Mendel @ 200

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Abstract
2022 marks the 200th anniversary of the birth of Gregor Mendel who, with his experiments in pea and common bean, is generally accepted as having founded the science of Genetics. In this presentation I will review what is known, at the molecular level, about the pea genes Mendel studied. I will also discuss the implications of their genomic locations and some common misconceptions about Mendel’s analyses and interpretations.
Genetic discoveries in legume nodulation and symbiotic nitrogen fixation

Sonali Roy

Over the last two decades, various forward- and reverse-genetic approaches have uncovered over 200 genes required for symbiotic nitrogen fixation (SNF) in legumes. These discoveries have advanced our understanding of the evolution of SNF in plants and their relationship with other beneficial endosymbioses, signaling between plants and microbes, the genetic basis of rhizobial infection of plant cells, the regulation of plant cell division leading to nodule development, autoregulation of nodulation, intracellular accommodation of bacteria, nodule oxygen homeostasis, the control of bacteroid differentiation, metabolism and transport supporting symbiosis, and the control of nodule senescence. In the last three years, several gene editing techniques have been developed for both model and crop legumes to further understand these processes. CRISPR-Cas9-based tools, in particular, are outpacing other comparable gene editing technologies used in legume hosts and their microbial symbionts to understand the molecular basis of symbiotic nitrogen-fixation. Gene editing has helped identify new gene functions, validate genetic screens, resolve gene redundancy, examine the role of tandemly duplicated genes, and investigate symbiotic signaling networks in non-model plants. In this talk, I will discuss the advances made in understanding the legume-rhizobia symbiosis through the use of gene editing and highlight studies conducted under varying environmental conditions. We reason that future climate-hardy legumes must be able to better integrate environmental signals with nitrogen fixation by fine-tuning long distance signaling, continuing to select efficient rhizobial partners, and adjusting their molecular circuitry to function optimally under variable light and nutrient availability and rising atmospheric carbon dioxide.
Characterization and association mapping of morphological traits in faba bean (Vicia faba L.)

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Abstract

Faba bean (Vicia faba L.) is an important crop with high protein content. Tens of thousands of faba bean accessions are available in germplasm collections throughout the world. Morphological characterization of these materials can enrich the collection and aid in the selection of genotypes for use in breeding programs. In this study, 26 morphological characters were analyzed for 61 faba bean landraces and 53 cultivars over two seasons in Izmir, Turkey. The genotypes had high diversity for several yield traits including number of pods per plant, dry seed yield, and 100-seed weight. Association mapping was conducted for the morphological characters using 711 alleles from 100 SSR markers and a general linear model based on the Q matrix. A false discovery rate of 0.20 was used to test the significance of marker-trait associations resulting in 75 loci detected for 20 of the morphological characters (p ≤ 0.001). Overall, 44% of the quantitative trait loci (QTL) were found for seed traits, with 24, 15, and 17% of QTL identified for vegetative, inflorescence and pod traits, respectively. The phenotypic data and marker-trait associations generated by this work can help breeding programs in the selection and improvement of faba bean.
Allelic expression of a transcription factor gene controlling peanut nodulation

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Abstract

Peanut as a legume species can establish a symbiotic relationship with rhizobia to fix nitrogen from the atmosphere. Over a hundred genes involved in legume symbiosis have been identified. A GRAS family transcription factor gene, *nodulation signaling pathway 2* (*NSP2*) plays a critical role in the symbiotic signaling pathway. Through a map-based cloning approach previously, two homoeologous genes, *AhNSP2-A08* or *N*$_a$ and *AhNSP2-B07* or *N*$_b$ were identified to control peanut nodulation. Interestingly, some peanut plants with *n*$_a$n$_aN_b^n_b$ genotype produce nodules (Nod+ phenotype) and some not (Nod– phenotype). To further understand the genetic mechanism of Nod– phenotype of the *N_b^n_b* plants, allelic expression was investigated in peanut roots and flowers. The results showed that only a single allele at *N_b* locus was expressed in the peanut roots. Particularly, in Nod– *N_b^n_b* plants, only a mutant allele *n_b* was expressed. In peanut flowers, *N_b* gene expressed significantly low in ovary than in pollen. The results indicated that the expression of *N_b* gene in ovary was inhibited or maternally silenced. This study firstly reported an allele-specific expression in tetraploid peanuts, which provided fundamental knowledge of epigenetic regulation in ploidy plants.
Development and characterization of a unique genetic resource for allele mining and peanut improvement in Africa

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Cultivated peanut (Arachis hypogaea L.) has high morphological diversity but low variability at the DNA level. Diving into breeding lines, improved and local varieties diversity is important for mining alleles that can be used in breeding programs. To reach this objective, core collections have been reported as meaningful genetic resources for QTL mapping and gene discovery. We assembled wide collection of peanut breeding lines, cultivars and landraces from ten breeding programs in Africa. We genotyped this collection using a 40k Affymetrix SNP array and used the data for describing the genetic diversity and its structure. This was done using discriminant analysis of principal components and a genealogical analysis. We also defined a core collection by combining breeders’ knowledge and diversity data, that has been phenotype in 5 countries in West-Africa. Overall, breeders in Africa hold large diversity with all botanical and commercial peanut types represented. However, this diversity is not evenly distributed, youngest breeding programs managing less variability than others. The analysis of population substructure showed a clustering based on geographical origin with groups composed mainly by Spanish variety from West Africa or Virginia from East and Southern Africa. The phenotyping of the core-collection showed large variation for trait related to yield component and disease resistance. High genotype and location interactions have also been observed. We developed a unique genetic resource for peanut breeding and alleles mining, that will allow breeder in Africa to efficiently tap in the useful diversity for varietal improvement.
Adaptation of chickpea to terminal drought: Physiological and molecular approaches

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Chickpea (*Cicer arietinum* L.) growth is sensitive to drought during the reproductive stage. Experiments were undertaken in both the field and glasshouse to understand the agronomic and physiological responses to drought. A two-fold variation in seed yield among more than 100 chickpea genotypes was observed at three dryland field sites in the grainbelt of Western Australia over two years. Ten contrasting genotypes were compared in the glasshouse using large bins containing 106 kg of soil to better simulate soil drying in the field. Terminal drought imposed from early podding in the glasshouse significantly reduced vegetative growth, reproductive growth, seed yield and water use efficiency for grain production in all genotypes. Terminal drought at least doubled the percentage of flower abortion, pod abscission and empty pods. Although the 10 genotypes used similar amounts of water during the drought stress, the slower water use in the cultivar Neelam when the drought treatment was first imposed maintained higher plant-available soil water (PASW) for a longer period during the reproductive phase thereby contributing to its higher yield. Two genotypes were further used for the detailed physiological studies. Pollen viability and germination of both genotypes decreased significantly when 82% PASW was transpired; however, at least one pollen tube in each flower reached the ovary. The young pods developed from flowers tagged when 50% PASW was used had viable embryos in the first 7 days after flowering and had higher concentrations of abscisic acid (ABA) than the well-watered plants, but all pods ultimately aborted. Seed set stopped at the same soil water content as stomata began to close and ABA increased to high concentrations strongly suggesting a role for ABA in the failure to set seed either directly through abscission of the developing pod/seed, or indirectly through the reduction in assimilate supply to the seed.

Genetic improvement of grain legumes (including chickpea), like other crops, is mostly based on pedigree and performance-based selection over the past half century. To achieve faster genetic gains in grain legume in in rainfed conditions, the integration of modern genomics approaches, high throughput phenomics, physiology, and simulation modelling in support of crop improvements that leads to improved cultivars that perform with appropriate agronomy.
Capturing the genetic variation in mungbean germplasm for crop vigour and canopy size using 3D cloud points

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Canopy size, structure, and vigour determined by leaf development and expansion are key component traits of yield that are also closely associated as an indicator of water use by the crop. Screening for such traits using 3D point cloud-based image analysis is now possible with high-throughput plant phenotyping facility, LeasyScan, at ICRISAT. In this study, a pool of mungbean germplasm comprising of 296 minicore lines and 52 elite lines (Vadez et al., 2015) were screened for canopy traits. The plants were sown in four replicates on 11 Feb 2020 and maintained under well-irrigated conditions until 20 Mar 2020. Eight plants per sector (i.e., 32 plants m⁻² density) were maintained until 30 days after sowing. Plants were thinned to four plants per sector on 13 Mar 2020. Of these several canopy parameters computed from 3D point cloud images from PlantEye® scanners, 3D-leaf area (3DLA), projected leaf area (PLA), and plant height (PH) measured between 638–660 degree days after sowing was used for studying genetic variation along with plant biomass (BM) which was measured destructively at harvest. In this preliminary experiment, canopy traits across 343 genotypes showed significant variation (p <0.001) for all four canopy traits. Large variation was observed in the minicore lines for plant biomass harvested at 744-degree days after sowing (8–43 g, and canopy size (3DLA = 28067–117060 cm²; PLA = 18310–83307 cm²). The range of biomass, 3DLA, and PLA of elite lines ranged from 17–34g per sector, 69165–114335 cm², and 40825–83344 cm², respectively. Plant height of elite lines ranged from 154–283 mm whereas that of minicore lines ranged from 137–314 mm. Identification of genotypes with high vigour and canopy size from the minicore and elite line collection will help in deciphering the building blocks for yield and in further understanding crop and water use relations in mung bean.
Winged bean (*Psophocarpus tetragonolobus* (L.) DC.) first QTL analysis for nutritional traits

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Abstract

Climate change, population growth and lack of diversity in our diets are threatening food security and quality of nutrition in human beings. There is a need to incorporate alternative foods especially protein sources into the human diet to reduce carbon dioxide emissions and diversify agriculture in order to meet the challenges of climate change. Legumes are an important source of protein across the world. Winged bean (*Psophocarpus tetragonolobus* (L.) DC.) is an underutilised tropical legume with high protein content (34.3 - 40.7%) and oil content (16.4 - 21.3%). Nevertheless, winged bean seeds have antinutritional factors such as protein inhibitors, tannins and phytic acid. In this study, the F2 population of a cross was utilised to identify for the first time QTLs (Quantitative Trait Locus) in winged bean protein and oil content as well as QTL for the yield related trait, 100seed weight. A significant QTL explaining less than 10% of the protein variation and a significant QTL explaining above 15% of the variation of seed weight were detected on chromosome 3 and 1, respectively. Whereas three putative QTLs for oil content explaining above 10% each were identified on chromosomes 2, 5 and 9. Further work is underway to identify QTLs for saturated, mono- and poly-unsaturated fatty acids composition. Exploring further the genetic mechanisms that underly the fatty acid composition in winged bean seeds could lead to better breeding selection through marker-assisted methodologies. Equally important to the nutritional value of winged bean seeds is their amino acid composition, which resembles soybean. Amino acid analysis of winged bean seeds and soybean meal showed that several of the winged bean accessions have a similar proportion of amino acids as soybean meal. These results suggest that winged bean has the potential to be a new soybean for the tropics.
Genome-wide association study of drought-related resistance traits in faba bean

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Faba bean (Vicia faba L.) is one of the highest protein crops and the sixth global temperate legume in production. The crop is adapted to diverse climatic and soil conditions and used in rotations, providing benefits like increasing fertility of soil, plant health and sustainability, etc. Faba bean however, is highly sensitive to water shortages. This majorly impacts the flowering and pod-filling which are the most sensitive and severely depressed periods of the growth cycle. In the wake of changing climate, drought and heat stress have become the most important limiting factors to productivity, preventing farmers from cultivating faba beans as one of the important crops. Thus, a better understanding of drought response patterns and associated traits are a key for identifying drought-tolerant genotypes and developing efficient molecular breeding approaches to attenuate the global warming impacts.

Our study was undertaken to exploit the genetic variation in a faba bean collection of diverse origin so as to: (i) assess the selection criteria for identifying drought tolerant faba bean genotypes, (ii) to evaluate the performance of a faba bean collection of diverse origins under well-watered and drought stress conditions using ten morphological, phenological and physiological traits (iii) to conduct a genome-wide association study (GWAS) to identify single nucleotide polymorphism (SNP) markers associated with the drought tolerance indices.

Our results intend to contribute to a better understanding of the genetic architecture governing drought tolerance in faba bean and provide a foundation for marker-assisted breeding in this crop.