

Editorial

Special Issue “Genetics, Genomics, and Breeding of Legume Crops”

Guo-Liang Jiang

Agricultural Research Station, Virginia State University, P.O. Box 9061, Petersburg, VA 23806, USA;
gjiang@vsu.edu or gljiang99@yahoo.com; Tel.: +1-804-524-5953

Legume crops are grown in the world primarily for their grain seeds that are widely used for human and animal consumption or for the production of oils for industrial uses. Broadly, legumes include well-known crops: soybean, common bean or dry bean, peanut, peas, chickpeas, cowpea, lentils, alfalfa, clover, etc. From a nutritional standpoint, legume crops are a significant source of protein, oil, dietary fiber, carbohydrates and dietary minerals. Economically, they also play an important role in international trade. Genetic improvement has been key to the growth of crop production and will continuously contribute to sustainable agriculture and food security. For the present, plant genetic improvement is in the middle of its evolution from field-based traditional breeding to a new era of application of multiple novel techniques such as marker-assisted selection, genomic prediction and gene-editing, which will be integrated with conventional methods in practical breeding. Research has involved all the traits of importance, including yield, quality, resistance to pests/diseases and abiotic stresses. In this Special Issue, fifteen articles are included, addressing a wide range of research topics in legume crops.

Abiotic stress like drought and salinity is a major limiting factor in crop productivity worldwide. Evaluation and genetic understanding of stress tolerance is essential for development of varieties adapted to the abiotic stresses. In light of insufficient studies of drought response in large, seeded genotypes of Andean origin, Sedlar et al. (2020) constructed a novel Andean intra-gene pool genetic linkage map for quantitative trait locus (QTL) mapping of drought-responsive traits using a recombinant inbred line population derived from a cross of two cultivars differing in their response to drought [1]. They detected 49 QTLs for physiology, phenology, and yield-associated traits under control and/or drought conditions, and validated the QTLs by projection on common bean consensus linkage map. These results confirmed the potential of Andean germplasm in improving drought tolerance in common bean. Tani et al. (2018) evaluated the seedling response of *Medicago sativa*, *M. arborea*, and their hybrid (*Alborea*) to salt shock and salt stress treatments [2]. They concluded that different components of salt tolerance mechanisms were regulated in the populations of *M. sativa* and *M. arborea*. It appears that the knowledge of different parental mechanisms of salt tolerance could be helpful for incorporating both mechanisms in *Alborea* populations.

In soybean, seed composition or nutritional quality is of importance to uses and market values. Bulatova et al. (2019) studied a soybean germplasm collection to identify accessions with low trypsin inhibitor content in seeds [3]. They selected and analyzed twenty-nine accessions, parental plants, and two hybrid populations using genetic markers for alleles of the *Ti3* locus, encoding Kunitz trypsin inhibitor (KTI). By marker-assisted selection with Satt228, they obtained some prospective homozygous *ti3/ti3* lines which might be further used in the breeding program for soybean quality improvement. To investigate the variation in seed fatty acid composition of soybeans of different origins, Abdelghany et al. (2020) evaluated a diverse germplasm set of 633 soybean accessions originated from China, United States of America (USA), Japan, and Russia [4]. Their results indicated that the unique accessions identified could be used in the soybean breeding programs to fit various human nutrition patterns across the world.



Citation: Jiang, G.-L. Special Issue “Genetics, Genomics, and Breeding of Legume Crops”. *Agronomy* **2021**, *11*, 475. <https://doi.org/10.3390/agronomy11030475>

Received: 5 February 2021

Accepted: 8 February 2021

Published: 4 March 2021

Publisher’s Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2021 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Short petiole is a valuable trait for the improvement of plant canopy of ideotypes with high yield [5]. Liu et al. (2019) identified a unique soybean mutant line called derived short petiole (*dsp*) with an extremely short petiole, which is also obviously different from most short-petiole lines identified previously. Genetic analysis with 941 F₂ individuals and subsequent segregation analysis of 184 F_{2:3} and 172 F_{3:4} families revealed that the *dsp* mutant was controlled by two recessive genes, named as *dsp1* and *dsp2*. These two recessive genes were located on two nonhomologous regions of chromosome 07 and chromosome 11. A total of 36 and 33 gene models were located within the physical genomic interval of *dsp1* and *dsp2* loci, respectively. They concluded that the identified markers linked with genomic regions responsible for the short-petiole phenotype of soybean could be effectively used in developing ideal soybean cultivars through marker-assisted breeding [5].

Pleiotropy is considered to have a significant impact on multi-trait evolution, but its roles in the evolution of domestication-related traits in crop species remain unclear [6]. In soybean, several maturity loci or quantitative trait loci (QTL) controlling maturity are known to have major effects on both flowering and maturity in a highly correlated pleiotropic manner. Sedivy et al. (2020) conducted a QTL mapping experiment by creating a population derived from a cross between domesticated soybean *G. max* and its wild ancestor *G. soja* that underwent stringent selection for non-pleiotropy in flowering and maturity [6]. Their results suggested that pleiotropy in flowering and maturity could be genetically separated, although pleiotropic loci such as *E* loci that control both flowering and maturity have been preferred by artificial selection during soybean domestication and diversification. The non-pleiotropic loci identified in the study may be helpful to improve soybean yield potential against diverse environments and cultivation systems.

Large seed size in the kabuli chickpea (*Cicer arietinum* L.) is preferred in the market for its high price and superior seedling vigor as well [7]. Comparatively, the double-podded chickpea has advantages in yield and stability over the single-podded chickpea. Kivrak et al. (2020) presented a study with the aim of integrating extra-large-seeded and double-podded traits in the kabuli chickpea, and increasing variation by transgressive segregations [7]. Heritability of important agro-morphological traits were also estimated in their study using F₂ and F₃ populations.

Cooking characteristics in food legume crops have been rarely investigated, although they are a central factor for consumer's choice. Interestingly, Harouna et al. (2019) explored the cooking time and the water absorption capacity upon soaking using 84 accessions of wild *Vigna* legumes [8]. For the first time, they elucidated the relationships between the cooking time and water absorbed during soaking.

Peanut is widely grown around the world, predominantly in China followed by India, Nigeria, the USA and Sudan in terms of total production. Konate et al. (2020) presented a review of the progress in the peanut breeding in Burkina Faso, a relatively small peanut producer with unique climate conditions and cropping systems [9]. They also provided crucial information about opportunities and challenges for peanut research in Burkina Faso, and particularly emphasized the need for institutional attention to genetic improvement of the crop.

Lupinus mutabilis (tarwi) is a species of Andean origin with high protein and oil content, and regarded as a potential crop in Europe [10]. The knowledge of intra-specific genetic variability of the collections helps successful introduction of this crop and establishment of breeding and conservation programs. Guilengue et al. (2020) assessed genetic and genomic diversity of tarwi accessions under Mediterranean conditions using morphological traits, inter-simple sequence repeat (ISSR) markers and genome size [10]. Their results revealed important levels of diversity, which is unrelated to phenotypic diversity, and reflected the recent domestication of the crop.

A unique nature of legume crops is the nitrogen-fixing function. Most legume crops have symbiotic nitrogen-fixing bacteria in structures called root nodules. Therefore, in addition to use of grains for human food and animal feeds, some legume species are grown for cover crop or livestock forage. Crimson clover (*Trifolium incarnatum* L.) is the most

common legume cover crop in the United States [11]. However, limited genetic variation for crimson clover was previously found within the National Plant Germplasm System (NPGS) collection. Focusing on traits important for cover crop performance, Moore et al. (2020) assessed the phenotypic and nodule microbial diversity within the NPGS crimson clover collection [11]. They discovered that accession effect was significant for the traits of fall emergence, winter survival, flowering time, biomass per plant, nitrogen (N) content in aboveground biomass, and proportion of plant N from biological nitrogen fixation (BNF). The information generated should be useful for cover crop breeding and production.

Mutation is a powerful tool in creating genetic variability, and mutation breeding has been successfully used in the development of new varieties with unique traits in plants. Based on phenotypic traits, Kim et al. (2020) chose 208 soybean mutants as a mutant diversity pool (MDP), and then investigated the genetic diversity and inter-relationships of these MDP lines using target region amplification polymorphism (TRAP) markers [12]. They suggested that the MDP would have great potential for soybean germplasm enhancement and that TRAP markers are useful for the selection of mutants in soybean mutation breeding. In order to enhance peanut genetic variability, Chen et al. (2020) treated two widely cultivated peanut genotypes, using different concentrations of the mutagen ethyl methyl sulfonate (EMS) for different durations [13]. They found that mutants induced by EMS differed in various phenotypic traits, such as plant height, number of branches, leaf characteristics, and yield and quality in plants of the M₂ generation. They also identified some potentially useful mutants among individuals of the M₂ generation, which were associated with dwarfism, leaf color and shape, high oil or protein content, seed size and coat color. Mutations were stably inherited in M₃-generation individuals.

As a new powerful tool, genomic selection (GS) has attracted increasing attention since it was proposed. An aim of GS is to incorporate molecular information directly into the prediction of individual genetic merit by predicting genomic estimated breeding value (GEBV). Using regularized quantile regression (RQR), Nascimento et al. (2019) predicted the individual genetic merits of the traits associated with flowering time (DFF—days to first flower; DTF—days to flower) in the common bean [14]. They also compared the predictive abilities in predicting the genetic merit between RQR and other methods such as random regression best linear unbiased predictor (RR-BLUP), Bayesian LASSO (BLASSO) and BayesB.

A trend of the present and future plant breeding is the application of integrated multiple methods including state-of-the-art technologies and extensive collaboration. Saxena et al. (2020) reported such an attempt. In order to overcome the productivity barrier for pigeonpea production, a translational pigeonpea genomics consortium (TPGC) was established across multiple states in India [15]. The team has been engaged in deploying modern genomics approaches in breeding and popularizing modern varieties in farmers' fields to augment pigeonpea productivity and production. Through the collaborative effort including farmer's participation, new genetic stock has been developed for trait mapping and molecular breeding initiated for improving resistance to fusarium wilt and sterility mosaic disease [15]. Meanwhile, genomic segments associated with various traits have been identified and participatory varietal selection trials involving a total of 303 farmers have been conducted. It is expected that further progress can be achieved in the near future.

Funding: This research received no external funding.

Acknowledgments: I thank the USDA-NIFA Evans-Allen Research Program for funding in support of this work. I appreciate the great efforts that the authors have made in contributing to the collection of the special topic. I especially thank all the reviewers for their time and dedications to review the manuscripts received. It would not have succeeded without their prompt, thoughtful and constructive reviews. I would also thank the editors in the Editorial Office, especially Aileen Song, the managing editor of this Special Issue, for their excellent in support.

Conflicts of Interest: The author declares no conflict of interest.

References

1. Sedlar, A.; Zupin, M.; Maras, M.; Razinger, J.; Šuštar-Vozli, J.; Pipan, B.; Megli, V. QTL mapping for drought-responsive agronomic traits associated with physiology, phenology, and yield in an Andean intra-gene pool common bean population. *Agronomy* **2020**, *10*, 225. [[CrossRef](#)]
2. Tani, E.; Sarri, E.; Goufa, M.; Asimakopoulou, G.; Psychogiou, M.; Bingham, E.; Skaracis, G.N.; Abraham, E.M. Seedling growth and transcriptional responses to salt shock and stress in *Medicago sativa* L., *Medicago arborea* L., and their hybrid (Alborea). *Agronomy* **2018**, *8*, 231. [[CrossRef](#)]
3. Bulatova, K.; Mazkirat, S.; Didorenko, S.; Babissekova, D.; Kudaibergenov, M.; Alchinbayeva, P.; Khalbayeva, S.; Shavrukov, Y. Trypsin inhibitor assessment with biochemical and molecular markers in a soybean germplasm collection and hybrid populations for seed quality improvement. *Agronomy* **2019**, *9*, 76. [[CrossRef](#)]
4. Abdelghany, A.M.; Zhang, S.; Azam, M.; Shaibu, A.S.; Feng, Y.; Qi, J.; Li, Y.; Tian, Y.; Hong, H.; Li, B.; et al. Natural variation in fatty acid composition of diverse world soybean germplasms grown in China. *Agronomy* **2020**, *10*, 24. [[CrossRef](#)]
5. Liu, M.; Wang, Y.; Gai, J.; Bhat, J.A.; Li, Y.; Kong, J.; Zhao, T. Genetic analysis and gene mapping for a short-petiole mutant in soybean (*Glycine max* (L.) Merr.). *Agronomy* **2019**, *9*, 709. [[CrossRef](#)]
6. Sedivy, E.J.; Akpertey, A.; Vela, A.; Abadir, S.; Khan, A.; Hanzawa, Y. Identification of non-pleiotropic loci in flowering and maturity control in soybean. *Agronomy* **2020**, *10*, 1204. [[CrossRef](#)]
7. Kivrak, K.G.; Eker, T.; Sari, H.; Sari, D.; Akan, K.; Aydinoglu, B.; Catal, M.; Toker, C. Integration of extra-large-seeded and double-podded traits in chickpea (*Cicer arietinum* L.). *Agronomy* **2020**, *10*, 901. [[CrossRef](#)]
8. Harouna, D.V.; Venkataramana, P.B.; Matemu, A.O.; Ndakidemi, P.A. Assessment of water absorption capacity and cooking time of wild under-exploited *Vigna* species towards their domestication. *Agronomy* **2019**, *9*, 509. [[CrossRef](#)]
9. Konate, M.; Sanou, J.; Miningou, A.; Okello, D.K.; Desmae, H.; Janila, P.; Mumm, R.H. Past, present and future perspectives on groundnut breeding in Burkina Faso. *Agronomy* **2020**, *10*, 704. [[CrossRef](#)]
10. Guilengue, N.; Alves, S.; Talhinhas, P.; Neves-Martins, J. Genetic and genomic diversity in a tarwi (*Lupinus mutabilis* Sweet) germplasm collection and adaptability to Mediterranean climate conditions. *Agronomy* **2020**, *10*, 21. [[CrossRef](#)]
11. Moore, V.; Davis, B.; Poskaitis, M.; Maul, J.E.; Kucek, L.K.; Mirsky, S. Phenotypic and nodule microbial diversity among crimson clover (*Trifolium incarnatum* L.) accessions. *Agronomy* **2020**, *10*, 1434. [[CrossRef](#)]
12. Kim, D.-G.; Lyu, J.I.; Lee, M.-K.; Kim, J.M.; Hung, N.N.; Hong, M.J.; Kim, J.-B.; Bae, C.-H.; Kwon, S.-J. Construction of soybean mutant diversity pool (MDP) lines and an analysis of their genetic relationships and associations using TRAP markers. *Agronomy* **2020**, *10*, 253. [[CrossRef](#)]
13. Chen, T.; Huang, L.; Wang, M.; Huang, Y.; Zeng, R.; Wang, X.; Wang, L.; Wan, S.; Zhang, L. Ethyl methyl sulfonate-induced mutagenesis and its effects on peanut agronomic, yield and quality traits. *Agronomy* **2020**, *10*, 655. [[CrossRef](#)]
14. Nascimento, A.C.; Nascimento, M.; Azevedo, C.; Silva, F.; Barili, L.; Vale, N.; Carneiro, J.E.; Cruz, C.; Carneiro, P.C.; Serão, N. Quantile regression applied to genome-enabled prediction of traits related to flowering time in the common bean. *Agronomy* **2019**, *9*, 796. [[CrossRef](#)]
15. Saxena, R.K.; Hake, A.; Hingane, A.J.; Kumar, C.V.S.; Bohra, A.; Sonnappa, M.; Rathore, A.; Kumar, A.V.; Mishra, A.; Tikle, A.N.; et al. Translational Pigeonpea Genomics Consortium for accelerating genetic gains in pigeonpea (*Cajanus cajan* L.). *Agronomy* **2020**, *10*, 1289. [[CrossRef](#)]