Exploring Genetic Diversity in Common Bean From Unexploited Regions of Jammu & Kashmir-India

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Abstract

Genetic diversity analysis is a first essential step in understanding the genetic base of the germplasm. Our group is focusing on the common bean, and in the present study, for its improvement a genetic diversity study has been initiated in the laboratory. Since our focus is on the regions (in Jammu and Kashmir, India), which are unexploited and are dominated by the resource-poor farmers, we believe that the genetic stock collection in our hands is unique. It is emphasized that this project forms a platform for the initiation of multidimensional research aspects. In this context, OMICS (phenomics, genomics, transcriptomics, proteomics, and metabolomics) based approaches will be powerful tools and their integrated mode essential in deciphering the regulatory mechanisms governing various traits. As a first step, the cataloging of this unique germplasm will form a foundation for identification of unique characters in each genotype. Hence, our immediate focus will be to estimate total protein and important micronutrients (mainly zinc and iron) among these genotypes and design a strategy to introgress stress tolerance genes in the different genetic backgrounds for the improvement of common bean as a future target.

Keywords

Common beans; Diversity; Molecular markers

1 Importance of common beans: Source of livelihood for the people

Common bean (Phaseolus vulgaris L.) is an important legume crop, which constitutes a traditional food for many people around the globe. It is one of five cultivated species from the genus Phaseolus. Common bean is considered third in importance after soybean and peanut, but first in direct human consumption (Broughton et al., 2003). Among the consumers and farmers with few other food or crop options, common beans are important for nutritional well-being as well as poverty alleviation. It has been observed that small farms ranging from 1-10 ha land holding are mostly involved in bean production (Voysest, 1994). In many areas, common bean is considered as a second most important source of calories after maize. In sub-Saharan Africa, more than 200 million people depend on this crop as a primary staple food. In Latin America and Africa, it is an important source of house hold income for millions of small-scale farmers. (http://www.cgiar.org/our-research/crop-factsheets/beans/).

Common bean is considered as a source of protein, essential vitamins and minerals, soluble fiber, starch, phytochemicals along with having a low fat content (Nyombaie et al., 2007). It also serves as a functional food as it contains lot of bioactive compounds like enzyme inhibitors, lectins, phytates, oligosaccharides, and various phenolic substances (Diaz-Batalla et al., 2006). It has also been observed that consumption of beans reduces the cholesterol level (Rosa et al., 1998) and coronary heart diseases (Bazzano et al., 2001), cancer (Hangen and Bannink, 2002), diabetes, and obesity (Geil and Anderson, 1994). In nutritional terms, beans are often called the “poor man’s meat” as it has high proteins and their rich content of minerals (especially iron and zinc) and vitamins (Beebe et al., 2000). In various countries bean provides as much as 15% of total daily calories and greater than 30% of the
daily protein intake. In humans, iron and zinc play important roles in proper functioning of various metabolic processes. Iron is essential for preventing anemia and for the proper functioning of many metabolic processes while zinc is essential for adequate growth and sexual maturation and for resistance to gastro-enteric and respiratory infections, especially in children (Bouis, 2003). Since a large part of the world is at a risk of micro-nutrient intake (Brown and Peerson, 2001) hence food rich in micronutrients are important in this concern. Iron (Fe) deficiency has been found to be very prevalent around globe affecting two billion people (Welch, 1999). Similarly 49% of the world population is at a risk for low zinc (Zn) intake (Brown and Peerson, 2001). In numerous developing countries with widespread poverty, malnutrition is a major threat and it is an aggravating factor for diseases like HIV-AIDS and tuberculosis. Both Fe and Zn have been found depleted in individuals suffering from AIDS. As such common beans rich in Fe and Zn can improve the health status of HIV infected patients (http://www.csrees.usda.gov/business/reporting/stakeholder/pdfs/pl_common_bean.pdf). Since beans are rich in Fe and Zn, the importance of this food source cannot be ignored. The heritability of Zn trait has no maternal affects, so breeding for increased Zn content in seeds of common bean can be done successfully (da Rosa et al., 2010). Similarly in another study the QTLs for Fe and Zn have been identified and it has opened a way for marker assisted selection to breed new varieties of common beans with commercial seed type along with high micronutrient concentration (Blair et al., 2009). A range of 30 to 110 ppm Fe and 25 to 60 ppm Zn was found in the germplasm and the high Fe containing genotypes, G14519 and G21242 were selected for development of common bean varieties rich in Fe and Zn contents (Beebe et al., 2000, Islam et al., 2002).

1.1 Importance of common bean as a model crop

Various unique genomic features contribute to the desirability of common bean as an experimental crop species. It is diploid in nature with 11 pairs of chromosomes having genome size, estimated to be about 450 to 650 million base pairs (Mb)/haploid (Bennett and Leitch, 1995), comparable of rice genome which generally is considered to have the smallest genome among major crop species. Nearly all loci are single copy (Vallejos et al., 1992; Freyre et al., 1998; McClean, 2002), and the traditionally large families, such as resistance gene analogs (Rivkin, 1998) and protein kinases (Vallad, 2001), are of moderate size. In addition to it there is also an availability of good linkage map (Freyre et al., 1998). Looking at the importance of this crop and feasibility of being a model crop, initiatives have been taken in complete genome sequencing of the common bean. Its immediate applications will help in developing fine maps which can be used in identification and introgression of various biotic and abiotic stress tolerance genes in desirable background through molecular breeding approach. The whole genome sequence will also help in candidate gene discovery not only in common bean but also other for other legume crops.

2 Need for genetic diversity studies in common beans: Cataloging of collected germplasms

The importance of common bean has been discussed in earlier section and it is evident that there is an urgent need to design a road map for improvement of this crop. Further, as per a report published by Commodity Online on December 01, 2010, the Indian government is mulling to import around 9,00,000 tonnes of the legume. (http://www.commodityonline.com/news/Indian-export-embargo-on-pulses-may-continue-33976-3-1.html). So designing strategies for improvement of this crop is to be done on a high priority basis.

Since, for the improvement of any crop, it is necessary to have knowledge about the germplasm of that crop. The best way to understand the potential of the available germplasm is by analyzing its genetic diversity and to characterize it. The genetic diversity can be analyzed by various means, but the main objective is to understand the genetic makeup of each and every genotype. By analyzing large number of genotypes of a particular crop, it is possible to get some desirable cultivars that can withstand harsh/abnormal conditions (biotic as well as abiotic
stress factors) and have better quality traits. The importance of genetic diversity can be understood further, as United Nations General Assembly declared 2010 as the International Year of Biodiversity (resolution 61/203) with the slogan, “Biodiversity is life. Biodiversity is our life.” Devoting a year to biodiversity indicates genetic diversity importance in human development and survival. The immense genetic diversity of landraces of crops is the most directly useful and economically valuable part of our planet’s biodiversity.

In the present investigation, the areas of our study were Rajouri, Poonch, and Shopain, which lie in the foothills of the Himalayas, and are well-known for their rich biodiversity. The utilization of this biodiversity by people inhabiting these regions for various purposes like medicine, food, fodder, timber, etc., is quite evident (Samant and Dhar, 1997). In addition to these locations, we have collected the germplasms from Quazigund, Baramulla and Bandipora also. These regions falling in the foot hills of Himalayas are mostly dominated by poor farmers, where common bean is cultivated as a crop for food and feed. To the best of our knowledge and expectations we have succeeded in the collection of some unique germplasms of common bean, mostly the landraces. These land races can serve as a source of essential genes involved in enhancing yield and quality of the common bean. The list of genotypes collected from various locations of Jammu and Kashmir (India) is presented in Table 1.

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Main regions</th>
<th>Local areas</th>
<th>No. of genotypes collected</th>
<th>Name of the genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Poonch</td>
<td>Bufliyaz, Loran, Maniyal, Dunaro, Sabzian, Chandimarg</td>
<td>19 (P1 to P19)</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Rajouri</td>
<td>Falni, Kewal, Budhal, Thana mandi</td>
<td>10 (R1 to R10)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Shopian</td>
<td>Chowgam, khudpora, achgoza keler</td>
<td>11 (KS1 to KS11)</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Bandipora</td>
<td>Wanigam, Bandipora plan ward 3</td>
<td>5 (K12, K14, K15, K16,K18)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Baramulla</td>
<td>Sangria, shuva, Zangeer</td>
<td>3 (K13,K17, K19)</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>Quazigund</td>
<td>Quazigund main</td>
<td>1 (K20)</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>Baderwah</td>
<td></td>
<td>2 (B1, B2)</td>
<td></td>
</tr>
</tbody>
</table>

3 Our vision and future work plan: Experimental strategy and design

As a first step, the common bean germplasm were collected and catalogued, as shown in Figure 1–Figure 3. The immediate need is to obtain the pure germplasms. To do so, the single plant seed collection was done (Figure 2) represents the selection of individual plants, where seed purification was done. As discussed in the earlier section about importance of genetic diversity analysis, our plan is to employ SSR and RAPD markers to detect the polymorphism among the diverse genotypes. Many studies in past have been conducted on bean germplasm diversity analysis by using different approaches (Metais et al., 2000; Gaitan-Solis et al., 2002; Maras et al., 2008). However, the use of molecular markers can generate greater polymorphism. These molecular markers will be selected based on their availability, reproducibility, and accuracy. In a number of studies, we observed that in case of beans, RAPDs and SSRs have been extensively used for determination of genetic diversity (Metais et al., 2000; Gaitan-Solis et al., 2002; Maras et al., 2008).

Figure 1 Locations of the common bean germplasm collection
et al., 2008). Molecular markers have demonstrated a potential to detect genetic diversity and to aid in the management of plant genetic resources (Virk et al., 2000; Song et al., 2003).

The second immediate focus of our investigation will be to assess the germplasm for water stress tolerance in field conditions and to know its micronutrient composition (mainly Fe and Zn) and seed protein content. These works will be carried out in the near future, with a focus on i) water stress tolerance under laboratory conditions and field conditions, ii) estimation of micronutrients, and ii) total proteins (amino acid analysis, and profiling polypeptide patterns using one-dimensional gel electrophoresis) of each collected germplasm/seed.

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