

First International Workshop
on
SYSTEMS BIOLOGY FOR HUMAN & PLANT NUTRITION
CENTER OF EXCELLENCE IN GENOMICS & SYSTEMS BIOLOGY
ICRISAT, Hyderabad, India
March 22-24, 2018



Program
Abstracts
List of participants
Logistics



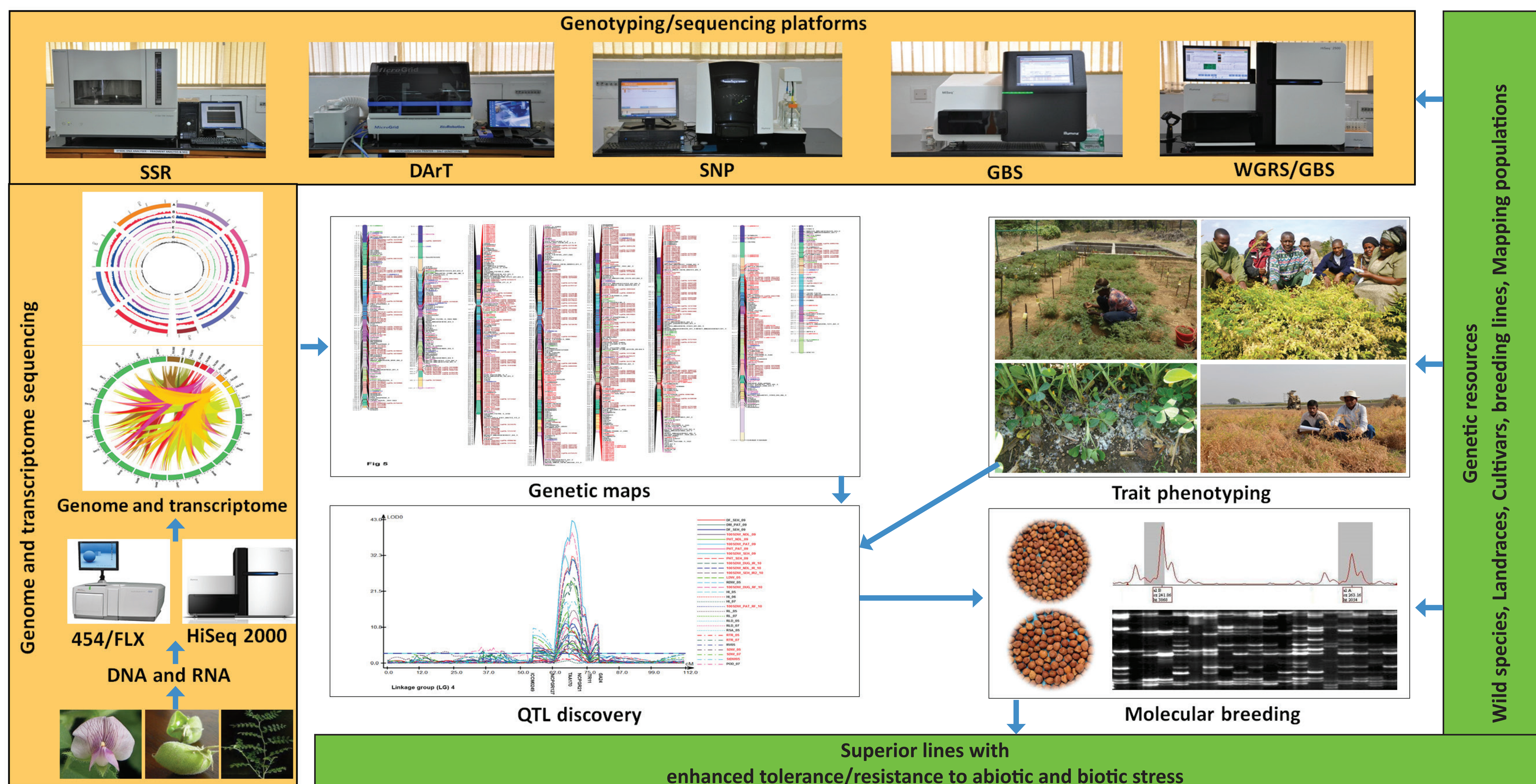
ICRISAT
INTERNATIONAL CROPS RESEARCH
INSTITUTE FOR THE SEMI-ARID TROPICS



Accelerating Genetic Gains in Crop Breeding Programs through Center of Excellence in Genomics (CEG)



Integrated genomics and breeding activities



Genome sequences

- Pigeonpea (Nature Biotech 2012, 30:83-89)
- Chickpea (Nature Biotech 2013, 31:240-246)
- Groundnut – A & B genomes (Nature Genetics 2016, 48:438-446), (PNAS 2016, 113: 6785-6790)
- Sorghum (available through US-led team)
- Pearl millet and finger millet (in progress)
- 3000 chickpea genome sequencing
- 1000 pearl millet genome sequencing
- Re-sequencing initiatives in sorghum, groundnut and pigeonpea

Molecular breeding

- Chickpea: drought tolerance and resistance to Fusarium wilt and Aschochyta blight
- Groundnut: resistance to rust and oil quality
- Sorghum: drought tolerance, resistance to shoot fly and Striga
- Pearl millet: resistance to blast, downy mildew and Fe and Zn
- Pigeonpea: markers for enhancing precision and efficiency of hybrid breeding

Marker resources

- Diagnostic markers for key traits
- >10,000 SSRs across mandate crops
- >10,000 SNPs across mandate crops
- High density DArT arrays for chickpea, pigeonpea and groundnut
- Affymetrix 50K+SNP arrays in chickpea, pigeonpea and groundnut
- High throughput & low cost genotyping platform (US\$ 1.5 per sample including DNA sample for 10 markers)

High performance computational genome analysis

- Number of cores 408
- Storage ~580 TB
- RAM 6 TB

Decision support tools

- ISMAB for molecular breeding
- GDMS for data management
- ISMU for mining SNPs based on NGS
- ISMU v 2 for deploying Genomic Selection
- GOBII for high-density genotyping data

Program

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Technical Program

Thursday, March 22, 2018
(212 Conference Hall)

08:30- 09:00 - Registration

09:00 – 10:00 hrs	Inaugural Session	
09:00 – 09:15	Welcome & Introduction	Rajeev Varshney <i>ICRISAT, India</i>
09:15 – 09:20	Inaugural Address	Peter Carberry , DDG- Research <i>ICRISAT, India</i>
09:20 – 09:30	About the workshop	Rajeev Varshney
09:30 – 10:00	Inaugural lecture: The gut microbiome in health and diseases – moving from mice and pigs to humans	Karsten Kristiansen <i>BGI-Shenzhen, China & University of Copenhagen Denmark</i>
10:00 – 10:30	<i>Group photo & Tea / Coffee Break</i>	
10:30 – 12:30 hrs	Session I: Human Gut/ Oral Microbiome Chair: <i>Karsten Kristiansen, BGI-Shenzhen, China & University of Copenhagen, Denmark</i> Rapporteur: <i>Lekha Pazhamala, ICRISAT, India</i>	
10:30 – 11:00 hrs	The Vienna Metabolomics Center – Applications in clinical studies and systems biology	Wolfram Weckwerth <i>University of Vienna Austria</i>
11:00 – 11:30 hrs	Molecular analysis of human Intestinal, oral and skin microbiome across the age groups in Indian patrilineal joint families	Dhiraj Dhotre <i>National Centre for Microbial Resources India</i>
11:30 – 12:00 hrs	The undernutrition story: Gut microbiome perspectives	Sourav Sen Gupta <i>Rajiv Gandhi Centre for Biotechnology India</i>
12:00 – 12:30 hrs	Factors influencing the human microbiome: genetics, environment, diet, and antibiotics	Liam Shaw <i>University College London UK</i>
12:30 – 13:30 hrs	<i>Lunch- 204 Banquet Hall</i>	

13:30 – 15:00 hrs	Session II: Human Gut/ Oral Microbiome Chair: Wolfram Weckwerth, University of Vienna, Austria Rapporteur: Sarita Pandey, ICRISAT, India	
13:30 – 14:00 hrs	Microbial role shift: Gut microbiota can be an asset or a problem to human host	V Deepak Bamola <i>All India Institute of Medical Sciences (AIIMS)</i> India
14:00 – 14:30 hrs	Role of legume derived synbiotic on immune modulation in mouse model- Relevance to gut health in humans	Himaja Nallagatla & Vasanthi Siruguri <i>ICMR-National Institute of Nutrition</i> India
14:30 – 15:00 hrs	Computational genomics of gut pathogens	Sabiha Shaik <i>International Centre for Diarrhoeal Disease Research</i> Bangladesh & <i>University of Hyderabad, India</i>
15:00 – 15:30 hrs	<i>Tea / Coffee Break</i>	
15:30 – 17:10 hrs	Session III: Country reports on nutrition (max 20' min each) Moderator: Rajeev Varshney, ICRISAT, India Rapporteur: Rakesh Kumar, ICRISAT, India	
	India- Country report on nutrition	KV Radhakrishna <i>ICMR- National Institute of Nutrition, India</i>
	Ghana- Country report on nutrition	Kwaku Tano-Debrah <i>University of Ghana, Ghana</i>
	Senegal- Current status of nutrition in Senegal: What is the contribution of the nutrition laboratory?	Nicole Idohou-Dossou <i>University Cheick Anta Diop of Dakar, Senegal</i>
	Mali- Country report on nutrition	Fatou Diawara Mme Traoré <i>Centre for Research and Documentation on Child Survival, Mali</i>
	Gambia- Country report on nutrition	Modou Jobe <i>MRC Unit The Gambia (MRCG), The Gambia</i>
18:00 hrs	Cocktails & Dinner - IMOD Plaza	

Friday, March 23, 2018
(Venue: 307 Conference Hall)

08:30 – 09:00 hrs	Session II: Human Gut/ Oral Microbiome continued Chair: Wolfram Weckwerth, University of Vienna, Austria Rapporteur: Sarita Pandey, ICRISAT, India	
08:30 – 09:00 hrs	Microbiome signatures in colorectal cancer	Manimozhiyan Arumugam <i>University of Copenhagen</i> Denmark

09:00 – 12:00 hrs	Session IV: Plant/Soil Microbiome & Trait Biology Chair: Apparao Podile, University of Hyderabad, India Rapporteur: Pallavi Sinha, ICRISAT, India	
09:00 – 09:30 hrs	Plant microbiome: Unravelling the biota black box	Vadakattu Gupta <i>Commonwealth Scientific and Industrial Research Organisation (CSIRO)</i> Australia
09:30 – 10:00 hrs	A critical role for pore connectivity in microbiome behaviour and metabolism in soil	Andrew Neal <i>Rothamsted Research</i> UK
10:00 – 10:30 hrs	<i>Tea / Coffee Break</i>	
10:30 – 11:00 hrs	Taxonomic structure and functional association of foxtail millet root microbiome	Tao Jin <i>BGI-Shenzhen</i> China
11:00 – 11:30 hrs	Proteomics to understand stress responsive mechanism in plants	Palak Chaturvedi <i>University of Vienna</i> Austria
11:30 – 12:00 hrs	Deciphering the dynamic biology of a pigeonpea environment-sensitive male sterile line	Lekha Pazhamala <i>ICRISAT</i> India
12:00 – 13:00 hrs	<i>Lunch- 204 Banquet Hall</i>	
13:00 – 17:00 hrs	<i>Brainstorming sessions</i>	
13:00 – 13:30 hrs	Proposed research activities @CEGSB-ICRISAT	Rajeev Varshney <i>ICRISAT</i> India
13:30 – 15:00 hrs	Gut Microbiome Brainstorming	Moderator: Manimozhiyan Arumugam <i>University of Copenhagen</i> Denmark
15:00 – 15:30 hrs	<i>Tea / Coffee Break</i>	
15:30 – 16:30 hrs	Soil Microbiome / Trait Biology Brainstorming	Moderator: Tao Jin <i>BGI-Shenzhen</i> China
16:30 – 17:00 hrs	Data Integration Brainstorming	Moderator: Prasad Bajaj <i>ICRISAT</i> India
17:00 – 17:30 hrs	Closing Session	
	Feedback about workshop Closing remarks Vote of thanks	Workshop delegates Peter Carberry Rajeev Varshney
18:00 hrs	<i>Dinner - Academic Court</i>	

1. ICRISAT Research Facilities

March 21, 2018	<i>14:00 hrs onwards</i>
	<ul style="list-style-type: none">* SAT Venture* Center of Excellence in Genomics & Systems Biology (CEGSB)* Genebank* Platform for Translational Research on Transgenic Crops (PTTC)

2. Hyderabad City / Monuments tour

March 24, 2018	<i>10:00 hrs onwards</i>
	<ul style="list-style-type: none">* Charminar* Golconda Fort* Qutub Shashi Tombs* Shilparamam

Abstracts

The gut microbiome in health and diseases – moving from mice and pigs to humans

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Monogenic diseases offer clear insight into the relation between genome and diseases, but the importance of the host genome in relation to more complex multifactorial diseases has proven more difficult to establish. During the last decade it has become well established that the gut microbiota may play an even more important role in relation to metabolism and immune functions, and evidence has been presented that the gut microbiota may also affect behavior. However, the exact molecular mechanisms by which bacteria in the gut exert their actions still remain elusive. In this lecture I will summarize recent work from Copenhagen and Shenzhen demonstrating how early life events and life styles modulate the development of the gut microbiota, how distinct changes the gut microbiota are associated several multifactorial diseases, how analyses of the oral or gut microbiota can be used for early non-invasion detection and stratification of patients prior to treatment, and how we can move from association to causality. I will conclude the lecture by discussing possible functional consequences and perspectives of these findings.

The Vienna Metabolomics Center – Applications in clinical studies and systems biology

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Metabolomics, the unbiased profiling of all small molecules in biological samples, has developed into a core technology for functional genomics, biobased economy and personalized medicine in the last decade. Recently, metabolomics has also emerged in ecosystem research and metagenomic studies. The Vienna Metabolomics Center (<http://metabolomics.univie.ac.at/>), headed by Univ.-Prof. Dr. Wolfram Weckwerth, provides state-of-the-art metabolomics technology with high quality preparation workflows and mass spectrometric standard operation protocols comprising gas -, liquid – and ion chromatography coupled to either triple quadrupole or high resolution mass spectrometry. Comprehensive metabolite libraries and workflows for structural elucidation of unknown structures as well as standard operation procedures for multi- and univariate statistics and genome-scale metabolic modelling are used for postprocessing and data mining 1-3. Furthermore algorithms for multi-omics and phenotypical metadata integration are established. Typically, genetic algorithms and machine learning processes are applied for feature selection and multiple regression methods4. In a complementary step biomathematical models of biochemical regulation are combined with data covariance structure analysis into a hybrid modelling approach revealing causal biochemical processes3. Applications will be presented ranging from fundamental aspects of data interpretation up to large-scale clinical studies investigating aging, diabetes, metabolic syndrome and the relation to gut microbiome dynamics.

Molecular analysis of human Intestinal, oral and skin microbiome across the age groups in Indian patrilineal joint families

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Human microbiome plays central role in the health and wellbeing of the host and is affected by variety of intrinsic and extrinsic factors such as host ethnicity, age, diet and geographic location. Composition of microbiota evolves throughout the life from birth to old age. Indian joint family structure provides the distinctive opportunity to study the effect of age on human microbiome by keeping other microbiome confounding factors almost similar. Here, we investigated human microbiome from 54 healthy individuals belonging three generations and six families staying in six separate households with the homogeneity in the diet, living standard and environment of the subjects. Gut and oral microbiome samples showed dominance of genus *Prevotella* in core microbiome wherein, 122 and 117 OTUs were found to be the part of core microbiome respectively. Similarly, in the skin microbiome 28 OTUs were found to be core in the present study population, suggesting transient nature of the skin microbiome. Analysis of gut microbiome showed the changes in the relative abundance of phylum *Proteobacteria* and genus *Bacteroides* with the age. Similarly, *Streptococcus*, *Granilicatella*, *Fusobacterium* and *Trepanoma* showed changes with the age in the oral microbiome. Microbiome inheritance reveals the sharing of the gut microbiome ranges up to 85% across the generations. The microbiome profile of the present study population from India also explained the significant differences in microbiome composition in with other populations in the world. Future work studying pan Indian microbiome with larger cohorts across diverse Indian population will aid in separating the effects of age and other factors.

The undernutrition story: Gut microbiome perspectives

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Undernutrition contributes to about one-third of deaths among children under five years of age. Undernutrition simply does not mean the lack of food but is now being perceived as an inadequate response of the host gut microbiome to caloric deficit. It is astounding to see that in the developing world, both malnourished and healthy children coexist in the same family with the same access to calories. Even, sustenance of healthy growth after nutritional therapy in similar cases of undernutrition can be significantly varied. This makes treating undernutrition, a clinician's nightmare. Our group has embarked on studying the gut microbiome of uncomplicated severe acute malnourished children from India in an attempt to understand the role of the millions of bacteria that reside in the gut, in the nutritional well-being and adequate growth of children.

Factors influencing the human microbiome: genetics, environment, diet, and antibiotics

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Research into the human microbiome promises to reveal a great deal about its role in health and disease. Recently there has been a great deal of interest in the possibility of manipulating the microbiome in order to improve nutrition and global health. However, it is first necessary to understand how the composition of the human microbiome can be affected by multiple factors. These factors include host genetics, the environment, diet, and antibiotics. In this talk, I will present recent work from our group that aims to understand the strength of the influence of these factors, and how they relate to each other. In the context of the salivary microbiome, we find that individuals who share a common household have a more similar microbiome composition and that host genetics does not play a significant role. We also find evidence that differences in the oral microbiome can be associated with a Western diet when compared to the diet of traditional hunter-gatherers and farmers. Finally, the most dramatic perturbation the microbiome can receive is antibiotics. As well as growing concerns about the dangers of antibiotic resistance, our modelling work suggests that even a week-long course of antibiotics can shift the composition of the gut microbiome into an alternative community state that persists for at least a year afterwards.

Microbial role shift: Gut microbiota can be an asset or a problem to human host!

Bamola VD¹ and Rama Ch^{1*}

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Microbes cause variety of illnesses to human host but they are also crucial to life on Earth and play important role in decomposition of dead bodies, atmospheric nitrogen fixation etc. Microbes have also been used to make fermented dairy products from ancient time. In the recent past, bacteria have been extensively used as a source of antibiotics and contributed to longer and quality life to human population. Human body contains an enormous number of microbes which normally follow a symbiotic relationship with the host but can have adverse effects in stressed conditions that leads to local and systemic consequences. Like all healthy ecosystems, richness of microbial species characterizes the human gut microbiome in healthy individuals and a loss in species diversity is a common in several disease states. The factors determining gut bacterial diversity are gastric conditions, immunity, gestational & delivery conditions and food habits. Alteration of gut microbial composition may be a factor in the pathogenesis of several disease condition like obesity, diabetes, inflammatory bowel disease (IBD) and colon cancer. Since the dietary habits of Indian population are different from that of the Western world, findings of studies on Western population cannot be extrapolated to their Indian counterparts. Therefore studies have been initiated by our group to assess gut microbial profile in Indian subjects with different food habits and disease conditions including IBD and colon carcinoma.

Fecal samples have been collected from different groups including healthy vegetarian, non-vegetarian, IBD and colon-cancer patients and 16S ribosomal RNA Amplicon Sequencing have been carried out using Illumina MiSeq Platform. In all groups Operational Taxonomic Units (OTUs) and relative abundance of bacteria were analyzed using the pre-processed consensus sequences. In vegetarian group a total of 5,392 OTUs and in non vegetarian group a total of 4,950 OTUs were identified. While in IBD group a total of 4,372 OTUs were identified and in Colon cancer patient group a total of 3,621 OTUs were identified. Analysis indicates that the bacterial genera Bifidobacterium, Eubacterium, Ruminococcus, Faecalibacterium, Prevotella, Bacteroides and Lactobacillus were found to be core genera in all groups. Further analysis revealed the significant difference in the OTUs in different groups and which also exhibited the presence of particular genera and species, unique to subject and group. Results of the study indicated that Indian healthy controls and patients have different microbial diversity compared to Western data and the reason is likely to be the Indian dietary practices. Results are clearly reflecting the role of gut microflora in colonic health and provide insight into microbial community in health and disease but, the association between gut microbial profile and different health conditions in Indian population may require further large scale study cohorts and analysis approach to draw specific conclusions and to establish precise microbial biomarkers for different disease.

Role of legume derived synbiotic on immune modulation in mouse model- Relevance to gut health in humans

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Increased clinical evidences suggest that plant derived foods have various potential health benefits and their consumption has been growing at a rate of 5-10% per year. Our research group focused upon the possible role of immune modulation with prebiotic derived from whole green gram (*Vigna radiata*) in combination with probiotic (*Lactobacillus rhamnosus* GG) as synbiotic. We studied the role of prenatal and postweaning supplementation effects on immune programming in animal model (mice) on vaccine responses. Further, amelioration of allergy was also studied.

Antibody titres against Hepatitis-B surface antigen (HBsAg) with prenatal synbiotic supplementation were comparable to control whereas, prenatal probiotic supplementation improved them by 2.9-fold. However, results were promising with postweaning synbiotic supplementation which showed improvement in the antibody titres by 4-fold and probiotic supplementation by 3.2-fold compared to control. Prenatal synbiotic supplementation efficiently ameliorated the symptoms of allergy among the ovalbumin induced allergy model compared to prenatal probiotic supplementation and control. Similarly, postweaning synbiotic supplementation showed better protection from allergy compared to probiotic and control groups. Influence of the supplementations on the gut bacterial population showed significance in terms of Bifidobacteria and Lactobacilli numbers. It was observed that synbiotic supplementation improved the Bifidobacterial population significantly whereas, probiotic supplementation improved Lactobacilli population compared to control. Interestingly, Bifidobacterial population thrived for 4 months postweaning even without supplementation. Hence prebiotics from legumes carry immense scope as functional food and more comprehensive research is required in this aspect.

Computational genomics of gut pathogens

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Whole genome sequencing can provide higher resolution by comparing genomic content of organisms from different backgrounds. Though it is much easier to sequence regions of single genomes, the downstream job of reconstructing the genomes from the millions of sequence reads followed by their high throughput comparative analysis is still challenging. To address the challenges faced in bacterial genomics, the following aspects will be discussed:

(1) An effort to improve upon the shortcomings associated with the construction of draft genomes with Illumina paired-end sequencing with Contig-Layout-Authenticator (CLA), an automated pipeline that can scaffold reference-sorted contigs based on paired end reads, resulting in better assembled bacterial genomes;

(2) Lessons from high resolution genomic analysis of gut bacterial lineages of *E. coli* named ST131 in comparison with three other extended-spectrum- β -lactamase (ESBL)-producing and globally distributed lineages (ST38, ST405 and ST648).

Findings from this study helped in understanding the differences in the genomic contents, constituents and coordinates of ST131 with respect to those of other STs. In general, these combined observations have implications for algorithm development and management of microbiome data emanating from clinics and environment.

Country report on nutrition: Ghana

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Seventy-five years on since the term Kwashiokor, used to describe a protein-energy malnutrition was created, Ghana, like many other developing countries have not yet achieved nutrition security. Though the country has made much progress in addressing nutritional diseases, several key developmental outcomes related to nutrition remain poor. Nearly a quarter of all children under 5 years of age are stunted; about six percent are wasted; micronutrient deficiencies among women and children are highly prevalent assuming public health challenges, especially the issue of anaemia. There is though much evidence that the nutrition status is not as it was in 1933 when Cicely Williams observed the prevalent condition that was termed Kwashiokor. Incidentally, as undernutrition is being tackled, there is the upsurge of metabolic diseases which are nutrition related. The increasing prevalence of obesity, Type 2 diabetes, cardiovascular diseases and cancers, has become another burden that needs equal or greater attention. It is estimated that about 40% of women 15-49 years and 16% men 15-59 years old are overweight or obese. In this presentation, the nutritional status of the country, based on the most recent Demographic Health Survey, and the double burden nature nutritional diseases will be outlined.

Current status of nutrition in Senegal: What is the contribution of the nutrition laboratory?

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Senegal, like most developing countries, is still faced with many nutritional challenges such as maternal and child undernutrition, micronutrient deficiencies, food insecurity, infectious diseases, and poor access to nutrient-rich foods and safe drinking water. In the national level, stunting and acute malnutrition affect 17% and 7% of children under five years, respectively (EDS-C, 2016). The first ever national micronutrient deficiency survey carried out by our laboratory in Senegal in 2011 has shown high prevalence of iron, zinc, folate, and vitamin A deficiencies among young children, pregnant and lactating women (Ndiaye et al., 2015; Ndiaye et al., 2017). The last national survey of food security shown also that 17% of households were affected by food insecurity, particularly in rural area (24%) (SECNSA, 2016). To tackle nutrition challenge, Senegal's government adopted a more multi-sectoral approach through National Policy for the Development of Nutrition (2015-2025) highlighting nutrition-sensitive priorities of different sectoral ministries.

The contribution of the Nutrition Laboratory to this challenge lies in the training. First objective is to strengthen capacity building in human nutrition, research and development. The Nutrition Laboratory has an active research program, actually located in the Groundnut Bassin of Central Senegal. Research topics are mostly focused on nutrition-sensitive agriculture through production and consumption of nutrient-rich foods, assessment of the impact of national strategy for fighting vitamin A deficiency, and assessment the impact of national communication strategies on exclusive breastfeeding rate. The effectiveness of using a vitamin and mineral enriched peanut-based solid food (RTUF) for recovery during severe malnutrition was tested for the first time in our laboratory (Diop et al, 2003). The functional properties of certain foods like okra, moringa, fonio and local rice have been also studied. The validation of alternative techniques for the assessment of childhood obesity are also part of the concerns of our laboratory.

Microbiome signatures in colorectal cancer

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The human microbiota are thought to have a tremendous influence on human health and diseases. Although it was virtually impossible to study them until a few years ago, next generation sequencing technologies have enabled us to access and characterize the microbiota in a culture-free manner. Cross-sectional studies have shown associations between changes in human gut microbiota and several diseases. Among them, a new family of studies known as metagenome-wide association studies (MGWAS) have reported significant associations between the gut microbiota and diseases. For most of these associations though, whether the relationship is causality or reverse causality still remains to be elucidated. This is only the beginning of a new trend to elucidate the role of host-associated microbiota in diseases, and bioinformatics is becoming increasingly important in this endeavor. Recently we reported significant changes in the gut microbiome associated with colorectal carcinoma in a Chinese cohort. We identified microbial gene biomarkers from fecal microbiome and validated them in multiple cohorts from Europe. Quantitative PCR measurements of some of these markers showed promising potential for affordable diagnosis of colorectal cancer using fecal microbiome. In this talk, our published and ongoing research on discovering microbiome-derived biomarkers for colorectal cancer will be discussed.

Plant microbiome: Unravelling the biota black box

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Plant's microbiome, above- and below-ground associated microbiomes, is an integral part of the wider genome of the plant and is now considered as the extended phenotype of all plants. The below-ground root-microbiome has been shown to have a major impact on plant health through interactions on growth and development, facilitation of nutrient uptake and ability to tolerate biotic and abiotic stresses. New tools in microbiome research are helping to unravel the complexities of its enormous diversity and functional potential and there is now new opportunity to develop 'Designer microbiomes'.

Our research targets towards the identification of key drivers of microbiome diversity and functionality along with understanding of spatial and temporal factors that operate under field conditions. The plant microbiome assemblage, in terms of composition and abundances of specific functional groups, is both soil type and host species dependent and could be modulated by management. For example, (i) within cereal crops and perennial grass species there is a plant type and variety specific enrichment of specific members of soil microbiome, (ii) clear differences in bacterial and fungal microbiomes exist between the domesticated modern bread wheats, landraces and wild relatives within the Triticeae, (iii) a diverse array of microbial communities that are well connected are involved in the continued effective expression of disease suppression in the field environment. Overall, the aim is to develop better connection between 'descriptive genomics' and 'functional gene analysis' that would allow deliberate selection of beneficial microbiomes through either targeted management or specific selection of crop genotypes.

A critical role for pore connectivity in microbiome behaviour and metabolism in soil

Neal A

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We understand a great deal about physical, biological and chemical processes that are important for soil function and how they fluctuate in space: we know far less about the temporal dimension, observable as system resilience. We do not understand the basis for resilience of soil function, nor how resilience is degraded e.g. via tipping points or gradual processes. A major barrier to progress has been the apparently intractable complexity that arises when we try to understand how physical, biological and chemical processes interact temporally. Thus, each process is usually considered in isolation. Consequently, treatment of the microbial microenvironment in current models is highly simplistic and at odds with a growing consensus that many macronutrient processes in soil are rate-limited by physical constraints, rather than by intrinsic chemical recalcitrance.

In this talk, I present new evidence from soils of a long-term field experiment that soil microstructure, including pore connectivity and hydraulic conductivity, exert a dominant influence upon a number of significant microbial behavioural (including secretion of exoenzymes and motility) and metabolic processes. These effects, observed at the functional gene level using metagenomics are not observed at the phylogenetic level, where instead chemical and nutritional factors exert a greater influence. This suggests that soil systems operate at two independent levels: one typified by prokaryote Class- or Phylum-level traits responsive to pH and nutrient availability, the second operating at the level of functional genes in response to constraints placed upon the diffusive transport of solutes and exoenzymes by soil microstructure.

Taxonomic structure and functional association of foxtail millet root microbiome

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The root microbes play pivotal roles in plant productivity, nutrient uptakes and disease resistance. The root microbial community structure has been extensively investigated by 16S/18S/ITS amplicons and metagenomic sequencing in crops and model plants. However, the functional associations between root microbes and host plant growth are poorly understood. We investigated the root bacterial community of foxtail millet (*Setaria italica*) and its potential effects on host plant productivity. We determined the bacterial composition of 2,882 samples from foxtail millet rhizoplane, rhizosphere and corresponding bulk soils from two well-separated geographic locations by 16S rRNA gene amplicon sequencing. We identified 16,109 OTUs, and defined 187 OTUs as shared rhizoplane core OTUs. The β -diversity analysis revealed that microhabitat was the major factor shaping foxtail millet root bacterial community, followed by geographic locations. Large-scale association analysis identified the potential beneficial bacteria correlated with plant high productivity. Besides, we construct a gene catalogue containing 67M unigenes based on the metagenome sequencing data. The pathways enriched in rhizoplane were identified, indicating the possible interaction between the host plant and microbes. Overall, our results demonstrated host plants enriched specific bacteria and functions in the rhizoplane. The potentially beneficial bacteria may serve as a valuable knowledge foundation for bio-fertilizer development in agriculture.

Proteomics to understand stress responsive mechanism in plants

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Plant acclimation to stress is associated with profound changes in proteome composition. Since proteins are directly involved in plant stress response, proteomics studies can significantly contribute to unravelling the possible relationships between protein abundance and plant stress acclimation. Here, we exemplify the extensive use of proteomics approach to understand pollen developmental mechanism and tissue-specific response of pearl millet under drought stress. Pollen development is a well programmed and crucial process which controls plant sexual reproduction and productivity. This process of development is highly sensitive to environmental changes like temperature, drought and nutrition, and thus crucial in the era of global climate change and decreasing plant productivity under abiotic stress. Recently, we have generated a first cell-specific reference-proteome of tomato pollen development which includes microsporocytes, tetrads, microspores, polarized microspores and mature pollen. Each stage showed a specific reprogramming of the proteome. These specific responses in pollen development were termed "developmental priming" in contrast to "defense priming". Here, the hypothesis that a genetic or epigenetic program controls expression and translation of protective proteins such as heat shock proteins that occurred already in the non - stressed state, to compensate for sudden changes in temperature during the maturation of the pollen. Further, a novel approach was introduced for peptide quantification based on mass accuracy precursor alignment (MAPA), considering a target list of "proteotypic peptides" in the ecotype Hazera cv.3017.

Pearl millet [*Pennisetum glaucum* (L.) R. Br] is the sixth most important cereal crop in the world after rice, wheat, maize, barley and sorghum. It is naturally hardy and tolerant to high temperatures; therefore, it is of prime importance to reveal the genes and proteins responsible for its sturdy nature. We have used a shotgun proteomics approach to identify protein signatures from different tissues (roots, seeds and leaves) under control and drought condition. The identified DRPs were involved in the function of lipid metabolism, signaling and transport which showed increased levels in the roots under drought stress and concomitantly observed increased root length which impaired shoot-root communication under drought stress.

Deciphering the dynamic biology of a pigeonpea environment-sensitive male sterile line

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Hybrid breeding has provided remarkable yield advantage to pigeonpea productivity in the semi-arid tropics. An alternative two-line hybrid technology is being explored for a less tedious and cost-effective system, for which environment sensitive male sterile line (ESMS) is a pre-requisite. An ESMS line has been characterized as a thermosensitive male sterile line (TSMS) in pigeonpea precisely responding to day temperature. Temperatures higher than the threshold temperature (24°C) promoted male sterility while lower temperatures rendered them male fertile. Cytological studies revealed a post-meiotic defect leading to undissociated tetrads in sterile plants, possibly the most critical stage for fertility transition. To understand the possible mechanism underlying fertility transition, sterile and fertile anther transcriptome profiling from five developmental stages was carried out using Illumina HiSeq 2500. Transcriptome analyses identified an involvement of phytohormones such as auxin in response to day temperature. We propose that auxin homeostasis is important for regulating sugar transport and cell wall modification, which otherwise would alter signalling with disruption in nutrient flow leading to microspore starvation in male-sterile plants. The role of auxin has also been experimentally shown to have practical implication in reverting the male-sterile line, thus holds great promise for developing two-line hybrid system in pigeonpea.

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Logistics

Logistics Information

Welcome to CEGSB Workshop at ICRISAT!

We are pleased to provide you the consolidated information on logistics and other vital details pertaining to your arrival and stay in Hyderabad, India. We hope that you will have a comfortable stay. Please do not hesitate to contact the following staff, in case you have any questions or need any assistance.

Ms Anu Chitikineni 91 8897270630

Mr B Anjaiah 91 9704444255

Agenda

Soft copy of the Workshop Programme is available at:

<http://cegsb.icrisat.org/wp-content/uploads/2018/03/Program-Systems-Biology-Workshop.pdf> and the same would be available in the abstract book.

Accommodation

Accommodation has been arranged for delegates at ICRISAT:

ICRISAT HOUSING FACILITIES:

Patancheru

Hyderabad

Telangana – 502324, India

(Tel: +91 40- 3071 3550)

Workshop venue

The Workshop will be held in **212 C Fred Bentley Conference Hall** on **22nd March** and **307 Great Lakes Conference Hall** on **23rd March, 2018** at ICRISAT. All participants are requested to wear their name badges throughout the workshop.

Hyderabad City / Monuments tour

We are planning to have a city tour on Mar 24, 2018. This tour will include visits to some historical monuments such as **Charminar, Golconda fort, Qutub Shahi Tombs and Shilparamam**. Please browse internet/ Wikipedia to know more about these places.

Food arrangements (Workshop Days)

Breakfast (22nd, 23rd, 24th Mar, 2018): **204 Banquet Hall, ICRISAT**

Lunch (22nd, 23rd, 24th Mar, 2018): **204 Banquet Hall, ICRISAT**

Dinner:

22nd Mar, 2018– IMOD Plaza, ICRISAT

23rd Mar, 2018 – 204 Banquet Hall, ICRISAT

24th Mar, 2018– Academic Court

Participants staying on other than the above dates are requested to have their meals in 204 Dining Hall by showing the meal card which will be given at the time of check-in.

Electric Plugs

At ICRISAT, we use British (**not Indian**) electricity plugs. So please carry the suitable adapters accordingly.



Hyderabad Weather

The average weather in March varies between a High of 36°C and a Low of 20°C. But don't worry for high temp- we expect to have cool and pleasant weather during the workshop.

Facilities @ICRISAT:

For those, residing at ICRISAT, can also contact the Housing Office, (extn 2550 from ICRISAT campus and 0091 40 3071 3550 from outside ICRISAT) round-the-clock.

Internet

All ICRISAT guestel/flatlets are networked, so participants can access internet on their laptops.

Medical

We don't expect anyone to fall sick during the workshop however for preventive measures First-aid kits are available at the Housing Office. Dr. Vinaykanth, Head, Medical Services, will be available for consultation in the Field Medical Unit (FMU) during working hours. After office hours, he may be contacted at his residence. His telephone numbers (from ICRISAT campus) are 2638 (FMU) and 2113 (home).

Recreation and Gymnasium

For participants staying at ICRISAT campus: The tennis court, table tennis room, cricket/football pitch, and basketball court are all situated to the East of the building complex and close to the dormitories. You are welcome to use these recreational facilities before/after working hours.

The Jim Ryan Recreation Center can be utilized by paying a nominal entry fee of Rs. 300 per day per person. Its working hours are: Monday through Saturday: 0600 hrs–1800 hrs, Sunday: 0600 hrs–1200 hrs.

Use of Swimming Pool is Complimentary.

Mamta Shop

A handicrafts shop, run by the ICRISAT Association for Community Development (IACD), is located on the ground floor in 204 Building (extn 2579), right below the Cafeteria. The items available here include Bidriware, sandal wood and camel bone carvings, the famous Hyderabad black metal figurines, batic paintings, Kalamkari and Pochampally fabrics and of course, the most famous of them all- a range of Hyderabad pearl jewelry that guaranteed to be of the highest quality. Also available are souvenir items with ICRISAT Logo - caps, T- shirts, scarves, key chains, pens and coffee mugs.

Profits from Mamta Shop are used for community development in the surrounding villages. It is open Monday through Friday from 0830 hrs to 1630 hrs and Saturdays from 0900 hrs to 1630 hrs.

Security

As a routine procedure, all persons (including ICRISAT staff) entering or leaving ICRISAT Campus may be stopped for a security check at the Main Gate. Though we have informed security about the workshop, we request you to cooperate with the security staff at all times.

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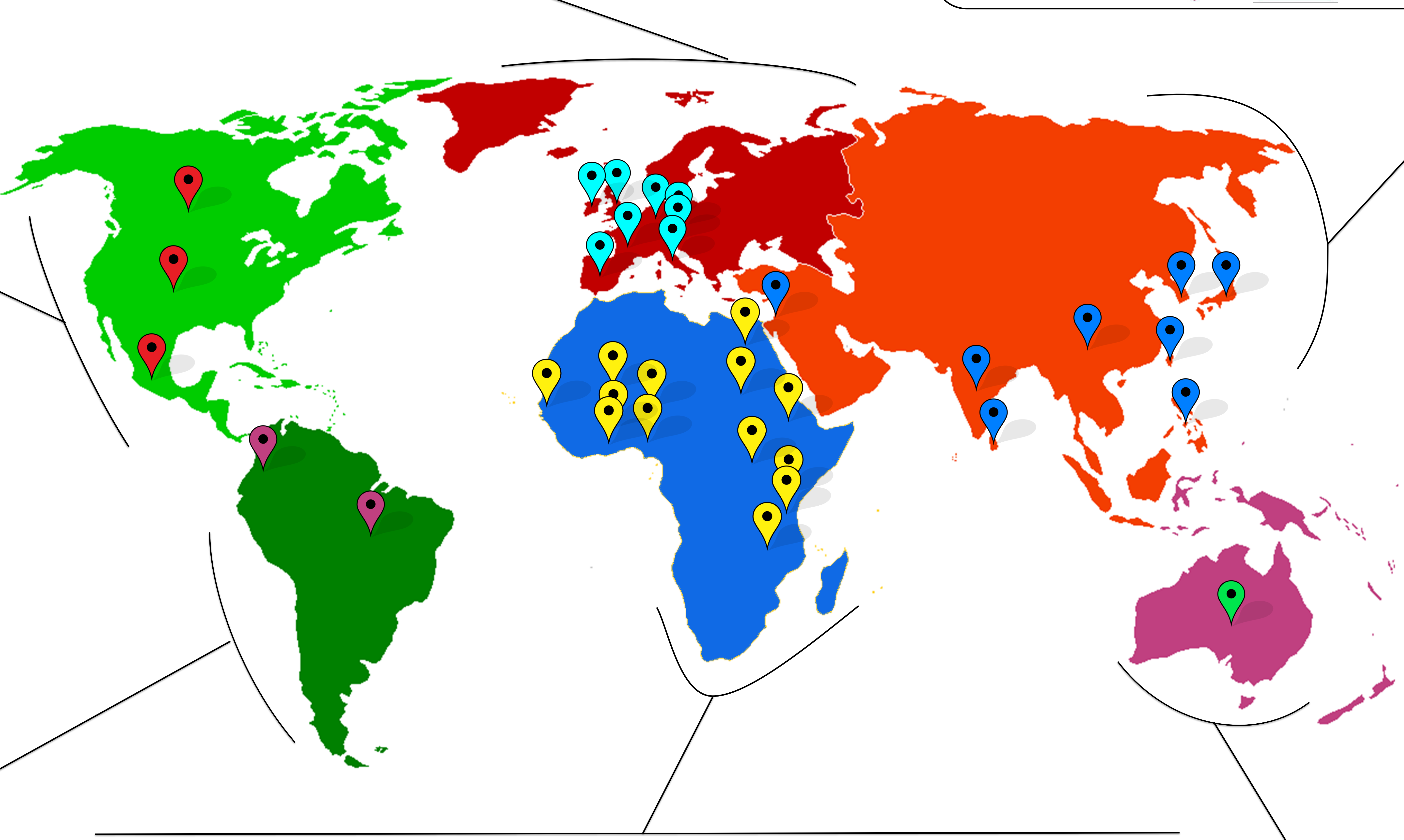
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We believe all **people** have a **right** to **nutritious food** and a **better livelihood**.

ICRISAT works in agricultural research for development across the drylands of Africa and Asia, making farming profitable for smallholder farmers while reducing malnutrition and environmental degradation.

We work across the entire value chain from developing new varieties to agri-business and linking farmers to markets.

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ICRISAT appreciates the support of CGIAR investors to help overcome poverty, malnutrition and environmental degradation in the harshest dryland regions of the world. See <http://www.icrisat.org/icrisat-donors.htm> for full list of donors.



About ICRISAT: www.icrisat.org



ICRISAT's scientific information: EXPLOREit.icrisat.org



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