm	Manpower Research infrastructure Inbreds for hybrid production Marketing for high value crops
Pakistan	Wheat, cotton, rice, tomato	Germplasm Know-how in traditional breeding Hot spots for screening	Technology Germplasm for some crops Manpower for MAS
Papua New Guinea, Salomon islands, Vanuatu	Sweetpotato, slippery cabbage, rice	Germplasm collection	Infrastructure Manpower
Philippines	Rice, banana, garlic, onion, yellow corn, tomato	Germplasm Genomics Center	Access to technology Trained manpower
Taiwan	Livestock, poultry	Breeding system for livestock	Reference lab for livestock MAS
Thailand	Rice, corn, sugarcane, cassava, tomato	Germplasm	MAS technology
Vietnam	Rice, soybean, maize	Field screening hotspots	MAS technology



Next steps:

Organize capacity development activities
Exchange germplasm
Develop joint project proposals

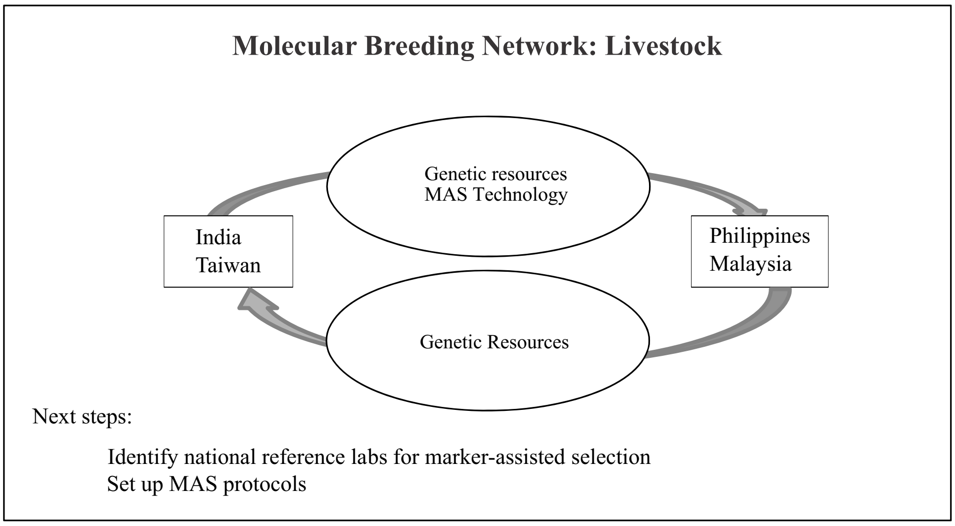
Figure 1: Anticipated exchange in molecular breeding networks for cereals.



Next steps:

Seek funding for network activities
Germplasm distribution via AVRDC and other international centers
Trait-based marker development (in collaboration with the Asia-Pacific Seed Association and similar organizations)

Figure 2: Anticipated exchange in molecular breeding networks for vegetables.



Next steps:

Identify national reference labs for marker-assisted selection
Set up MAS protocols

Figure 3: Anticipated exchange in molecular breeding networks for livestock.

GENERAL RECOMMENDATIONS

1. Molecular and genomic tools provide vast opportunities for improving the efficiency of crop and animal breeding. NARS of the Asia-Pacific region should actively adopt molecular breeding approaches to achieve improved agricultural productivity, nutritional quality and farm profitability.

2. In view of high investment in infrastructure and human resource development required for effective implementations of molecular breeding, the countries need to prioritize crops/animals and traits to be targeted for improvement through this approach. Along with the NARS should substantially increase their investments in molecular breeding R&D.

3. Molecular breeding needs to be integrated with high quality phenotyping to achieve the desired improvement objectives.

4. Molecular tools have an important place in search for new genes in wild germplasm. Application of these tools should be encouraged to enhance the use of diverse germplasm in breeding programs.

5. Both gene-based and neutral markers have their own merits for assessing genetic diversity. Appropriate choices of markers need to be made based on crops, availability of markers and project objectives.

6. Cooperation among Asia-Pacific countries in application of molecular tools for crop and animal improvement will benefit the region by way of enhanced technology uptake and implementation, sharing of germplasm and appropriate screening environments, and capacity development.

7. The three networks on rice, vegetables and livestock identified during this meeting need to be operationalized through appropriate national initiatives followed by regional group meetings among network partners.

8. AVRDC and APAARI should facilitate organization of group meetings and collaborative activities related to the identified networks. The support of COA for such activities should continue.

APAARI-AVRDC-COA

Asia-Pacific Symposium on Molecular Breeding

1-3 October 2013

AVRDC – The World Vegetable Center, Shanhua, Tainan, Taiwan
Auditorium and Conference Room, 3rd Floor of Chandler Hall

Program

30 September 2013 (Monday)		
Pick-up of the delegates at Kaohsiung Airport or at Tainan HSR Station		
Check-in at AVRDC Guesthouse		
1800	Dinner at AVRDC Cafeteria	
1 October 2013 (Tuesday) **Location: Auditorium**		
0830 – 0900	Registration	
0900 – 0945	Inaugural Session	Mr. Sing-Hwa Hu, Deputy Minister, Council of Agriculture, Taiwan Dr. Jawahir Karihaloo, Asia-Pacific Association of Agricultural Research Institutions (APAARI) Dr. Yin-Fu Chang, Deputy Director General, AVRDC – The World Vegetable Center, Taiwan
0945 – 1000	Introduction to the Asia-Pacific Symposium on Molecular Breeding	Dr. Roland Schafleitner, Head of Molecular Genetics, AVRDC – The World Vegetable Center, Taiwan
1000 – 1015	Group photo	
1015 – 1045	Coffee Break	
Technical Session I: Molecular Breeding		
Chairperson: Dr. Roland Schafleitner		**Speaker**
1045 – 1120	***Integrating molecular approaches with conventional breeding for accelerated crop improvement***	Dr. Darshan Brar, Honorary Adjunct Professor, Punjab Agricultural University, India
1120 – 1130	Q&A	
1130 – 1200	***Genomic selection in animal breeding***	Dr. Ming-Che Wu, Chief of Animal Breeding and Genetics Division, Livestock Research Institute, Council of Agriculture (COA), Taiwan
1200 – 1215	Q&A	
1215 – 1330	Lunch at AVRDC Cafeteria	

Technical Session II: Technological Advances in Molecular Marker Technologies

Chairperson: Dr. Jawahir Karihaloo		**Speaker**
1330 – 1400	***Whole genome sequencing and marker development for marker-assisted breeding and genomic selection***	Dr. Bill Chang, CEO, Yourgene Bioscience, Taiwan
1400 – 1415	Q&A	
1415 – 1445	***Challenges in bioinformatics for NGS and marker development***	Dr. Chien-Yu Chen, Assistant Professor, National Taiwan University
1445 – 1500	Q&A	
1500 – 1530	Coffee Break	
1530 – 1555	***Simultaneous discovery and genotyping of single nucleotide polymorphisms using restriction site associated DNA (RAD) sequencing***	Dr. Roland Schafleitner, Head of Molecular Genetics, AVRDC – The World Vegetable Center, Taiwan
1555 – 1600	Q&A	
1600 – 1630	***The SNP genotyping platform at NTU***	Dr. Chih-Wei Tung, Assistant Professor, National Taiwan University
1630 – 1645	Q&A	
1800 – 2000	Welcome dinner at AVRDC Cafeteria	

2 October 2013 (Wednesday)
Location: Auditorium

Technical Session III: Country Reports

Chairpersons: Dr. Darshan Brar **Ms. Abigail Oropesa Retuta**		**Speaker**
0900 – 0930	***Current status of molecular breeding in vegetable crops***	Dr. Avverahally Thammanna Sadashiva, Principal Scientist, Indian Institute of Horticultural Research (IIHR), India
0930 – 1000	***Application of DNA markers to plant breeding and researches in JIRCAS***	Dr. Naoki Yamanaka, Senior Researcher, Japan International Research Center for Agricultural Sciences (JIRCAS), Japan
1000 – 1030	Coffee break	
1030 – 1100	***Genomewide marker development and its application on Brassica rapa***	Dr. Jung Sun Kim, Senior Researcher, Rural Development Administration (RDA), Korea
1100 – 1130	***Status of marker assisted selection (MAS) in Malaysia***	Dr. Norzihan Abdullah, Coordinator, Malaysian Agricultural Research and Development Institute (MARDI), Malaysia

1130 – 1200	***Molecular marker assisted breeding on food crops: an opportunity in Nepal***	Mr. Resham Babu Amgain, Scientist, Nepal Agricultural Research Council, Nepal
1200 – 1300	Lunch at AVRDC Cafeteria	
Technical Session III : Country Reports (Continued}		
Chairpersons: Dr. Norzihan Abdullah **Dr. Avverahally Thammanna Sadashiva**		**Speaker**
1300 – 1330	***Molecular detection of adult plant rusts resistance genes in Pakistani bread wheats***	Dr. Maqsood Qamar, Senior Scientific Officer, National Agricultural Research Center, Pakistan
1330 – 1400	***Molecular breeding initiatives in Papua New Guinea and the Pacific***	Dr. Toshiro Shigaki, Principal Scientist for Biotechnology, Papua New Guinea National Agricultural Research Institute, Papua New Guinea
1400 – 1430	***Current status and prospects for molecular breeding in the Philippines***	Ms. Abigail May Oropesa Retuta, Science Research Specialist, Philippine Council of Agriculture, Aquatic and Natural Resources Research and Development (PCAARRD), Philippines
1430 – 1500	***R&D initiatives and extent of application of MAS in livestock and poultry production in the Philippines***	Mr. Alfredo Ryenel Manolo Parungao, Science Research Specialist, Philippine Council of Agriculture, Aquatic and Natural Resources Research and Development (PCAARRD), Philippines
1500 – 1530	Coffee break	
1530 – 1600	***QTL mapping and marker-assisted selection for bacterial wilt resistance in tomato***	Ms. Fang-I Ho, Assistant Specialist, AVRDC – The World Vegetable Center, Taiwan
1600 – 1630	***Molecular breeding of crop plants in Thailand***	Ms. Boonruanrat Ruangwised, Agricultural Research Specialist, Department of Agriculture, Thailand
1630 – 1700	***The achievements of marker-assisted selection in rice breeding at the Cuu Long Delta Rice Research Institute (CLRRI), Vietnam***	Dr. Thuy Kieu Tien Nguyen, Head, Department of Plant Genetics and Breeding, Cuu Long Delta Rice Research Institute, Vietnam
1700 - 1730	AVRDC biotechnology laboratory tour	Dr. Roland Schafleitner
1800 – 2000	Dinner at AVRDC Cafeteria	

3 October 2013 (Thursday) **Location: Conference Room**		
0800 - 0900	Tour through AVRDC Demonstration Garden	Willie Chen
Technical Session IV: Workshop on Regional Cooperation in Molecular Breeding		
0900 – 1000	Discussion on identifying needs and priorities: (Country-wise response with respect to priority crop, animals and traits, gaps in human resources, infrastructure, germplasm)	Facilitator: Dr. Jawahir Karihaloo, Asia-Pacific Association of Agricultural Research Institutions (APAARI)
1000 – 1020	Coffee Break	
1020 – 1115	Identification of network partners - Group work: Draft plan how to close the research gaps	Facilitator: Dr. Roland Schafleitner, AVRDC, The World Vegetable Center, Taiwan
1115 - 1145	Reporting from Group work	
1145 - 1200	Symposium Closing	Dr. Jawahir Karihaloo, Asia-Pacific Association of Agricultural Research Institutions (APAARI) Dr. Yin-Fu Chang, Deputy Director General, AVRDC – The World Vegetable Center, Taiwan
1200 – 1300	Lunch at AVRDC Cafeteria	
1300 – 1800	Field Trip of Tainan	Dr. Roland Schafleitner, AVRDC, The World Vegetable Center, Taiwan
1900 – 2100	Farewell Dinner at Da Zhen Restaurant, Shanhua	

Participants List

Last Name	First Name	Affiliation	Country	E-mail	Phone
Abdullah	Norzihan	MARDI	Malaysia	zihan@mardi.gov.my	03-89437550
Amgain	Resham Babu	Nepal Agricultural Research Council	Nepal	reshamamgain@yahoo.com	977 01 5539658
Brar	Darshan Singh	Punjab Agricultural University	India	d.brar@irri.org	0091-81462-97092
Chang	Bill	Yourgene Bioscience	Taiwan	bchang@yourgene.com.tw	02-26758068
Chang	Hui-Ju	TSS	Taiwan	tracyc@tss.gov.tw	0912375205
Chang	Jui-Hsin	Taichung DARES	Taiwan	changrs@tdais.gov.tw	0955283938
Chang	Sheng-Chih	TSS	Taiwan	james7309@tss.gov.tw	0912602572
Chang	Yin-Fu	AVRDC – The World Vegetable Center	Taiwan	yin-fu.chang@worldveg.org	06-5837801#110
Chen	Chien-Yu	National Taiwan University	Taiwan	chienyuchen@ntu.edu.tw	02-33665334
Chen	Hsuan	Academia Sinica	Taiwan	jearldchen@gmail.com	0987898196
Chen	Huei-mei	AVRDC – The World Vegetable Center	Taiwan	huei-mei.chen@worldveg.org	06-5837801#360
Chen	Jen-Ren	TSS	Taiwan	jrchen@tss.gov.tw	0920001551
Chien	Yi-Wen	TSS	Taiwan	sally0122@tss.gov.tw	0933802091
Chiu	Ericka Yen-Hsin	TSS	Taiwan	yhchiu@tss.gov.tw	04-25825471
Cho	Myeong-Cheoul	AVRDC – The World Vegetable Center	Taiwan	myeong-cheoul.cho@worldveg.org	06-5837801#390
Chou	Chien-Ming	TARI	Taiwan	cmchou@tari.gov.tw	0963419083
Chu	Shu-hui	AVRDC – The World Vegetable Center	Taiwan	julie.chu@worldveg.org	06-5837801#363
Dai	Hung Yu	TARI	Taiwan	hydai@tari.gov.tw	0953316719
Hanson	Peter	AVRDC – The World Vegetable Center	Taiwan	peter.hanson@worldveg.org	06-5837801#370
Ho	Fang-I	AVRDC – The World Vegetable Center	Taiwan	fang-i.ho@worldveg.org	06-5837801#440
Hsu	Selena	COA	Taiwan	selena@mail.coa.gov.tw	02-23124064
Hu	Sing-Hwa	COA	Taiwan	VC6005@mail.coa.gov.tw	02-23126005
Huang	Shih-Hung	Taiwan Banana Research Institute	Taiwan	xhshkimo@yahoo.com.tw	0911246533
Huang	Shu-mei	AVRDC – The World Vegetable Center	Taiwan	shu-mei.huang@worldveg.org	06-5837801#363
Jang	Seonghoe	Academia Sinica	Taiwan	florigen@gate.sinica.edu.tw	06-5053202
Karihaloo	Jawahir	APAARI	India	j.karihaloo@cgiar.org	9818872624
Kenyon	Lawrence	AVRDC – The World Vegetable Center	Taiwan	lawrence.kenyon@worldveg.org	06-5837801#350
Kim	Jung Sun	RDA	Korea	jsnkim@korea.kr	82-31-299-1632
Koh	Kah Wee	Academia Sinica	Taiwan	kohkww@hotmail.com	0913525729
Kumar	Sanjeet	AVRDC – The World Vegetable Center	Taiwan	sanjeet.kumar@worldveg.org	06-5837801#310
Kumar	Seerangan	Academia Sinica	Taiwan	ksctsinica@gmail.com	0972301496
Lin	Chia-Yu	Taitung DARES	Taiwan	631@mail.ttdares.gov.tw	0955326188
Lin	Jean-yu	AVRDC – The World Vegetable Center	Taiwan	Jean.lin@worldveg.org	06-5837801#363

Lin	Meng-Ying	National Taiwan University	Taiwan	r00621111@ntu.edu.tw	0975537223
Lin	Pih-yun	AVRDC – The World Vegetable Center	Taiwan	lucy.lin@worldveg.org	06-5837801#363
Lin	Tzu-Kai	TARI	Taiwan	kai@tari.gov.tw	0952252595
Liu	Li-yu Daisy	National Taiwan University	Taiwan	lyliu@ntu.edu.tw	0916966357
Lu	Hsiang Chia	Academia Sinica	Taiwan	Hsiangchia.lu@gmail.com	0935967108
Nguyen	Thuy Kieu Tien	Cuu Long Delta Rice Research Institute (CLRRI)	Vietnam	ntktien10@gmail.com	84909565991
Parungao	Alfred	PCAARD	Philip-pines	alfrmp@yahoo.com	63 932-881-7506
Peng	Rui-ju	Tainan DARES	Taiwan	jcpeng@mail.tndais.gov.tw	06-5912901#309
Qamar	Maqsood	National Agricultural Research Center	Pakistan	maqsoodqmr@gmail.com	92 346 5939219
Retuta	Abigail May Oropesa	PCAARRD	Philip-pines	abi.retuta@gmail.com	0917-603-4777
Ruangwised	Boonruanrat	Ministry of Agriculture and Cooperation	Thailand	boonruanr@yahoo.com	66-923323885
Sadashiva	Avverahally Thammanna	IIHR	India	atsbrs@gmail.com	9845097472
Schafleitner	Roland	AVRDC – The World Vegetable Center	Taiwan	roland.schafleitner@worldveg.org	06-5837801#380
Shigaki	Toshiro	Papua New Guinea National Agricultural Research Institute	PNG	toshiro.shigaki@nari.org.pg	675 475 1033
Sundara velpandian	Kalaipandian	Academia Sinica	Taiwan	sundarpbg@yahoo.com	0933472244
Tarng	Tracy	COA	Taiwan	tracyt@mail.coa.gov.tw	02-23126969
Tsai	Yuan-Ching	Academia Sinica	Taiwan	botsai@gate.sinica.edu.tw	0921692846
Tseng	Ching-Shan	TARI	Taiwan	samtseng@tari.gov.tw	0920383592
Tseng	Meng-Chun	Taoyuan DARES	Taiwan	cellist@tydais.gov.tw	0955260617
Tung	Chih-Wei	National Taiwan University	Taiwan	chihweitung@ntu.edu.tw	02-336-64756
Wang	Jau-Yueh	TARI	Taiwan	jywang@tari.gov.tw	0919028287
Wang	Jaw-fen	AVRDC – The World Vegetable Center	Taiwan	jaw-fen.wang@worldveg.org	06-5837801#450
Wang	Yen-wei	AVRDC – The World Vegetable Center	Taiwan	vivian.wang@worldveg.org	06-5837801#363
Wu	Ming-Che	TARI	Taiwan	wu@tari.gov.tw	0963105085
Wu	Ming-Che	TLRI	Taiwan	mcwu@mail.tlri.gov.tw	0932870380
Yamanaka	Naoki	JIRCAS	Japan	naokiy@jircas.affrc.go.jp	81-29-838-6649
Yang	Ai-Hua	Tainan DARES	Taiwan	ahyang@mail.tndais.gov.tw	0972822690
Yeh	Tzu-ying	Fengshan Tropical Horticultural Experiment Branch, TARI	Taiwan	tzuying139@fthes-tari.gov.tw	07-7310191#702
Yen	Yo-yi	AVRDC – The World Vegetable Center	Taiwan	joyce.yen@worldveg.org	06-5837801#363

About the organizers

The **Asia-Pacific Association of Agricultural Research Institutions** (APAARI) is a regional association that aims to promote the development of National Agricultural Research Systems (NARS) in the Asia-Pacific region through inter-regional and inter-institutional cooperation. The overall objectives of APAARI are to foster the development of agricultural research so as to promote the exchange of scientific and technical information, encourage collaborative research, promote human resource development, build organizational and management capabilities of member institutions and strengthen cross-linkages and networking among diverse stakeholders. The **Asia-Pacific Consortium on Agricultural Biotechnology** (APCoAB) is a program of APAARI with the mission to "Harness the benefits of agricultural biotechnology for human and animal welfare through the application of latest scientific technologies while safeguarding the environment".

AVRDC – The World Vegetable Center, an international non-profit research and development institute, is committed to alleviating poverty and malnutrition in the developing world through the increased production and consumption of nutritious and health-promoting vegetables. From its founding mandate in 1971 to support vegetable research and development in tropical Asia, AVRDC – The World Vegetable Center has expanded its focus to serve more continents, more countries, and more people. Today, Center researchers lead and participate in projects throughout Asia, Africa, Central America, and Oceania. The Center has more than 300 staff engaged in this spread of activities, and seeks to partner with governments, nongovernmental organizations, universities, research institutes, and the private sector to promote prosperity for the poor and health for all.

www.avrdc.org

AVRDC - The World Vegetable Center
Headquarters
PO Box 42
Shanhua, Tainan 74199
Taiwan

T +886 (0) 6 583-7801
F +886 (0) 6 583-0009
E info@worldveg.org

www.appari.org

Asia-Pacific Association of Agricultural Research Institutions (APAARI)
Headquarters
4th Floor, FAO RAP Annex Building
202/1, Larn Luang Road
Pomprab Sattrupai District
Bangkok 10100
Thailand

T +66 2 282 2918
F +66 2 282 2919

C/o ICRISAT
National Agricultural Science Center Complex
Dev Prakash Shastri Marg
New Delhi-110012

T +91 11 32472305, +91 11 65437870
F +91 11 25843243