Food Science and Technology
ISSN 0101-2061 (Print)
ISSN 1678-457X (Online)

DOI: https://doi.org/10.1590/fst.42117

Nutritional and health benefits of legumes and their distinctive genomic properties

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Abstract

Legumes are indispensable for human diet in respect to their valuable and nutritive bioactive molecules. Legumes and derivative foodstuffs are rich in fiber, proteins, vitamins and some valuable phytochemicals, which exhibit important biological activities. Due to their remarkable molecular content, they are receiving great attention by researchers. Recent developments in genomics and bioinformatics led to cumulative data about legume genomes. These data could provide important information to accelerate breeding and to develop new traits for biofortification. The main focus of this review is to present their distinctive genomic properties by summarizing significant studies conducted with relatively newly developed techniques revealing the beneficial effects of bioactive molecules from legumes on human health.

Keywords: *Leguminosae*; nutritional properties; health; bioactive compounds; legume genomes.

Practical Application: Nutritional and health benefits of legumes and their distinctive genomic properties.

1 Introduction

Legumes are the third largest family of angiosperms belong to Fabaceae/Leguminosae (Gepts et al., 2005). Pulses are the important components of a healthy diet and take an important place in the traditional diets throughout the World (Malaguti et al., 2014). This family includes peas, lentils, beans, peanuts and other podded plants that are consumed as food (Messina, 1999). They provide a range of essential nutrients including protein, low glycemic index carbohydrates, dietary fibre, minerals and vitamins. Legumes are uniquely rich in both protein and dietary fibre (Table 1). In addition, legumes are richer in protein than other cultivated plants because of the nitrogen-fixing bacteria live in the nodules of legume roots (Kouris-Blazos & Belski, 2016). Protein derived bioactive peptides of legume plants have many important roles as health-enhancing compounds (especially interact with amino acids of enzymes related with diseases). Presence of these bioactive peptides in legumes may contribute to the food quality (López-Barrios et al., 2014; Ortiz-Martinez et al., 2014). Also, the observed effects on diseases including cardiovascular diseases, diabetes, cancer and obesity, may derive from the synergistic combination of bioactive compounds of legume seeds (Arnoldi et al., 2015). There are many reports regarding that these peptides have different activities and described as antimicrobial properties, blood pressure-lowering effects, cholesterol-lowering ability, antithrombotic, antioxidant activities, enhancement of mineral absorption/bioavailability, cyto- or immunomodulatory effects, and opioid-like activities (Mejia & Dia, 2010; Li et al., 2013; Möller et al., 2008; Zambrowicz et al., 2013). Among the legumes, soybean (*Glycine max* L.) is widely used in human and animal diet because of its nutritional value. Soybean seed has high quality proteins in the manner of nutrition when compared to other legume seeds (Natarajan et al., 2013). After the developments in genetic engineering technologies, modified soybean varieties has been developed to address insusceptible conditions (Zhang et al., 2016). Today, 83% of all soybeans planted is genetically modified (GM) soybean in the world (about 92.1 million hectares) (James, 2009).

Even though noteworthy progress has been made in decreasing hunger globally, 795 million people are still underweight, with over 2 billion people having micronutrient deficiencies, and approximated 161 million children under 5 years of age are undersized and, 99 million are undernourished (Amoroso, 2016). Regarding the global nutrient deficiencies, legumes play major role as a part of the farming structure of the developing world. To solve the global food shortage problem, improving the quality of legume grains using recent technologies can be adapted as a strategy. By means of research projects focusing on biofortification of the legume grains, which use genomics technologies, could rapidly meet the expectations. These technologies would help to explore whole genome in a short time, then enlighten the scientists to determine target gene regulating DNA regions related to biofortification (Gupta, 2014; White & Broadley, 2009). Rapidly growing methods in the genomic area have shown to be accurate analysis tools for plants (Bohra et al., 2015; Varshney et al., 2015). Decreasing costs along with rapid progress in next-generation sequencing (NGS) and bioinformatics analysis resources have facilitated discovery of whole genome sequences of legume plants. Consequently, new NGS assays like genotyping-by-sequencing (GBS) and whole genome re-sequencing (WGRS) could assist researchers in the evaluation of genetic diversity of model plants and also for the non-model grain legumes (Bohra et al., 2014; Poland & Rife, 2012).

The general view is that today it would be insignificant to discuss the legumes without taking into consideration of their genomic properties. The main aim of this review is to display the features of legumes in genomic perspective while discussing the present status of them on human nutrition and health.

Received 22 Dec., 2017
Accepted 11 Sept., 2018

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Table 1. Nutrient values of various legumes per 100 g*.

	Unit	Soybeans	Peas	lentils	Lupins	Chickpea	White bean	Black bean
Energy	kcal	172	118	116	119	164	139	132
Protein	g	18.21	8.34	9.02	15.57	8.86	9.73	8.86
Fat	g	8.97	0.39	0.38	2.92	2.59	0.35	0.54
Carbohydrate	g	8.36	21.10	20.13	9.88	27.42	25.09	23.71
Dietary Fiber	g	6	8.3	7.9	2.8	7.6	6.3	8.7
Minerals								
Calcium, Ca	mg	102	14	19	51	49	90	27
Iron, Fe	mg	5.14	1.29	3.33	1.20	2.89	3.70	2.10
Magnesium, Mg	mg	86	36	36	54	48	63	70
Phosphorus, P	mg	245	99	180	128	168	113	140
Potassium, K	mg	515	362	369	245	291	561	355
Sodium, Na	mg	1	2	2	4	7	6	1
Zinc, Zn	mg	1.15	1.00	1.27	1.38	1.53	1.38	1.12
Vitamins								
Vitamin C	mg	1.7	0.4	1.5	1.1	1.3	0.0	0.0
Thiamin	mg	0.155	0.190	0.169	0.134	0.116	0.118	0.244
Riboflavin	mg	0.285	0.056	0.073	0.053	0.063	0.046	0.059
Niacin	mg	0.399	0.890	1.060	0.495	0.526	0.140	0.505
Vitamin B-6	mg	0.234	0.048	0.178	0.009	0.139	0.093	0.069
Folate, DFE	µg	54	65	181	59	172	81	149
Vitamin B-12	µg	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Vitamin A, IU	IU	9	7	8	7	27	0	6
Vitamin D	IU	0	0	0	0	0	0	0
Vitamin E	mg		0.03	0.11			0.94	0.87
Vitamin K	µg		5.0	1.7		4	3.5	3.3
Lipids								
Fatty acids, total saturated	g	1.297	0.054	0.053	0.346	0.269	0.091	0.139
Fatty acids, total monounsaturated	g	1.981	0.081	0.064	1.180	0.583	0.031	0.047
Fatty acids, total polyunsaturated	g	5.064	0.165	0.175	0.730	1.156	0.152	0.231
Fatty acids, total trans	g	0.00	0.000	0.000	0.000	0.000	0.000	0.000

*Values from USDA standart reference release 28 and based on edible portions of mature seeds, cooked, boiled without salt. National Nutrient Database for Standard Reference Release 28.

2 Importance of legumes regarding bioactive compounds and human health

There are numerous groups which can be classified as bioactive protein and peptide derivatives, phytosterols, isoflavones, saponins, alkaloids and bioactive carbohydrates. Mostly studied, lunasin, Bowman-Birk protease inhibitor (BBI) and soy isoflavones are bioactive components of the legumes. Lunasin is found in soybean and also detected in wheat, barley, rice, rye, triticale and amaranth (Jeong et al., 2007; Jeong et al., 2009; Jeong et al., 2010; Park et al., 2005). It is encoded within 2S albumin (GM2S-1) gene and composed of 43 amino acid residues with molecular weight of 5.5 kDa. Health-promoting effects of lunasin can be sorted as anti-inflammatory, cholesterol lowering, anticancerous and antioxidant activity (Hsieh et al., 2018). Its bioactive properties come from the capability of arresting cell division in cancer cells, inhibiting core histone acetylation in mammalian cells and protecting DNA from oxidative damage. Generally, it is estimated that the mechanism of lunasin to act as anticancer agent is to disturb histone acetylation and deacetylation. Hereby, inactivation of some tumor suppressor proteins as Rb, p53 and pp32 is reported (Lumen, 2005; Galvez et al., 2001; Hernández-Ledesma et al., 2011; Jeong et al., 2007; Jeong et al., 2002). Bowman-Birk inhibitor (BBI) is one of the major classes of legume produced protease inhibitors, and composed of 70-80 amino acids with a molecular weight of 8 kDa. It is found in soy as well in lentil and pea. BBI has many functions such as regulation of protease activity during seed germination and protection of plants from insects and microorganisms, also there are studies reporting the preventive effect of BBI against prostate, breast and colon cancers (Chan et al., 2013; Mejia & Dia, 2010; Hernández-Ledesma et al., 2009; Park et al., 2005). Proteasome activity is known to be increased in many cancer cells compared to non-transformed cells (Souza et al., 2014) and proteasome inhibition may result homeostasis disruption of the cancer cells. Based on this information, proteasome inhibitors might be used for cancer therapy, also BBI may be an important compound that has a potential to be used in cancer prevention. The proposed mechanism is the induction of tumor suppressor gene connexin 43 (Cx43) and cell cycle arrest in G1/S phase (Chen et al., 2005; Saito et al., 2007).

Another group of bioactive proteins is lectins, which have the ability to agglutinate cells due to their binding to specific carbohydrate residues on the cell surface. Liener (1991), first reported that soybean aglutinin could inhibit tumor growth in a rat model demonstrating of anticancer properties of soybean lectins. Boland et al. (1992) demostrated that soybean lectins improve the life expectancy in a lymphoma mouse model.

Besides these bioactive peptides, other phytochemicals (isoflavones, saponins, alkaloids) in legumes have been reported to have potential benefit in human health. It is reported that isoflavones are largely isolated from the Fabaceae family (Leguminosaea) (Rochfort & Panozzo, 2007). Isoflavones have been shown to have several biological activities including reduction in osteoporosis, prevention of cancer and cardivovascular disease (Table 2) (Cooke, 2006; Manach et al., 2005; Martínez et al., 2006; Messina et al., 2006; Trock et al., 2006). Isoflavones can also be used for the treatment of symptoms of menopause (Li et al., 2015). Saponins are another class of phytochemicals, and they are included as soya saponins classified into group A, B, and E saponins on the chemical basis of the chemical structure of their aglycone. They have been also reported to be found in lupins (Woldemichael et al., 2003; Woldemichael & Wink, 2002), lentils (Rochfort & Panozzo, 2007; Ruiz et al., 1996), chickpeas, various beans, as well as soy (Shi et al., 2004). It has been suggested that legumous saponins may have anticancer activity, and be beneficial for hyperlipidemia (Chang et al., 2006; Ellington et al., 2006; Shi et al., 2004; Zou et al., 2006).

Alkaloids from edible legumes have been reported from lupins. One of the alkaloid trigonelline has been reported from peas (Hammouda & Ahmed, 1962), also low levels of alkaloids were detected from chickpeas and lentils. One of the report discusses the enhancement of insulin secretion by lupin quinolizidine alkaloids (López et al., 2004).

Legumes can reduce cholesterol, blood pressure, inflammation, weight and blood pressure lead to cardiovascular disease (CVD) due to their valuable content (Abeysekara et al., 2012; Flight & Clifton, 2006; Hermsdorff et al., 2011; Nilsson et al., 2013). Low serum cholesterol and and low-density lipoprotein cholesterol (LDL-C) have an inverse correlation with coronary heart disease (CHD) mortality because of the high levels of saponins and phytosterols (Kouris-Blazos & Belski, 2016). There are some studies reporting the reduce of CHD by consumption of legumes because of their high saponin and phytosterol contents (Afshin et al., 2014; Bazzano et al., 2001; Nagura et al., 2009). The consumption of dry legumes with a low saturated-fat diet may help improve the lipid homeostasis and as a result reduce the risk of CVD (Duranti, 2006).

The prevalence of *diabetes mellitus* (DM) is rapidly increasing worldwide as a result of population growth, ageing, urbanization and lifestyle changes leading obesity and physical inactivity (Chen et al., 2011; Zimmet et al., 2001). Legumes have been demonstrated to improve the glycemic control in type 2 DM patients because of higher amount of resistant starch and amylose content (Thorne et al., 1983). The increased consumption of resistant starch is related to improved glucose tolerance and insulin sensitivity (Jukanti et al., 2012). Short-term studies have shown that legume consumption lowers blood glucose and insulin responses and increases insulin sensitivity (Nestel et al., 2004). The protective effect of legumes on type 2 DM may be as a result of high fiber content, low glycemic index and a range of potentially bioactive nutrients including isoflavones and lignans (Kalogeropoulos et al., 2010).

The glycated hemoglobin A1c (HbA1c) is considered as the gold-statement to determine blood sugar control over time and acceptable HbA1c levels are below 6.5% according to the American Diabetes Association (2011) and The World Health Organization (2011). When legumes were consumed in low-glycaemic index (GI) diets, HbA1c level also was lowered in both diabetic and non-diabetic individuals. Legumes in high-fibre diets also significantly reduced FBG (Fasting Blood Glucose) and HbA1c level. Thus, the consumption of legumes, alone or in low-GI or high-fibre diets, improves markers of longer term glycaemic control in humans (Sievenpiper et al., 2009). The recent randomised controlled studies have also demonstrated that legumes, as part of a low GI diet, are associated with long-term improvements in HbA1c and lowered risk of developing type 2 DM (Dong et al., 2011; Jenkins et al., 2012). Legumes also have been shown to improve insulin sensitivity, whilst they are as part of high carbohydrate and GI diets (Simpson et al., 1981).

Overweight and obesity have been related chronic diseases and contributed to morbidity and mortality, including cardiovascular and metabolic disorders as well as certain types of cancers such as colorectal cancer, lung cancer, esophageal adenocarcinoma and breast cancer (Abete et al., 2010; Calle et al., 2003; Jemal et al., 2011). Legumes are rich in low glycemic index carbohydrates, resistant starch, oligosaccharides and fibre, and also demonstrated to decrease hunger and acute food intake therefore consumption of legumes, can aid in the management of obesity and obesity-related mortality (Muzquiz et al., 2012; Rebello et al., 2014; Wanders et al., 2011). Bean extracts containing digestive enzyme α-amylase inhibitors were demonstrated to reduce starch digestion leading to significantly reduction of body weight, body mass index (BMI) and fat mass (Celleno et al., 2007).

Legumes, particulary, beans contain bioactive components like phenolic compounds (flavonoids, tannins, and anthocyanin), protease inhibitors, phytic acid, and saponins. These components have helped in the inhibition of colon cancer (Table 2) (Harland & Morris, 1995; Kennedy, 1994; Kinjo et al., 1998). Colon rectal cancer (CRC), being highly metastatic and resistant to anticancer treatment strategies, is the third most common cause of cancer death in the developed and developing countries (Markle et al., 2010; Siegel et al., 2014). The case-control studies have shown that legume consumption is related to a decrease in the risk of CRC (Aune et al., 2009). Furthermore, preclinical research has also revealed that feeding of laboratory animals with 100 g of diet including 75 g black or navy beans can reduce both the incidence and the number of colon tumors by 50% (Bennink, 2002). There are a number of phytochemicals in legumes shown anticarcinogenic activity; these include phytoestrogens, a variety of phenolic acids, phytosterols, protease inhibitors, saponins, phytates, fiber, proteins, and fatty acids (Mathers, 2002; Messina, 1999).

Protein extracts from some legume seeds, particularly albumins and globulins, can reduce cell migration in colon carcinoma cells. Effectiveness of seed proteins in inhibition of gelatinases (MMP-9) activities which is known to be linked to

Table 2. Effects of legumes on cardiovascular diseases, diabetes and cancers.

Legume Source	Involved metabolism	Type of study	Beneficial effect	Reference
Dry beans, peas and peanuts	Cardiovascular	Epidemiologic Follow-up Study	22% reduction in coronary heart disease (CHD) and 11% reduction in cardiovascular disease (CVD)	Bazzano et al. (2001)
Legumes	Cardiovascular	Meta-analysis	Decreased risk of 10% in both CVD and CHD	Marventano et al. (2017)
Baked beans	Hypercholesterolemia	unblinded, 2 × 2 randomized crossover with baked bean treatment and a control treatment	5.6% reduction in total cholesterol and 5.4% in low-density lipoprotein cholesterol	Winham & Hutchins (2007)
Cooked beans, chickpeas or lentils	Cardiovascular and diabetic	randomized controlled trial	Reduced hemoglobinA1c (HbA1c) level and reduction in coronary heart disease (CHD) risk	Jenkins et al. (2012)
Five cups/week yellow peas, chickpeas, navy beans and lentils)	Metabolic syndrome	Randomized Controlled Trial	Reduced risk factors of the Metabolic syndrome	Mollard et al. (2012)
Beans with low-GI diet	Glycaemia and obesity	randomized, crossover study	Improvement in metabolic control in type 2 obese diabetic patients and weight loss	Jimenez-Cruz et al. (2003)
Azuki bean juice	Hypertriglyceridemia	Randomized double-blind parallel-group trial	Reduction in triglyceride by suppression of lipase inhibitory activity	Maruyama et al. (2008)
Legume seed extracts	Colon cancer	Test-tube Lab Research	Inhibition of MMP-9 activity and cell migration in colon carcinoma cells.	Lima et al. (2016)
Raw or cooked- bean extracts	Colon cancer	Animal Research Studies	Inhibition of aberrant foci crypt development in rat colon	Feregrino-Perez et al. (2008)
Lunasin peptides isolated from soybean	Colon cancer	Test-tube Lab Research	Lunasin caused a G2/M cell cycle arrest on HT-29 colon cancer cells	Caccialupi et al. (2010)
Protein isolates of germinated soybean	Cervical cancer	Animal Research Studies	Decreased in the expression of PTTG1 and TOP2A (2 genes considered as therapeutic targets) causing apoptosis of cancer cells.	Robles-Ramírez et al. (2012)
Soybean soyasaponin I	Skin cancer	Animal Research Studies	Decreased in the expression of α-2,3-linked sialic acid on the cell surface, which in turn suppresses the metastatic potential of melanoma cells	Chang et al. (2006)
Lunasin peptides isolated from soybean	Skin cancer	Test-tube Lab Research	Chemopreventive agent	Galvez et al. (2001)
Brown Kidney Bean Bowman–Birk Trypsin Inhibitor	Breast cancer	Test-tube Lab Research	Inhibition of the proliferation of human breast cancer cells	Chan et al. (2013)

progression of CRC (Herszényi et al., 2012), is varied to legumes species. For example, mediterranean-type legume seeds contain most efficient MMP-9 inhibitors among the analyzed legumes, while pea seeds were less effective on HT29 cell proliferation and cell migration tests (Lima et al., 2016).

3 Prominent genomic features of legumes

Because of their nutritional, agricultural and ecological value, the legume biology has been of particular interest. The special features of the legumes such as nutritional value, Rhizobia-Legume symbiosis, and genetic characteristics that confer these phenotypic traits have long been investigated. The habitats of majority of the legumes are unfavorable environments including salinity, cold, drought, and variety of biotic stress (Dita et al., 2006). Therefore, it is important to investigate the stress response mechanisms in legumes not only to obtain more resistant varieties but also to understand their uniqueness among the other plant groups. These investigations have been carried out at the transcriptome, proteome and metabolome level. For example, proteomic analysis gives detailed information regarding the protein content associated with variety of stress responses (Kosová et al., 2011). It has been reported that symbiotic relationship between *Medicago truncatula* and *Sinorhizobium meliloti* strain 2011 affects drought responsive protein levels (Larrainzar et al., 2007). Besides, since the metabolites are direct indicators of regulatory mechanisms, it is important to detect their abundance and dynamic composition when legume specific responses to environmental perturbations are concerned (Obata & Fernie, 2012). Scherling et al. (2010) demonstrated the differential metabolic profiling between legume and non-legume plants which grown in different conditions and found that changing environment had profound impact both on primary and secondary metabolism.

Nutritional breeding of legumes for high protein and mineral content stays critical to people. In order to allocate the biosynthetic pathways that highlight nutrient synthesis, nutrient accumulation and their transportation to the relevant plant parts, researchers need to lay emphasis on comprehending the complex mineral network. An enormous genomic pool promoting high-throughput recovery of DNA markers for instance SSRs (Single Sequence Repeats), single nucleotide polymorphisms (SNPs) and insertion-deletions (InDels) was exhibited by genome assemblies (Bohra & Singh, 2015; Varshney et al., 2013). After analysing 90 genomes, diverse additional chickpea genome polymorphisms including both SNPs and InDels were revealed in addition to determining SSRs and SNPs based on genome scanning and RNA-seq analysis. By sequencing, genomic selection and genome-wide association studies, these resources will facilitate genomic-based breeding approaches like genotyping (Varshney et al., 2013). In genomics-based biofortification researches, the determination of the location of the important genes/quantitative trait loci (QTL) is an indispensable requirement. There is strong correlation with QTL determination and robust DNA marker determination. The correct molecular markers for edible plant parts could noticeably hasten the biofortification progress (Bohra et al., 2014). In order to identify the genomic location of gene(s)/QTLs which have quantitative effects on the phenotype, two QTL mapping methods like family-based linkage mapping and association analysis (so called LD mapping) are executed (Bohra, 2013; Mackay & Powell, 2007; Mitchell-Olds, 2010; Würschum, 2012). For the detection of QTLs responsible for increased mineral concentrations in seeds, QTL analysis was conducted in two model legumes: *Medicago truncatula* and *Lotus japonicus*. As a result, 46 important QTLs altering mineral concentrations were determined in *Medicago truncatula*, and more than 100 QTLs were gained from *Lotus japonicus* (Klein & Grusak, 2009; Sankaran et al., 2009). Forty QTLs of *Medicago* which affects nearly 18 different traits related to seed mineral concentrations, total nitrogen: total sulfur (N:S) ratio in seed, cysteine and methionine concentrations, were found out important (Ramamurthy et al., 2014). Furthermore, Scanning genomes of 94 different accessions with 1129 single nucleotide polymorphism (SNP) markers, a genome-wide association analysis was conducted recently in chickpea. As a result, SNPs were detected contributing towards Fe and Zn accumulation (Diapari et al., 2014).

Crops that typically have lower genetic diversity, can be introgressed by the pan-genome. Association between agronomic phenotypes, which inferred from homology and comparison with mapped QTLs, and genes with structural variation and large-effect variation can be used in order to develop molecular markers. These kind of data should empower the crop breeding community for more effective usage of molecular approaches. For instance, genomic selection in order to reduce the yield drag often accompanied with introgression from wild species (Bohra & Singh, 2015). Because it determines the protein composition in particular organs and tissues at a given time, protein reference maps contribute greatly to understand the legume specificity (Watson et al., 2003). Lei et al. (2005) analysed the comprehensive proteome of *M.truncatula* and identified 1367 proteins and obtained 907 unique protein accession numbers. They also revealed that these proteins function in tricarboxylic acid cycle, glycolytic pathway and ubiquitin pathway and identified many enzymes involved in flavonoid/isoflavonoid, chalcone, and lignin biosynthesis using two-dimensional electrophoresis and nanoscale HPLC-MS/MS. Since symbiosis with rhizobia is a characteristic attribute, defining nodule proteome is especially important for the legumes. For this reason, reference maps have been constructed also for nodules in different species. Results obtained from these studies provide valuable insights into different features of protein dynamics in nodules. For example, it has been shown that post-translational modifications in proteins are more apparent in nodules in comparison with roots (Dam et al., 2014). In the same study, it was also shown that protein composition in nodules dramatically changed prior to and during nitrogen fixation. Dynamic changes in concentration and intertissue compartmentalization of proteins significantly affect the nutritional value of legume seeds. Legume seeds are highly rich in protein and other nutritious components as a distinguishing feature. The most important reason for this trait is the symbiotic relationship with nitrogen-fixing bacteria.

Legume genomes present distinct features as well. As a common characteristic, about 58 million years ago (Mya), a whole-genome duplication (WGD) took place in important legume families, and the best-knowns are *M.truncatula, L. japonicus and G. max*. It is thought that approximately 7.000 legumes share the same genome duplication event (Pfeil et al., 2005) and it seems that these events largely affected two distinctive features, nodulation and symbiosis (Young et al., 2011). In addition, WGD events cause novel disease-resistance and developmental mechanisms to emerge. It is thought that, during legume evolution, a rapid expansion occured in well-conserved disease resistance genes and this expansion was followed by a contraction. Some resistance genes emerged after divergence of legumes. This dynamic pattern caused a much faster evolution of disease resistance genes than other genes as an essential need to adapt to dramatically changing environmental conditions. Moreover, it seems that, during domestication, especially the resistance genes, which directly involved in the plant-pathogen interaction pathway, were selected (Zheng et al., 2016).

Subsequent duplications also ocurred and shaped the genomes and evolution of characteristic traits of the legumes. For example, a second genome duplication took place about 13 Mya and as a result, splitting of soybean occurred (Shoemaker et al., 1996). Therefore, one genomic region of *M.truncatula* or *L. japonicus* probably corresponds to two glycine regions. It is thought that these duplication events confer higher adaptability to rigorously changed environment and harsh conditions (Fawcett et al., 2009). One of the advantages that these duplication events provide the availability of nitrogen thanks to the evolution of nodulation and symbiosis regulative genes. Presence of nitrogen frees legumes of the need for the key constraint that other plants have to obtain, and thereby increases their adaptive capacity in more drastic environments (Cannon et al., 2009). In addition to this naturally occurred selection, artificial selection also shaped the legume genomes. When wild and cultivated soybean genomes compared, it is revealed that differentiated genome regions in cultivated soybean correlates with variation in harvest index and yield (Huang et al., 2008).

Sequenced legume genomes reflect the significant similarity between legume groups. It is reported in a more recent study that in *Lotus* and *Medicago* genomes there are many colinear, extensive syntenic regions and that gene densities are relatively homogeneous (Cannon et al., 2006). Legumes have higher numbers and increased complexity in the gene families such as lipoxygenases (Shin et al., 2008). LysM (Lysin motif) receptor kinases (Zhang et al., 2007) and enzymes that function in flavonoid synthesis (Young et al., 2011). Furthermore, soybean, *Lotus* and *Medicago* genomes harbour high numbers of F-box domain protein coding genes and Medicago genome contains special cysteine-rich peptides coding gene family. It is noteworthy that the products of these genes function especially in nodules (Young & Bharti, 2012). The genomes of some legumes contain distinct genes observed only in legume genomes. For example, *Medicago truncatula* genome express 566 defensin-like genes which have unique *cis*-element motifs in the upstream 1,000 bp promoter regions of nodule cysteine rich family (Nallu et al., 2013). These genes expressed only in nodules at various stages of development and sometimes have important function in rhizobial biology. Other well known nodulation related proteins are nodulins, early nodulation proteins (ENOD 16 and 8), ascorbate metabolic enzymes, and putative rhizobial effectors (Rathi et al., 2016). Schmutz et al. (2010), sequenced *G. max* genome and identified 283 putative legume-specific gene families which are absent in grapevine, poplar, *Arabidopsis*, papaya and grass genomes. Therefore, the analysis of the functions of these specific gene families enables to understand the legume biology more comprehensively. In addition to gene gaining, throughout their evolution, legumes have lost some genes known as legume lost genes (LLGs). These lost genes, like the gained genes, have also contributed to evolution of symbiotic relationship with rhizobia. For example, it is reported that 34 LLGs might have lost in, one of the sub-family of leguminosae, Papilionoideae family and orthologs of 21 LLGs in nonlegume plants function in plant defence mechanisms. Accordingly, it seems that gene lose has also a considerable impact on distict features of Papilionoidae family (Gu et al., 2016).

The genetic diversity and taxonomic structure of Glycine species have been investigated and their results suggest that wild soybean should be conserved to maintain the genetic diversity of soybean (Wang et al., 2016; Wang et al., 2015a; Wang et al., 2015b). Wild crop relatives are more genetically diverse than their domesticated counterparts so resequencing is limited in point of capturing many types of structural variation. Besides, presence-absence variation and copy number variation that are generally associated with agronomic traits, may also be missed. In order to capture the majority of genetic diversity within species, *de novo* construction of a pan-genome for species which consists of a core genome shared among individuals is compulsory. Li et al. (2014), by sequencing and assembling seven *G. soja* accessions *de novo*, constructed a pan-genome with the aim of completely characterizing the genomic content and molecular evolutionary history of *G. soja*. In this pan-genome, nonessential gene set was found to have evolved more promptly and be more variable than the core gene set and also genes under selection displayed relatively little overlap between the seven *G. soja* lineages showing that local adaptation may have affected non-overlapping sets of genes. As a consequence, researchers considered that the divergence time between *G. soja* and *G. max* was nearly three times earlier than a previous consideration (Bohra & Singh, 2015).

4 Conclusion

The research summarized in this review, clarify the potential of legume plants for human nutrition because of their remarkable molecular content, health benefits, nutritional value and distinctive genomic features. Soybean and derivative food products are prominent in the world. Newly developed technologies such as next generation sequencing, will serve as powerful tools to understand new features and advantages of these plants. Revealing the genomic potentials and characteristic properties of legumes will help to improve their nutritional capacity and resistancy to harsh conditions. However, still, there is a great need for collaborations of agronomists, plant geneticist and bioinformaticicons to utilize the gigantic data and develop new traits in the context of nutritional value.

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