

-BOOK OF ABSTRACTS-

International Workshop

Applied Mathematics and Omics Technologies for Discovering Biodiversity and Genetic Resources for Climate Change Mitigation and Adaptation for Sustainable Agriculture in Drylands

Rabat, Morocco 24–27 June 2014



Co-organizers

ICARDA, INRA Morocco, CGIAR (CAAFS), Concordia University, University of Helsinki, ARCAD, NordGen, CIMMYT, GRDC, and IAV Hassan II



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Bennasser Alaoui
Oumekaltoum Essahli
Meryam El Alauoui
Hind Outouairi

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Zakaria Kehel, CIMMYT, Mexico

Contacts and support:

S. Dayanandan, Concordia University, Montreal, Canada
Ardeshir (Adi) Damania, University of California, Davis, USA
Oumekaltoum Essahli, ICARDA, Rabat, Morocco

Edited by:

A. Damania, S. Dayanandan, and A. Bari

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Summary

Innovative approaches using applied mathematics for agricultural genebank mining for climate change resistant traits improve the effectiveness of breeding programs and of food security for dry areas.

Dry areas represent more than 40% of global land cover and are home to over 2.5 billion people.

Crop cultivars with improved tolerance to heat and drought, and resistance to emerging virulent pests and diseases are urgently needed to sustain and increase agricultural productivity under the current changing climatic conditions in drylands.

Identifying stress tolerance and resistance traits from more than seven million accessions held in the world's 1,700 major agricultural genebanks, is not a trivial exercise. Today, developing innovative approaches to mining these agricultural gene banks is more important than ever.

The latest innovations include methods that use applied mathematics – including the Bayes-Laplace inverse and the Stone-Weierstrass approximation theorems in combination with phenomics and genomics – for rapid and cost-effective identification of crop plants with climate change adaptive genetic traits.

Applying these approaches as a standard practice for genebank mining in the world's breeding programs will improve the effectiveness of these organizations help accelerate crop improvement, to maintain biodiversity, food security, and improve livelihoods of communities living on the world's marginal lands and dryland areas.

Co-organizers



ICARDA

The International Center for Agricultural Research in the Dry Areas (ICARDA) is the global agricultural research center working with countries in the world's dry areas, supporting them for the sustainable productivity of their agricultural production systems; increased income for smallholder farmers living on dry lands and in fragile ecosystems; and nutrition and national food security strategies. With partners in more than 40 countries, ICARDA produces science based-solutions that include new crop varieties (barley, wheat, durum wheat, lentil, faba bean, kabuli chickpea, pasture and forage legumes); improved practices for farming and natural resources management; socio-economic and policy options to support countries to improve their food security. ICARDA works closely with national agricultural research programs and other partners worldwide – in Central Asia, South Asia, West Asia, North Africa, sub-Saharan Africa.

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Dryland Systems

The CGIAR Research Program on Dryland Agricultural Production Systems (known as Dryland Systems) embodies a new approach to integrated and 'holistic' agro-ecosystems research. It combines many research disciplines, from biophysical to socioeconomic. The goal of Dryland Systems is to identify and develop resilient, diversified, and more productive combinations of crops, livestock, rangeland, and agroforestry systems that increase productivity and production stability, increase resilience, reduce hunger and malnutrition, and improve the quality of life for the rural poor.

<http://drylandsystems.cgiar.org/>



Climate Change, Agriculture and Food Security (CCAFS)

The CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS) addresses the increasing challenge of global warming and declining food security to agricultural practices, policies, and measures through a strategic collaboration between CGIAR and Future Earth. Led by the International Center for Tropical Agriculture (CIAT), CCAFS is a collaboration involving all 15 CGIAR Agricultural Research Centers and coordinates with the other CGIAR Research Programs.

<http://ccafs.cgiar.org>



Institut National de la Recherche Agronomique (INRA) is a public autonomous research organization under the auspices of Morocco's Ministry of Agriculture. INRA was established on 8 April 1981 and evolved from its predecessor, the Directorate of Research. Within its new mandate, INRA's responsibilities include:

- Carrying out research and technical activities to develop the agricultural and livestock sectors
- Carrying out prospective research studies, particularly those related to natural resources and the environment
- Undertaking experimental trials – either at INRA's own initiative or at the request of other parties – to improve plant or animal production and to develop tools and technologies to use or to transform plant and animal produce
- Ensuring, within areas in which INRA has a comparative advantage, the supervision of research and studies for better livelihoods in Morocco
- Dissemination of relevant information and knowledge related both to its own research and to research undertaken elsewhere
- Defining the scientific practicability and applicability of its own research results and advising extension services and farmers
- Disseminating research results, studies and other activities

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Institut Agronomique et Vétérinaire Hassan II (IAV Hassan II)

IAV Hassan II provides three integrated core tasks – training, research and development. It became a polytechnic center of multidisciplinary expertise and provides initial training and continuing education to specialists in science and technologies (engineers, veterinarians, and doctors of agricultural sciences). It actively contributes to the effort to modernize agriculture by conducting innovative research programs that meet the expectations and needs of a changing worlds' agriculture. Skills at IAV extend to the following areas of agriculture and agricultural resources: (i) rural development and spatial planning, (ii) environmental and natural resources management, (iii) agro-industrial processing, (iv) biotechnologies of plants, animals, and microorganisms, (v) veterinary public health, and (vi) services associated with agricultural production, distribution, and marketing.

www.iav.ac.ma



Concordia University

The global imperative to meet the challenges of environmental destabilization begins with the recognition that human well-being depends on maintaining environmental quality and adopting sustainable systems. Concordia's strengths in these areas have been developed through multiple research activities related to environmental science and engineering, energy, and natural resources. This includes scientific assessments of human impact on the environment, implications for policies and actions regarding resource efficiency, and sustainable consumption and production, as well as understanding how to adapt to climate change. Concordia has established strengths in both fundamental and applied research. Its researchers are generating foundational knowledge, nurturing discoveries, fostering innovation, and making evidence-based contributions that respond to the needs of society, including the growing imperatives of adaptability and sustainability as experienced by people, communities, markets, industries, institutions, and countries around the world. Concordia's research and research creation activity spans a wide range of disciplines and fields, utilizing an impressive diversity of methodological approaches. Its two major research clusters comprise six unifying research themes and 17 unique domains of excellence for which it is widely recognized.

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University of Helsinki

University of Helsinki belongs to the League of European Research Universities (LERU) and its Faculty of Agriculture and Forestry is Finland's only tertiary provider of agricultural sciences education. The Department of Agricultural Sciences conducts research on plant production in agriculture and horticulture, animal production, and technologies pertaining to them. It provides the highest level education and has societal influence based on its research.

www.helsinki.fi/agriculturalsciences/index.html



NordGen

Nordic Genetic Resource Centre (NordGen) is the joint Nordic institution for conservation and sustainable use of genetic resources. Biodiversity, and the underlying genetic diversity, is the basis for all human existence and the base for constant adaptation to change. Access to genetic resources is a prerequisite for adaptation to new growth conditions, to climate change, for providing resistance to new diseases of plants and domestic animals, for increased food production, for low environmental impact, or to meet new requirement from our consumers. NordGen contributes to safeguarding the livelihoods of our region today and for our future.

www.nordgen.org



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On normalizing transformations of the coefficient of variation for a normal population with an application to the evaluation of the uniformity of plant varieties

Adaptation of farmers to climate change: a systems approach. A case study of cereal production in Benslimane region, Morocco

S. B. Alaoui, A. M. Adan, Y. Imani, and O. Lahlou

Department of Production, Protection and Biotechnology, Institut Agronomique et Vétérinaire Hassan II, Rabat Morocco.

E-mail: M.El-Alaoui@cgiar.org

Abstract

The recorded variations in temperature and precipitation caused by climate change affect agricultural production and threaten the availability of food and food security overall. Therefore, an adaptation is necessary to overcome this problem. This study focuses on the identification of effective adaptation options, within a systems approach perspective, to limit the negative effects of climate change. The study has a framework of the effects of global warming on agricultural production in Morocco.

The negative effects on Moroccan agriculture result from a decline in and variability of rainfall combined with a rise in temperature. It results in a reduction in the length of the crop growing cycles and increased evapotranspiration from plants. Hence, these factors would require new, adapted varieties. Climate change increases the plants' water deficit, especially in dryland farming, which applies to most of the arable land in Morocco.

The challenge for Morocco is to mitigate the effects of climate change and increase production to meet the needs of a growing population with limited land and water resources available. Based on research results and agricultural techniques practiced by some farmers who are performing well, it appears that some cultural practices will be decisive in the production process of cereals to adapt to unstable climate during difficult years. Therefore, some farmers have adopted a systems approach by combining efficient practices, which attempt to reduce the effect of weather perturbations, with the practice of early seeding using short-season varieties. The latter option allows the crop cycle of the newly adapted varieties to coincide with the rainy season.

Other adaptation measures can also improve the performance of agriculture. These include the expansion of irrigation, adaptation of technical packages, introduction of new technologies – such as conservation agriculture – and integrated crop management.

Crop genetic resource conservation and its threat in the case Ethiopia

T. G. Alganesh

Ethiopian Institute of Biodiversity, Addis Ababa, Ethiopia

Email: alganeshgellaw@yahoo.com

Abstract

Ethiopian economy is based on agriculture where 83% of the total population of the country is engaged in agricultural sector. There is however low productivity with risk for food security. This will be more demand on genetic resources in the face of climate change with also high risk of erosion the countries genetic resource in time that would be critically needed.

Ethiopia, has diversified agro ecological zones with a diversified fauna and flora, these situation coupled with the farmers selection criteria favors the country to be the center of origin and diversity for many economically important crops, such as; *Eragrostis tef*, *Guizotia abyssinica*, *Enset ventricosum*, *Coffee arabica*, *Catha edulis*, *Rhamnus prinoides*, *Hygenia abyssinica*, *Coleus edulis*, *Cuccinia abyssinica* and *Brassica carinata* *Triticum durum*, *Hordeum vulgare*. Ethiopian farmers through their selection criteria may also selected for traits related to climate change with potential to sustain agriculture production .

According to Ethiopian flora, 6000 plant species are found in the country 12% of which are endemic. More than 200 wild and cultivated species were documented. However, 35 crops as macro nutrients with high kcal (High protein, carbohydrate and fats) and 10 crops are micro nutrient (vitamins & minerals) have been utilized others are underutilized and 6 of which are globally significant crops.

Findings of the assessment of demand for and supply of technologies for mitigation and adaptation to climate change

Tom Apina

Sustainet East Africa

E-mail: tom.apina@sustainetea.org

Abstract

Agriculture is of critical importance to the development of Africa; 80% of the population is involved in agricultural production, and it accounts for 30% of GDP on the continent. A recent study, commissioned by the German Federal Ministry for Economic Cooperation and Development (BMZ), through Deutsche Gesellschaft für Technische Zusammenarbeit (GIZ), covering 17 countries in Africa, showed that even though a large number of research outputs match with the farmers' needs, the most important problems of farmers are not met by research.

Most technologies focus on improving the traits/genetic resources of both crop and livestock varieties, and a few, but growing number of technologies, try to understand markets and seek to add value to production. Most of the top technologies covered in a study of the work of International Agricultural Research Centers have not reached more than 5000 households each, and the diffusion potential of a considerable number is rather limited. A major constraint to successfully up-scaling the technologies is attributed to scientists largely being evaluated on the number of articles they publish rather than on their engagement with farmers or extension agents.

Assessing the resource status, input application level, and cost of innovations, the study found that more than two-thirds of the technologies are not affordable to the majority of farmers. Technologies continue to play crucial roles in climate change adaptation and mitigation processes. The study found that the majority of actors felt that climate change is having a negative impact on farmers, and despite a range of coping mechanisms being promoted, more research on better coping mechanisms is necessary to keep up with the speed of change. The study concludes that the main bottleneck to the adoption of technologies by farmers is not that the technologies developed do not match their needs, but rather that farmers do not have access to them.

Climate change, agro-biodiversity and food security in West Africa

Aichatou Assoumane^{(1),(2)}, Abdulai Jalloh⁽²⁾, and Aboubakar Njoya⁽²⁾

⁽¹⁾ Department of Biology, University of Niamey, Niger

⁽²⁾ West and Central Africa Council for Agricultural Research and Development (CORAF/WECARD),
Dakar, Senegal

E-mail: aichatou.assoumane@gmail.com

Abstract

Weather-related crop failures, collapse of fisheries, and livestock deaths, in addition to losses of property, are causing economic losses and undermining food security in West Africa. Climate change will have far-reaching consequences for the poor and marginalized groups. The majority depend on agriculture for their livelihoods and have a lower capacity to adapt. Against the backdrop of the rainfall changes is an increase in temperature – on average 2°C in all the countries – with at least one model showing a rise in temperature of up to 3.5°C in Liberia, Niger, and Sierra Leone based on a CORAF/WECARD, CCAFS and IFPRI study in the region.

High temperatures, above the ranges tolerated by crops, will definitely affect the physiology of plants, including the staple crops of the region. One consequence will be decreased productivity, which will affect food production. In contrast, a drastic increase in rainfall in hitherto dry areas could pose serious challenges to adaptation and the conservation of biodiversity, at least in the short run. Increased humidity and flooding could threaten the existence of plants and animals adapted to the dry conditions in the Sahel.

This situation could be compounded by genetic erosion arising from the inability of plants to survive harsh conditions. Acting now could help save the 10 to 15% of species that will otherwise likely be lost in an Africa that is 2°C warmer than preindustrial days (Parry et al. 2007). This situation will demand actions on many fronts, including conservation of biodiversity, water conservation and the development of irrigation, and capacity building at various levels, all of which will require adequate resources and policy frameworks.

Patterns of genetic variability and their implications for exploring genetic resources for adaptation and mitigation to changes in the climate

Abdallah Bari⁽¹⁾, Selvadurai Dayanandan⁽²⁾, Hamid Khazaei⁽³⁾, Yogendra P. Chaubey⁽²⁾, Frederick L. Stoddard⁽³⁾, Damon Matthews⁽²⁾, Kenneth Street⁽¹⁾, Mikko J. Sillanpää⁽⁴⁾, Lhassane Sikaoui⁽⁵⁾, Hassan Ouabbou⁽⁵⁾, Bennasser Alaoui⁽⁶⁾ and Chandrashekha Biradar⁽⁷⁾

⁽¹⁾ *International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco*

⁽²⁾ *Concordia University, Montreal, Canada*

⁽³⁾ *University of Helsinki, Helsinki, Finland*

⁽⁴⁾ *University of Oulu, Oulu, Finland*

⁽⁵⁾ *Institut National de la Recherche Agronomique, Morocco*

⁽⁶⁾ *Institut Agronomique et Vétérinaire Hassan II, Rabat, Morocco*

⁽⁷⁾ *International Center for Agricultural Research in the Dry Areas (ICARDA), Amman, Jordan*

E-mail: a.bari@cgiar.org

Abstract

Patterns of genetic variation can be detected at various scales, ranging from traits, as networks of genes, to populations, as a spatially structured network of individuals. The presence of such patterns implies the possibility of quantifying genetic variability to predict and capture traits, such as water use efficiency (WUE) that could withstand extreme environmental conditions resulting from changes in the climate. At the trait level, the expression of some of the genes involved may increase or decrease the expression of other genes, forming a complex network of interactions. There are many such complex networks of genes that involve genotype x environment interactions and also epistatic interactions between genes regulating trait variation.

The interaction and functioning among these networks of genes could be predicted if these networks were sufficiently understood and appropriately quantified. At the population level, the resulting patterns are partly the result of boundaries set by ecological and evolutionary processes. Such patterns have facilitated the tracing of the origin of crops, their genetic diversity, and identifying the traits associated with extreme environments. These patterns have been explored for predicting the occurrence of traits adaptive to changes in climate based on the assumption that a trait, as a response variable, is driven by stochastic, ecological, and evolutionary processes that could be predicted through mathematical modeling approaches.

This paper presents current progress in identifying traits adaptive to expected changes in the climate as a result of exploring the patterns of genetic variability, and discusses future prospects in addressing uncertainties in the phenological shifts induced by climate change.

Geoinformatics and genetic resources under changing climate

Chandrashekhar Biradar⁽¹⁾, Abdallah Bari⁽¹⁾, Prashant Patil⁽¹⁾, Murari Singh⁽¹⁾, Ahmed Amri⁽¹⁾, C.Jeganathan⁽²⁾

⁽¹⁾ International Center for Agricultural Research in the Dry Areas (ICARDA), Amman, Jordan

⁽²⁾ International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

⁽³⁾ Birla Institute of Technology (BIT), Mesra, Ranchi, India

E-mail: c.biradar@cgiar.org

Abstract

Each species requires a minimum/optimum area for its survival, evolution, and gene exchange. Analysis of habitat condition, function, composition, fragmentation, patchiness, interspersed, and juxtaposition has an impact on the ecology and evolutionary process. The greater the variety of types of habitat, the greater is the diversity of genetic resources and the better the chances of mitigating the extinction risk from the ever changing climate. However, spatial representations of the habitat and genetic resources at a scale which can be used for genetic resources management and conservation planning are lacking.

This paper presents an application of geoinformatics technology in the characterization of genetic resources at the landscape level. The resultant outputs in the geospatial domain help in delineating the biodiversity-rich hot-spots, their spatial pattern, and variability under the influence of biophysical, socioeconomic, and climatic conditions. These will further assist in the identification of the potential areas for germplasm collection, in situ biodiversity conservation, and exploring the various traits for climate smart agriculture. It also discusses bio-prospecting of the genetic resources and the implications of this in climate change adaptation and mitigation.

Testing, screening, and improving the salt tolerance of durum wheat genetic resources

Ramzi Chaabane⁽¹⁾, Abdelkader Saidi⁽¹⁾, Mustapha Rouissi⁽¹⁾, Masanori Inagaki⁽²⁾, Abdallah Bari⁽²⁾

⁽¹⁾ Applied Plant Biotechnology Laboratory, National Agronomic Research Institute of Tunisia (LBAA-INRAT), Tunisia

⁽²⁾ International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

E-mail: ramzic2003@yahoo.it

Abstract

Fresh water is a scarce resource. According to the World Meteorological Organization, only 2.5% of the total water volume on the Earth is fresh water, the remainder is saline. Irrigation with saline water induces salt stress and considerably reduces crop growth and yield. Agricultural losses caused by salinity are expected to increase with increasing climatic changes. Changes in climatic variables, such as precipitation and temperature, can significantly alter the hydrologic cycle and exacerbate the salinity problems. Improving the salt tolerance of plants has been proposed as part of the solution to some of these problems.

Developing plants with such multi-genetic complex trait improved, involves overcoming a variety of difficulties. First we have to define a valuable genetic resources screening method for this trait. Based on this method, we have to screen a huge number of available genetic resources. Finally we have to use various breeding technologies to develop new salt-tolerant cultivars. Both traditional plant breeding and biotechnology-based techniques are needed to produce plants with the desired quality traits. The present study is an example of combining different strategies, approaches, and techniques to overcome these difficulties to improving the salt tolerance of durum wheat.

On normalizing transformations of the coefficient of variation for a normal population with an application to the evaluation of the uniformity of plant varieties

Yogendra P. Chaubey

Department of Mathematics and Statistics, Concordia University, Montreal, QC, Canada.

E-mail: yogen.chaubey@concordia.ca

Abstract

The variance stabilizing transformation (VST), which was formally introduced by Bartlett (1947), is quite popular in statistical applications because of its approximate normalizing property. This property mainly arises because the VSTs may be more symmetric compared to the untransformed statistics. Chaubey and Mudholkar (1983) developed a differential equation, analogous to Bartlett's, for obtaining an approximately symmetrizing transformation and illustrated its use in some common examples. In general, the transformation may be computationally intensive, as illustrated in Chaubey et al. (2013), in terms of the coefficient of variation from normal samples. In this talk we review these transformations in this light and examine some new transformations along with an application to evaluate the uniformity of plant varieties.

Fruit genetic resources facing increasing climate uncertainty

O. Saddoud Dabbebi⁽¹⁾, S. Mnasri⁽¹⁾, S. Abdelaali⁽¹⁾, and M. Mars⁽²⁾

⁽¹⁾ Banque Nationale de Gènes, Boulevard du Leader Yesser Arafet, Charguia 1, Tunis, Tunisia

⁽²⁾ Unité de Recherche Agrobiodiversité, Institut Supérieur Agronomique de Chott Mariem, Sousse, Tunisia

Email: olfa.lf@gmail.com

Abstract

In Tunisia, fruit genetic resources are well diversified and economically significant. Fruit crops occupy nearly 2.2 million ha and represent more than 34 species. Most of the species have local or autochthonous varieties or cultivars adapted to local environmental and agrotechnical conditions. Arid lands cover about two-thirds of Tunisia and the country is increasingly vulnerable to climate change. During the last decades, frequent variability in precipitation, winter and summer temperatures, floods, and rising sea levels were observed. Additionally, economic pressure has compelled farmers to substitute local varieties with new, more productive ones. This fact may anticipate the genetic erosion of very well adapted varieties.

The fruit trees group in the Tunisian National Gene Bank (BNG) is working on the evaluation and conservation of fruit genetic resources in order to improve their management and for a better valorization of this heritage. Taking into account these considerations, many surveys and meetings were organized and allowed an inventory of collections to be established and the degree of the genetic erosion threat identified. Our work is focusing on the genetic evaluation of adapted varieties. The main objective is to better use and conserve these resources for a better adaptation to climate change.

Targeted search for crop germplasm with climate change adaptive traits to sustain agriculture in dryland systems

Selvadurai. Dayanandan^{(1),(2)} and Abdallah. Bari⁽³⁾

⁽¹⁾ Centre for Structural and Functional Genomics and Biology Department, Concordia University, Quebec, Canada

⁽²⁾ Quebec Centre for Biodiversity Sciences, Montreal, Quebec, Canada

⁽³⁾ International Center for Agricultural Research in the Dry Areas, Rabat Institute/Rabat, Morocco

Email: daya.dayanandan@concordia.ca

Abstract

The predicted increases in temperature and frequency of drought associated with global climate change will have significant negative impacts on agricultural production in the drylands, which constitute more than 40% of global land cover and are home to over 2.5 billion people. Crop cultivars with tolerance to heat and drought, and resistance to emerging virulent pests and diseases are urgently needed to sustain agriculture in dryland systems under changing climatic conditions. Crop improvements to meet these challenges will largely depend on the identification and effective use of naturally occurring variants of genes related to traits adaptive to changes in the climate.

Although many suitable natural variants of these genes or alleles are present in crop accessions stored in more than 1700 national and international genebanks, finding such alleles in over 7 million accessions of crops is a daunting task. An integrative, multidisciplinary approach, involving analyses of these crop accessions, using emerging mathematical modeling techniques and high throughput omic technologies, including phenomics, genomics, proteomics, and transcriptomics, are needed. This will help to achieve the rapid and cost efficient identification of genes or genomic regions associated with climate change adaptive traits and accelerate crop improvement programs to maintain biodiversity, food security, and livelihoods under changing climatic conditions.

Barley genetic resources under climate changes: a possible way in field study

A. Jilal, M. Maatougui, and H. Ouabbou

Chercheur chargé du programme national l'amélioration génétique de l'orge (Barley Breeder) Institut National de la Recherche Agronomique (INRA) Rabat, Morocco

Email: abderrazek_2001@yahoo.fr

Abstract

The untapped reservoir of useful genes in barley genetic resources for biotic and abiotic stresses needs to be exploited. Time and field space consumed in identifying useful genes has led to a new way of thinking about field assessment. The use of head planting in early generation seed increase, associated with a honeycomb design, could be an effective way for evaluating barley landraces. Identifying 10,000 accessions in one hectare for tolerance to stresses and intra-plant competition might be a new tool for the rapid development of the FIGS (Focused Identification of Germplasm Strategy) subset and core collection.

Identifying climate patterns during the crop growing cycle from 30 years of CIMMYT elite spring wheat international yield trials

Zakaria Kehel, Jose Crossa, and Matthew Reynolds

International Maize and Wheat Improvement Center (CIMMYT)-Mexico: CIMMYT, Mexico, D.F., Mexico

Email: z.kehel@cgiar.org

Abstract

In total, 954 location × year combinations, characterized by 22 climatic variables during three wheat development stages, were used to identify spatio-temporal patterns in CIMMYT elite spring wheat international yield trial locations globally from 1986 to 2009. We used linear and non-linear data mining methods to gain a better understanding of when and where most climate change occurred in major wheat growing regions. Clear temporal change was found in most climatic variables studied, especially temperature, during three wheat stages – vegetative, reproductive, and grain filling.

Results revealed that the wheat cycle is facing a significant rise in temperature, especially the maximum temperature, and in particular at the end of the cycle. Most climatic variables showed a strong spatial pattern. Locations with high temperatures during grain filling are found in the same geographic regions. The maximum temperature showed an unpredictable pattern during the reproductive and vegetative stages mainly in the Mediterranean region and along the Nile River. Principal component analysis did not identify any pattern in these data, but summarized them into a few axes that can be explained by climatic factors and/or/ by specific wheat development periods. Additionally, we demonstrated the capability of self-organized maps to identify, both analytically and visually, regional and temporal climate changes that have occurred in CIMMYT yield trial locations since 1986.

Mining CIMMYT germplasm bank for assessing breeding targets for climate change adaptation

Zakaria Kehel, Jose Crossa, Thomas Payne, and Matthew Reynolds

International Maize and Wheat Improvement Center (CIMMYT)-Mexico: CIMMYT, Mexico, D.F., Mexico

Email: z.kehel@cgiar.org

Abstract

Every year CIMMYT sends promising lines coming from the breeding pipelines of the global wheat program to a large number of partners located globally. Each location represents certain mega environments already defined for wheat. The mega environments are used by the breeders to plan and target their breeding efforts. Many institutions are evaluating these lines and send feedback on grain yields, phenotypic information, and pest and disease scorings.

This data set, spanning several decades, is used to analyze the effect of climate variability on grain yield in a large variety of environments. Data from two of the CIMMYT international yield trials – elite spring (ESWYT) and semi-arid (SAWYT) – were preserved and analyzed for genotype x environment (GE) interaction. GE analysis was undertaken each year the genotypes were sent to collaborators and locations and from which CIMMYT obtained the different data from one year to the next. Thus, 92 combinations of climatic variables, characterizing the locations for three physiological stages of the wheat (vegetative, reproductive, and grain filling) were used to dissect the climate/stage driving the yield variability for SAWYT and ESWYT over the years.

Several climatic covariates were significant and are capable of explaining some of the GE. Genotypic sensitivities to specific climatic variables were then computed and helped identify genotypes favored by abiotic stresses. High density genotypic data was also used, together with climate, to predict genotypic performance under specific climatic conditions and to estimate missing phenotypic values of wheat germplasm accessions.

Root trait differences between wet- and dry-adapted sets of faba bean accessions selected by FIGS

Hamid Khazaei⁽¹⁾, Abdallah Bari⁽²⁾, Kenneth Street⁽²⁾ and Frederick L. Stoddard⁽¹⁾

⁽¹⁾ Department of Agricultural Sciences, University of Helsinki, Helsinki, Finland

⁽²⁾ International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

Email: hamid.khazaei@helsinki.fi

Abstract

Grain legumes, such as faba bean (*Vicia faba* L.), are important sources of protein, particularly for people in developing countries where climate change is expected to result in higher temperatures and changing precipitation patterns. Among grain legumes, faba bean is thought to be relatively sensitive to drought. Deeper roots and larger root biomass have been shown to be important contributors to crop performance under drought conditions. Thus root traits could be used as the selection criteria for drought adaptation. During 2010–2011, two sets of faba bean accessions, from 'wet' and 'dry' regions, each containing 201 accessions, were chosen using the Focused Identification of Germplasm Strategy (FIGS). FIGS uses the environmental data (geographic and agro-climatic information) associated with the collection sites of plant genetic resources to identify sets of accessions 'most likely' and, in this case, 'least likely' to express the trait of interest. The two sets were screened for a variety of morpho-physiological leaf traits related to drought adaptation.

The results showed that FIGS successfully differentiated between material selected according to collection site moisture availability. From these results, it was hypothesized that root traits of the two FIGS sets would reflect their different geographic origins. Hence, root traits of six representative accessions from each set (chosen by principal component analysis) were evaluated under well watered conditions and then, under water deficit. Under well watered conditions, the 'dry' set had significantly higher root biomass than the 'wet' set, but no differences for root length and gas exchange traits. When the plants were exposed to water deficit, root length, root, and shoot biomass decreased significantly more in the 'wet' set than in the 'dry' one. The 'dry' set showed higher gas exchange than the 'wet' set under water deficit.

These results, together with those on leaf traits, confirm the ability of the FIGS to identify germplasm for breeding for drought resistance in faba bean, and this may be extended to other crops and to other traits related to abiotic stresses and adaptation to climate change.

Olive of Marrakesh: an opportunity to study the behavior of olive genotypes with respect to climate change

Sikaoui Lhassane⁽¹⁾, Abdelmajid Moukhli and Abdallah Bari⁽²⁾

⁽¹⁾ Institut National de la Recherche Agronomique (INRA) Marrakech, Marrakesh, Morocco

⁽²⁾ International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

Email: sikaouilhassane@yahoo.fr

Abstract

The olive crop (*Olea europaea* L.) is characterized by its large diversity because of its local domestication and breeding in different regions surrounding the Mediterranean over the centuries and across civilizations. There has been continuous characterization of this diversity in these different olive-growing regions with the collaboration of the International Olive Oil Council. A total of 1200 accessions have been identified with more than 3000 names. Forty varieties of them are grown in large areas in different countries. These accessions are maintained in three different germplasm banks: in Cordoba (Spain), representing the north of the Mediterranean; Marrakesh (Morocco), for the south; and Izmir (Turkey), representing the east.

The Marrakesh collection currently contains approximately 600 genotypes from 15 olive-growing countries. This collection is available to the scientific community to undertake research studies on their behavior in the Mediterranean olive-growing areas, mostly to the south. Molecular characterization has identified a core collection of 98 genotypes. In relation to climate change, this collection provides an interesting opportunity to study the behavior of the olive in a very difficult environment in terms of rainfall (200 mm annually), water scarcity, and sudden increases in spring temperatures, with significant implications for phenology, such as flowering, in some varieties. It was found that some varieties do not bloom possibly because of an inadequate cold spell. This is also an opportunity for the Moroccan olive varietal with a less diversified profile. The timing of the phenological stages could extend the period, which would avoid any climate incidents and diversify olive products

Technology transfer into agriculture: an operational framework

Jean A. Nyemba

Consultant for Innovation in Agriculture, (Former ICRISAT Regional Coordinator for West and Central Africa), Yaoundé, Cameroon

Email: jnyemba@gmail.com

Abstract

The operational framework proposed takes into account key elements of the process of innovation development, innovation transfer, and adoption.

1. From a conceptual perspective, the activities cover very well agricultural innovation, supply and demand, coordination and partnerships for the diffusion of innovations, and the strategic linkages to be strengthened for sustainability and adaptation to climate change.
2. From an operational standpoint, the ideas proposed could help develop a strategy and tools for understanding the innovation development process, its outcomes and impacts for the different stakeholders involved in the process of research, innovation development, and use with climate change and demand/market-driven perspectives.

It is important to pay attention to the private sector, from the perspective of a market-driven approach. The elements proposed are constructed from a structural model involving:

- The innovation development process: knowing the strategic crops targeted by the selected research institutions, and the relevance for food security and/or private sector investment; knowing the strategic crops grown by households and private investors, and the relevance for food security and/or private sector involvement; understanding how climate change is addressed in the process of innovation development and relevance to needs
- Innovation dissemination outcome: existence of an innovation supply chain to address innovation availability and access; existence of an organized system of innovation demand/access to address households and private investors' innovation needs; how climate change is understood and addressed by actors in the supply chain
- Innovation adoption impact: key elements include impact for research institutions; increased research capacity/funding and assets, staff development, extension/outreach, partnerships, networking, and private sector involvement; impact for households and private investors, increased production and productivity, increased income levels, increased levels of innovation use, increased and strengthened business for local agro-dealers; impact for sustainable natural resources management: soils, watershed, lowland, forest.

Genomic diversity and domestication of soybean

Ying-hui Li⁽¹⁾, Jianxin Ma⁽²⁾, Guangyu Zhou⁽³⁾, Scott Jackson⁽⁴⁾, Rui-qiang Li⁽³⁾, Li-juan Qiu⁽¹⁾

⁽¹⁾ The National Key Facility for Crop Gene Resources and Genetic Improvement (NFCRI), Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing, China

⁽²⁾ Department of Agronomy, Purdue University, West Lafayette, IN, USA

⁽³⁾ Novogene Bioinformatics Institute, Beijing, China

⁽⁴⁾ Center for Applied Genetic Technologies, University of Georgia, Athens, GA, USA

Email: qiulijuan@caas.cn

Abstract

Domestication is a multi-faceted process that is amenable to study by a wide range of disciplines, including archaeology, anthropology, molecular genetics, and evolutionary biology. Domesticated soybean (*Glycine max* (L.) Merr.), and its wild progenitor, *G. soja*, exhibit substantial morphological differences in growth habits, seed-coat color, seed size, etc. Our genealogical analyses of 420 *G. max* and *G. soja* accessions indicated that cultivated soybean tended to form a monophyletic clade with respect to *G. soja*, and the primary division of genetic diversity was between the wild and domesticated accessions. To elucidate the consequences of artificial selection accompanying the domestication of soybean, we analyzed 55 whole-genome re-sequencing accessions as well as seven representative de novo sequencing *G. soja* accessions.

We found that artificial selection during domestication led to a pronounced reduction in the genetic diversity of soybean. Inter-genomic comparisons identified 1978 genes with copy number variation, 338 genes with *G. soja*-specific presence-absence variation, and 2094 genes affected by artificial selection during domestication for preferred agricultural traits. Comparing candidate domestication-related genes with previous QTLs, as well as their homologs, we found some genes may contribute to variation of agronomic traits, such as pathogen resistance, seed composition, flowering and maturity time, organ size, and final biomass. Accordingly, our study of soybean domestication has yielded fundamental insights into the genes and biological mechanisms that underlie morphological change, and the strength and patterns of selection. The results will facilitate harnessing the untapped genetic diversity from wild soybean for enhancement of elite cultivars.

Adaptation of the potato crop to climate change

Roland Schafleitner⁽¹⁾, Julian Ramirez⁽²⁾, Andy Jarvis⁽²⁾, Daniele Evers⁽³⁾, Raymundo Gutierrez⁽⁴⁾, Mariah Scurrah⁽⁴⁾

⁽¹⁾ The World Vegetable Center (AVRDC), Shanhua, Tainan, Taiwan

⁽²⁾ International Center for Tropical Agriculture (CIAT), Cali, Colombia

⁽³⁾ Centre de Recherche Public (CRP) - Gabriel Lippmann, Belvaux, Luxembourg

⁽⁴⁾ International Potato Center (CIP), Lima, Peru

Email: roland.schafleitner@worldveg.org

Abstract

Potato (*Solanum tuberosum* L.) is the third most important global food crop, with an annual worldwide production of more than 300 million tonne. Demand for potato is increasing strongly, particularly in developing countries where the crop is recognized for its contribution to food security. Modern cultivars require moderate climates and a sufficient and regular supply of water for high yields. Climate change scenarios project a significant rise in average temperatures in the 21st century, accompanied by more frequent extreme weather events, such as droughts and heat waves. We have established climate change projections for potato growing areas using statistically downscaled outputs of selected global circulation models from the Intergovernmental Panel on Climate Change (IPCC) for 2010–2039 and emission scenarios from the IPCC Special Report on Emission Scenarios (SRES-A2).

The resulting climate scenarios were analyzed using the EcoCrop model to estimate regional changes in suitability for potato production. Changes in precipitation were predicted to remain relatively modest. Temperature changes may be more critical for potato production, as predominant cultivation areas overlap with regions with higher projected temperatures. The most significant losses in potato production suitability were predicted to occur in the tropics – yet the average expected change in suitability was positive (+1.3%). Although this gain represents a considerable area and amount, it is predicted to occur in very high latitudes or high altitudes, where the current climatic constraint is the minimum temperature. Our study suggests improving heat tolerance is crucial to mitigate climate change effects, and improving cold tolerance would allow expansion of production to new areas. In contrast, drought tolerance might contribute little to the adaptation of the potato crop to climate change.

Anticipated dryland expansion in scenarios of global warming

C.T. Simmons and H.D. Matthews

Department of Geography, Planning and Environment, Concordia University, Montréal, QC, Canada

E-mail: christophesimmons@gmail.com

Abstract

Climate models are an invaluable resource for assessing the responses of Earth systems to changes in atmospheric chemistry. In order to account for uncertainties in the future concentrations of greenhouse gases and aerosols, the Intergovernmental Panel on Climate Change (IPCC) has recently developed several standardized scenarios, called Representative Concentration Pathways (RCP), which have been incorporated into climate models to explore future changes in global temperatures and hydrology. Applying these pathways, recent modeling work, carried out as part of the Climate Model Inter-comparison Project (CMIP, Phase 5), shows dryland expansion over the next century for two RCP scenarios, and most notably in the business-as-usual case (RCP8.5).

These models project an average 10% increase in global dryland extent by the end of the century. In these model runs, climate regime shifts to arid conditions are most common in subtropical regions, such as the Mediterranean basin, southern Africa, central Asia, southwestern North America, and Australia. This is due in part to a simulated intensification of the Hadley Circulation. Modeled precipitation modestly increases in some mid-latitude and tropical regions; however, many of these areas also experience decreases in atmospheric humidity (and increases in evaporation) in response to the greater heating of land surfaces from greenhouse gas forcing. Despite the shift toward drier conditions over land areas in many simulations, model variability, poor resolution of convective precipitation, and uncertainties in the RCP scenarios themselves merit important consideration when interpreting model output and the predicted changes in dryland extent.

Efficacy of herbicides and genetic resistance for managing *Striga* infestations of sorghum in West Africa

Souley Soumana⁽¹⁾, Issoufou Kapran⁽¹⁾, Aboubacar Toure⁽²⁾, Mountaga Kayentao⁽²⁾, Kassim Al-Khatib⁽³⁾, Newton Ochanda⁽³⁾, Aad van Ast⁽⁴⁾, Lammer Bastiaans⁽⁴⁾ and Mitchell Tuinstra⁽⁵⁾

⁽¹⁾ Istituto Nazionale di Ricerca per gli Alimenti e la Nutrizione (INRAN), Niamey, Niger

⁽²⁾ Institut d'Economie Rurale (IER), Bamako, Mali

⁽³⁾ Kansas State University, Manhattan, Kansas, USA

⁽⁴⁾ Wageningen University and Research Center, Wageningen, Netherlands

⁽⁵⁾ Purdue University, West Lafayette, Indiana, USA

E-mail: nsoumana@yahoo.com

Abstract

Striga infestations are one of the greatest obstacles to sorghum production in Africa. Seeds of a herbicide tolerant sorghum hybrid (Atx623 x Tailwind) were treated as follows:

- 3 rates of imazapyr (0.018, 0.037 and 0.075 mg ai seed⁻¹)
- 3 rates of metsulfuron (0.003, 0.006 and 0.012 mg ai seed⁻¹)

Untreated seeds were used as a control.

Seven inbred lines and their testcross hybrids were evaluated in '*Striga* sick-plots' in Konni, Niger and Cinzana, Mali in 2005 and 2006. The study indicates that the metsulfuron and imazapyr herbicide seed treatments can significantly delay *Striga* emergence. The study indicated that Wassa and its hybrid were significantly more susceptible than SRN-39 or Brhan in trials in Niger. SRN-39 and Brhan were identified as the most resistant to *Striga* across locations.

Climate change and an increasing protein deficit: why Europe needs to exploit the genetic resources of protein crops now

Fred Stoddard

Department of Agricultural Sciences, University of Helsinki, University of Helsinki, Finland

Email: Frederick.stoddard@Helsinki.fi

Abstract

Europe suffers from a huge deficit in plant protein; 70% of its plant protein needs are imported. These imports are mostly in the form of soya bean from North and South America and mostly used to feed pigs and chickens. At the same time, its rotations are too narrowly based on the high-yielding small-grain cereals, particularly wheat and barley, so soil-borne diseases of cereals may become endemic. Furthermore, European agriculture relies heavily on inputs of nitrogen from fertilizer and, to a lesser extent, manure, with consequences for greenhouse gas releases and nitrate leaching. Many of these difficulties, and others, can be at least partially resolved by the increased use of grain legumes that fix their own nitrogen, provide high-protein seeds for food and feed use, leave at least some nitrogen-rich residue for following crops, and break the cycles of soil-borne diseases of cereals while promoting the growth of beneficial soil microorganisms.

The yields of legumes lag behind those of the cereals, as do their stress resistances, largely because of a relative lack of breeding effort for the past two to three decades. In order for European legume yields and yield stability to improve, and to withstand the increased stresses expected from climate change, new sources of stress resistance, yield, and quality urgently need to be identified for the major grain legume crops. The new traits then need to be transferred into agronomically viable cultivars by developing rapid, omics-supported methods. The European Parliament has been told that Europe needs to support legume farming appropriately, in order to reap the public-good benefits of legume-supported cropping systems, and the European Commission has been told that legume breeding needs research support in order to reduce the protein deficit. Our success with using FIGS and omics for drought adaptation in faba bean, discussed elsewhere in this conference, shows how these advances can be made, and future projects will focus on other crops, such as narrow-leafed lupin and alfalfa, and other stresses, such as water logging and acid soil tolerance, as these are already important in many countries and are expected to become more so.

Patterns and climate change-induced patterns and their implications in the predictions to explore genetic resources for adaption and mitigation

**Abdallah Bari⁽¹⁾, Selvadurai Dayanandan⁽²⁾, Yogen P. Chaubey⁽²⁾, Frederick L. Stoddard⁽³⁾,
Hamid Khazaei⁽³⁾, Damon Mathews⁽²⁾, Ken Street⁽¹⁾, Mikko J. Sillanpää⁽⁴⁾, and
Chandrashekhar Biradar⁽⁵⁾**

⁽¹⁾ *International Centre for Agricultural Research in the Dry Areas, Rabat, Morocco*

⁽²⁾ *Concordia University, Montreal, France*

⁽³⁾ *University of Helsinki, Helsinki, Finland*

⁽⁴⁾ *University of Oulu, Oulu, Finland*

⁽⁵⁾ *International Centre for Agricultural Research in the Dry Areas, Amman, Jordan*

Email: a.bari@cgiar.org

Abstract

Patterns in genetic variation can be detected at different scales, from the trait level as a network of genes, to the population level in terms of its spatial structure as a network of individuals. The presence of such patterns implies the possibility of quantification and prediction, thus allowing the capture and prediction of traits that withstand climate change such as water use efficiency, WUE. At the trait level, the expression of some of the genes involved may increase or decrease the expression of other genes, forming a complex network of interactions). There are many such complex networks of genes that involve genotype-by-environment interactions and also epistatic interactions between genes regulating trait variation (Cooper et al. 1999; Dennis 2002). At the population level, the patterns are also partly the result of boundaries set up by ecological and co-evolutionary processes. Such patterns have helped in tracing back the origin and diversity of crops and in locating new trait variation. These patterns have been explored in predicting the occurrence of traits related to climate change based on the assumption that a trait, as a response variable, is driven by stochastic ecological and co-evolutionary processes where modelling could be used for its prediction. This research focuses on the presence of patterns and the potential of exploring such patterns to predict and locate traits related to climate change. The paper presents current progress in identifying climate change related traits based on exploring the patterns, and discusses future prospects in addressing uncertainties in the phenological shifts induced by climate change.

Detecting selection along environmental gradients: analysis of eight methods and their effectiveness for outbreeding and selfing populations

Stéphane De Mita⁽¹⁾, Anne-Céline Thuillet⁽¹⁾, Lauréne Gay⁽²⁾, Nour Ahmadi⁽³⁾, Stéphanie Manel⁽⁴⁾, Joelle Ronfort⁽²⁾, Yves Vigouroux^{(1),(5)}

⁽¹⁾ Institut de Recherche pour le Développement (IRD), Montpellier, France

⁽²⁾ Institut National de la Recherche Agronomique (INRA), Montpellier, France

⁽³⁾ Centre International de la Recherche Agronomique pour le Développement (CIRAD), Montpellier, France

⁽⁴⁾ Université de Provence, Aix en Provence, France

⁽⁵⁾ Université Montpellier II, Montpellier, France

Email: yves.vigouroux@ird.fr

Abstract

Thanks to genome-scale diversity data, present-day studies can provide a detailed view of how natural and cultivated species adapt to their environment and, particularly, to environmental gradients. However, because of their sensitivity, up-to-date studies might be more sensitive to undocumented demographic effects, such as the pattern of migration and the reproduction regime. In this study, we provide guidelines for the use of popular or recently developed statistical methods to detect footprints of selection. We simulated 100 populations along a selective gradient and explored different migration models, sampling schemes, and rates of self-fertilization. We investigated the power and robustness of eight methods to detect loci potentially under selection; three were designed to detect genotype-environment correlations and five designed to detect adaptive differentiation (based on F_{ST} or similar measures).

We show that genotype-environment correlation methods have substantially more power to detect selection than differentiation-based methods, but that they generally suffer from high rates of false positives. This effect is exacerbated whenever allele frequencies are correlated, either between populations or within populations. Our results suggest that, when the underlying genetic structure of the data is unknown, a number of robust methods are preferable. Moreover, in the simulated scenario we used, sampling many populations led to better results than sampling many individuals per population. Finally, care should be taken when using methods to identify genotype-environment correlations without correcting for allele frequency autocorrelation because of the risk of spurious signals as a consequence of allele frequency correlations between populations.

Spatial and temporal variation in the selection of genes associated with varietal quantitative traits *in situ*

Cédric Mariac^{(1).(2)}, Issaka Salia Ousseini^{(1).(2).(3).(4)}, Abdel-Kader Alio⁽²⁾, Hélène Jugdé⁽²⁾, Jean-Louis Pham⁽¹⁾, Gilles Bezançon^{(1).(2)}, Joelle Ronfort⁵, Luc Descroix^{(2).(6)}, Yves Vigouroux^{(1).(2).(3)}

⁽¹⁾ Institut de Recherche pour le Développement (IRD), Montpellier, France

⁽²⁾ Institut de Recherche pour le Développement (IRD), Niamey, Niger

⁽³⁾ University Montpellier II, Montpellier, France

⁽⁴⁾ University Abdou Moumouni of Niamey, Niamey, Niger

⁽⁵⁾ Institut National de Recherche Agronomique (INRA), Montpellier, France

⁽⁶⁾ Institut de Recherche pour le Développement (IRD), Grenoble, France

Email: yves.vigouroux@ird.fr

Abstract

Current cases of polymorphism maintained by variable selection in space and time are very modest. One of the challenges of such a study is to assess selection *in situ*. In this study, we directly track the evolution of allele frequency in two genes associated with phenotypic variation *in situ*. We sampled 17 populations of cultivated pearl millet over two years. We track the evolution of allele frequencies in these populations by genotyping up to 7070 individuals. Inference of drift, based on microsatellite locus, concludes that several changes in allele frequencies are compatible with selection.

We also show that populations where changes in allele frequencies occur suggest selections were different geographically and from year to year. This result suggests a variable selection both spatially and temporally. Inference of selection in our experiment is high, but within the range of the strong selection coefficient published recently. Our study suggests that the polymorphism maintained by the genes studied might be partially explained by the variability of selection. We also discuss the particularity of our study system where human action had also a direct, potentially significant, impact.

Learning about the genetic basis of phenotypic variations: the limit of association study

**Abdoul-Aziz Saïdou^{(1),(2)}, Issaka Salia Ousseini^{(1),(3)}, Anne-Céline Thuillet⁽¹⁾, Marie Couderc⁽¹⁾,
Cédric Mariac⁽¹⁾ and Yves Vigouroux^{(1),(4)}**

⁽¹⁾ Institut de Recherche pour le Développement (IRD), Montpellier, France

⁽²⁾ University of Maradi, Maradi, Niger

⁽³⁾ University Abdou Moumouni of Niamey, Niamey, Niger

⁽⁴⁾ Université Montpellier II, Montpellier, France

Email: yves.vigouroux@ird.fr

Abstract

Association mapping studies offer great promise for identifying polymorphisms associated with phenotypes and for understanding the genetic basis of quantitative trait variation. To date, almost all association mapping studies based on structured plant populations examined the main effects of genetic factors on the trait, but did not deal with interactions between genetic factors and the environment.

In this paper, we propose a methodological prospect of mixed linear models to analyze genotype x environment interaction effects using association mapping designs. First, we simulated datasets to assess the power of linear mixed models to detect interaction effects. This simulation was based on two association panels composed of 90 inbreds (pearl millet) and 277 inbreds (maize). Based on the simulation approach, we reported the impact of effect size, environmental variation, allele frequency, trait heritability, and sample size on the power to detect the main effects of genetic loci and the diverse effect of interactions implying these loci. Interaction effects specified in the model included SNP x environment interaction, ancestry x environment interaction, SNP x ancestry interaction, and three way interactions. The method was finally used on real datasets from field experiments conducted on the two considered panels.

We showed two types of interaction effects contributing to genotype x environment interactions in maize: SNP x environment interaction and ancestry x environment interaction. This last interaction suggests a differential response at the population level in the function of the environment. Our results suggested the suitability of mixed models for the detection of diverse interaction effects. The need for samples larger than those commonly used in current plant association studies is strongly emphasized to ensure rigorous model selection and powerful interaction assessment. The use of the ancestry interaction component brought valuable information complementary to other available approaches. We also discuss the limit of association study for low frequency variants.

Geoinformatics and Genetic Resources under Changing Climate

**Chandrashekar Biradar⁽¹⁾, Abdallah Bari⁽¹⁾, Prashant Patil⁽¹⁾, Ahmed Amri⁽²⁾, Murari Singh⁽¹⁾,
C.Jeganathan⁽²⁾**

⁽¹⁾ International Centre for Agricultural Research in the Dry Areas (ICARDA), Amman, Jordan

⁽²⁾ International Centre for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco

⁽³⁾ Birla Institute of Technology (BIT), Mesra, Ranchi, India

Email: c.biradar@cgjar.org

Abstract

Each species requires minimum/optimum area for its survival, evolution and gene exchange. Analysis of habitat condition, function, composition, fragmentation, patchiness, interspersed and juxtaposition has an impact on the ecology and evolutionary process. Greater the variety of types of habitat, greater is the diversity of genetic resources and better the chances of mitigating the extinction risk from the ever changing climate. However, spatial representations of the habitat and genetic resources at a scale which can be used for genetic resources management and conservation planning are lacking. This paper presents application of geoinformatics technology in characterization of the genetic resources at landscape level. The resultant outputs in the geospatial domain help in delineation of the biodiversity rich hot-spots, its spatial pattern and variability under the influence of biophysical, socio-economic and climatic conditions. These will further assist in the identification of the potential areas for germplasm collection, in-situ biodiversity conservation, exploring the various traits for the climate smart agriculture. It also discusses bio-prospecting of the genetic resources and its implications in climate change adaptation and mitigation.

Key words: Genetic resources, Geoinformatics, Ecology, Climate Change

Toward better wheat adaptation to a changing climate: heat stress environments
OR
Wheat improvement for a changing climate: heat-stressed environments

Izzat S.A. Tahir

Wheat Breeder and Associate Professor, Agricultural Research Corporation (ARC), Wheat Research Program, Wad Medani, Sudan

Email: izzatahir@hotmail.com

Participants

Bennasser Alaoui	b.alaoui@iav.ac.ma
Tom Apina	tom.apina@sustainetea.org
Abdallah Bari	a.bari@cgiar.org
Chandrasekhar Biradar	c.biradar@cgiar.org
Ramzi Chaabane	ramzic2003@yahoo.it
Yogendra Chaubey	chaubey@alcor.concordia.ca
Olfa Dabbebi	olfa.lf@gmail.com
Ardeshir Damania	abdmania@ucdavis.edu
Selvadurai Dayanandan	daya.dayanandan@concordia.ca
Alganesh Gellaw	alganeshgellaw@yahoo.com
Yasmina Imani	y.imani@iav.ac.ma
Abderazek Jilal	abderrazek_2001@yahoo.fr
Zakaria Kehel	z.kehel@cgiar.org
Hamid Khazaei	hamid.khazaei@helsinki.fi
Ouiam Lahlou	ouiamlahlou@gmail.com
Mohamed Maatougui	m.maatougui@cgiar.org
Miloudi Nachit	m.nachit@cgiar.org
Jean Nyemba	jnyemba@gmail.com
Hassan Ouabbou	hassan.ouabbou@gmail.com
Lijuan Qiu	qiulijuan@caas.cn
Roland Schafleitner	roland.schafleitner@worldveg.org
Lhassane Sikaoui	sikaouilhassane@yahoo.fr
Christophe Simmons	christophesimmons@gmail.com
Souley Soumana	nsoumana@yahoo.com
Frederick Stoddard	Frederick.stoddard@Helsinki.fi
Izzat Tahir	izzatahir@hotmail.com
Sripada Udupa	s.udupa@cgiar.org
Yves Vigouroux	yves.vigouroux@ird.fr

