Towards establishment of comprehensive reference proteome maps of legume crops

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Abstract

Common bean and pigeon pea constitutes two legume crops par excellence consumed worldwide, including the Indian sub-continent where they serve to satisfy the energy requirements of the population. Importantly, they provide diverse nutrients, protein, and some essential micronutrients. Thus, these model legumes are excellent research materials for high-throughput omic analyses, including proteomics, which is the next frontier post-genome sequencing. The reasons for advancing proteomics databases are manifold, from understanding fundamental plant biology, growth and development, varietal differences, and to unraveling the factors involved in plant adaptability or susceptibility to adverse environmental conditions, among others. Finally, only an integrated omics analysis approach with the protein (proteome) at the center of the genome to metabolome will help fully understand the legumes and contribute to their survival and further advancement as a food crop. Here we discuss possibility and our efforts towards establishment to comprehensive reference maps of common bean and pigeon pea.

Opinion

Common bean (*Phaseolus vulgaris L.*) and Pigeon pea or red gram (*Cajanus cajan (L.) Millspaugh*) belongs to family Fabaceae. They are important food legumes for the people living in temperate, tropical and subtropical regions. These are the major sources of dietary protein in Indian food. As per reports, 91% of vegetarians and 85% of non-vegetarians in India are deficient in proteins which are indispensable for body growth, metabolism and repair (Department of Commerce, Govt. of India). Year 2016 has been declared as the International Year of Pulses by the United Nations indicating importance of pulses as an important component of our food.

Our research focus lies on two important legume crops i.e., common bean and pigeon pea. Although genomes of both crops have been sequenced but the proteome research on these crops is still in its infancy. We here propose of developing comprehensive proteome reference maps of these crops by considering different plant tissues of various developmental stages under varying environmental conditions/stresses. Therefore, it is pertinent to use proteomics in expediting the functional characterization of common bean and pigeon pea. This will provide a catalogue of proteins conducible for engineering improved varieties that could sustain optimal growth and development under adverse Indian agro-climatic conditions. Another important implementation of this work is to sustain the development under the Indian agro-chemical conditions. Li Z, et al. [1] demonstrated that worldwide regulatory jurisdictions in-

cluding India are struggling with the agro-chemicals regulation and management. This study can definitely help local regulatory agencies develop a systematic agro-chemical management strategy.

The data generated from this study would be made available in the public domain and would also be shared with geneticists and breeders of these crops. ICAR-National Research Centre on Plant Biotechnology, New Delhi has already established a central facility (under ICAR-Network Project on Transgenic Crops) for performing proteomics including characterization of novel proteins using MALDI-TOF/TOF and has been rendering services to various educational and research institutions across the country. The authors having expertise in proteome research [2-4] would like to have collaboration among different laboratories working on proteomics of other legumes for developing comparative proteome maps that may help in understand biology for attaining long term sustainability in legume production. We intend to invite members of plant proteomics community through the INPPO platform (http://www.inppo.com/). We here conclude that, proteomics linked with genomics and transcriptomics will likely enhance the agronomic merit as well as quality traits in the legumes by enabling us to first understand

regulatory pathways and then enable the manipulation of these regulatory pathways to develop an improved and more sustainable legume crops. **Figure 1**, depicts the strategy for establishing comprehensive proteome reference maps of legume crops.

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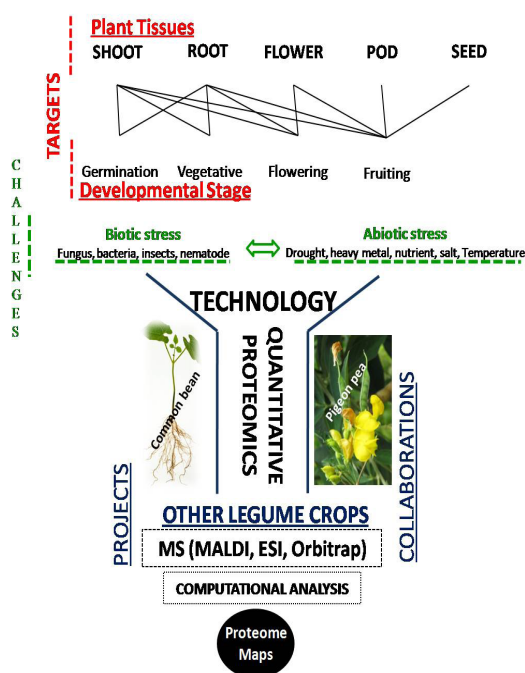
Figure

Figure 1