Role of conventional and molecular techniques in soybean yield and quality improvement: A critical review

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Abstract

The soybean is one of the most significant legume crops around the globe and serves as a source of dietary components for humans and animals. It has a higher percentage of protein compared to any other crop. Soybean yield and quality have been affected by many environmental factors. The genetic mechanism of yield and quality is still not clearly understood. Hence there is still a need to investigate the major potent factors to shed light on the mechanism behind yield and quality traits in soybean. Recently, a lot of significant work, including novel QTL, genes, and CRISPR-based genome editing in soybeans, has been done, which opened new doors of hope. The current review has presented detailed work done previously. We have also discussed the role of different breeding techniques in the conventional way of soybean improvement. The genetic factors regulating yield, quality, and disease resistance could be further cloned and transferred into elite cultivars to attain higher output in the current situation of changing environment. The integrated use of several techniques, like CRISPR/Cas9, next-generation sequencing, omics approaches, would be a fruitful way to improve soybean yield and quality. Besides this, hybridization, mass selection, pure line selection, backcross breeding, and pedigree selection should be adopted to develop novel soybean cultivars. This review concluded that soybean yield and quality improvement could be enhanced by exploring its genetic mechanism using several molecular and conventional methods.

Keywords: conventional methods; molecular techniques; soybean; yield; quality

Abbreviations: QTL: Quantitative traits loci; Soy: Soybean; Chr: Chromosomes; Gen: Genomics
Introduction

The soybean (Glycine max) is one of the important and oldest legumes known and consumed by human beings. This crop has a higher percentage of oil, protein, and other valuable products, and its production is increasing every year because of increasing demand day by day (Contini et al., 2013; Bao et al., 2019). The soybean contributes to 69% of oil and 30% of the protein consumed by livestock (Van and McHale, 2017). Genetic and environmental factors that impact the polygenic traits are difficult to improve by conventional breeding (Li, 2006). The huge genetic diversity among the lines makes it easy to differentiate the lines in the field trails. The yield is an ultimate goal of any breeding program in soybean, and it is generally associated with seed size and plant architecture. In general terms, plants with unified architecture are expected to have higher yields than plants with contrasting traits. To overcome this difficulty, breeders have selected relatively simple traits to enhance yield, which is least influenced by external factors and controlled by small genetic loci (Hartung et al., 1981).

Hence, understanding the genetic basis of small traits, their characterization, and their role in improving the yield and quality of soybean is helpful to speed up the breeding programs using different breeding methods (Cober and Morrison, 2010). In China, soybean production has decreased over the past few years due to the low yield trend during the last 50 years (Liu et al., 2018). The country imports 80% of the soybean for domestic use, and hence it’s become essential to make the country self-sufficient by increasing its yield by developing high-yielding varieties (Liu et al., 2018; Sharmin et al., 2020). The US-China trade war has negatively affected China’s soybeans yield and increased costs. This change in international soybean trade would lead to the noticeable growth of global environmental costs in the short term due to surplus soybeans in the US and the enhanced food transportation distance (He et al., 2019). The breeders have successfully targeted the genes contributing to high yields in soybean (Karikari et al., 2019).

China is now the 4th main soybean producer. China’s soybeans are grown over a large latitudinal variety and in varied ecological environments and cropping schemes that spread from the frigid areas of Northern China to the tropical expanses of Southern China (Wang et al., 2007). China has the highest genetic diversity of soybean germplasms (Liu et al., 2017b). Contemporary soybean breeding started in China in 1913 (Wang et al., 2007), about 30 years earlier than North America (Rincker et al., 2014). The first formally unrestricted soybean cultivar, ‘Huangbaozhu’, was described in 1923 (Zhou et al., 2000). In recent years, conventional breeding techniques have significantly contributed to the development of high-yielding soybean cultivars (Ahmar et al., 2020). However, the traditional method is not adequate to increase the yield to feed the rapidly growing population (Ashraf et al., 2010; Bhat et al., 2016). These methods applied to select phenotypic traits are not sufficient to meet the criteria of global food security (Mir et al., 2019). Advanced genomics and phonemtics techniques give excellent opportunities to adopt precision breeding at a higher level (Mir et al., 2019). For instance, the genomic assisted selection method allows understanding of major traits, but it needs a complete molecular understanding (Chaudhary et al., 2015; Steiner et al., 2019). Soybean yield is polygenic trait and controlled by many genes. The improvement of multigene traits is often challenging and not fruitful. There are many traits which contribute to yield improvement, and hence improvement of soybean yields via conventional breeding is very lengthy and costly process. Soybean quality is a monogenic trait which means that this trait is regulated by a single gene and its improvement is not challenged by environmental factors (Dong et al., 2004).

Genomic assisted breeding is emerging as a potent tool in large-scale breeding plans (Hickey et al., 2017). It unlocks new windows to select lines in early generations (Yao et al., 2018). These techniques enable the early selection of lines, reduce the field tests, and enhance reuse in breeding programs as parental material. Using this way, we can select lines earlier with less error. This exercise was only promising after developing high-density marker pieces that are presently accessible for numerous crops. Markers are extensively used to assume relations at the QTL level, assessing whether the LD among markers and QTL is practically high (Habier et al., 2007). A list of high-yielding genotypes is shown in Table 1. This review sheds light on recent insights about soybean yield and quality improvement. The study discusses the potent genetic factors regulating soybean yield and
quality improvement and highlights future directions. The reasons for the low soybean yield in China are shown in Figure 1.

![Figure 1. The key reasons for low soybean yield in China](image)

| Sr. No | Soybean genotypes         | Origin   |
|--------|---------------------------|----------|
| 1      | ‘Huangbaozhu’             | China    |
| 2      | ‘China-1’                 | China    |
| 3      | ‘Australia’               | Australia|
| 4      | ‘Bhat’                    | India    |
| 5      | ‘Kala soybean’            | India    |
| 6      | ‘Jinong 74’               | China    |
| 7      | ‘Jinong 75’               | China    |
| 8      | ‘Shidadou 1’              | China    |
| 9      | ‘Xindadou 1’              | China    |
| 10     | ‘Suinong 1’               | China    |

### Soybean domestication from wild to cultivated

Many genetic links occurred during the domestication and diversification of soybeans, particularly in Asian landraces (Hyten et al., 2006). Accidently half of the genetic diversity (Zhou et al., 2015) and about 81% of alleles (Hyten et al., 2006) were lost during the domestication of *Glycine soja* landraces. In the North American breeding pool, only 19 landraces have contributed to the genes of desired traits (Gizlice et al., 1996). It is stated that the modern-day soybean originated from a wild-type species in east Asia about 6000-9000 years ago (Carter et al., 2004; Kim et al., 2012). The origin of the soybean is still a mystery because of the lack of molecular studies and other evidence. Hence, modern research on molecular aspects and whole-genome sequencing have shed light on this valuable crop’s origin. The historical evidence suggested that the soybean originated from northeastern China in 2510BP, which led to the agricultural revolution (Ho, 1975). Most of the landraces diversity was discovered along the Yellow River (Dong et al., 2004; Li et al., 2010). Placed around this area, plenty of archeological, soybean specimens (Zhijun, 2004; Lee et al., 2011) around the Yellow River bowl as a main nominee for the source of soybean domestication. Otherwise, the Yangtze basin has also been recommended as a birth place of the soybean based on phylogenetic and clustering analyses with microsatellites and nucleotide variety (Guo et al., 2010).
Furthermore, archeological histories display larger soybean seeds in Japan and Korea related to seeds discovered in the Yellow River basin in China throughout the era 5000–3000BP (Lee et al., 2011). Specifically, soybean seed models from Japan were leading throughout this period. These results, composed of the long deviation time among *Glycine max* and *Glycine soja* as defined before, designate that there may have been multiple works to domesticate wild soybeans. Certainly, the existence of wild soybeans in grain imitations on ceramic was seen as early as 7000–5000BP in Japan (Obata and Manabe, 2011). The latest evidence show that the domestication process had improved several soybean traits. The photosynthesis, nitrogen content and stomatal conductance have been improved by using the domestication process in wild soybean lines (Togashi and Oikawa, 2021). Likewise, the *GmOLEO1* gene significantly improved the soybean oil quantity during domestication in the field (Zhang et al., 2019).

**Conventional breeding methods to improve soybean yield and quality**

*Ways towards a revolution in soybean yield*

Yield is a multigene trait governed by many genetic factors (Rasheed et al., 2020a, 2020b; Rasheed et al., 2020; Rasheed et al., 2021b; Rasheed et al., 2021c). The yield is influenced by the number of seeds, seed size, height, branch number, number of pods, and seeds per pod (EL Toum et al., 2020). The angle and the petiole length also distress the final harvest. For maximum planting density, a suitable breeding design is the first criteria to be considered (EL Toum et al., 2020). An additional breeding method is important to enhance PH and node number. Plants with tall heights are often lodged, while small plants are resistant to lodging (Panthée et al., 2007). Other possible optimization characteristics which may affect higher yields include the number of seeds per pod, seed size, and petiole length. Theoretically, the number of seeds per pod, as well as the size of the seed, can increase the final harvest (Rasheed et al., 2017; Rasheed et al., 2018; Rasheed et al., 2019), although short petiole and enhanced leaf size will be favorable to thick planting and photosynthetic effectiveness. Particularly, numerous environmental factors containing climate situation, synthetic features, and even planting date can also significantly influence final soybean yield (Robinson et al., 2009). Earlier findings also showed that adaptive changes could critically donate to the growth and production of soybean in the planting area (Yue et al., 2017).

Consequently, breeding the cultivars with developed environmental alterations is also significant for high soybean production (Liu et al., 2020b). Several breeding techniques are hybridization, mass selection, recurrent selection, pure line selection, speed breeding, backcross methods, and pedigree method; however, hybridization is the most successful breeding method used in crops. Soybean seed size and yield were improved using the mass selection breeding method (Cober and Voldeng, 2008). In the same way, Lee et al. (2015) used the pedigree selection method to improve soybean cultivars. The cultivars showed good yield and quality. The pedigree method would help the breeder to improve the soybean further. The main breeding objectives of soybeans are shown in Figure 2.

*Hybridization breeding*

In addition to the expansion of Green Revolution lines, other methods have also added greatly to crop yield rise during the last several periods. A good example is heterotic breeding, also called hybrid breeding, which means that hybrid vigor shows a higher yield than parental genotypes (Liu et al., 2020a). For instance, hybrid breeding has increased maize yield by 15% compared to inbreeding (Duvick, 2001). Initially, it was impossible to develop hybrid genotypes in self-pollinated crops, but later on, the discovery of sterile male lines made it possible to develop hybrids in rice. As a result of these efforts, hybrid cultivars have shown a 10-20% increase in yield compared to conventional varieties (Cheng et al., 2007), making it a significant development in current rice breeding programs. Newly, great development in wheat heterotic breeding has also been completed, and the hybrid genotypes with beneficial yield have been gained and sold in EU countries (Gupta
et al, 2019). The hybrid breeding program has been extensively used in numerous other crops, such as soybean and sorghum (Seiler et al., 2017).

\[ F_1 \] lines showed a 20% yield rise over that of their extraordinary parents (Palmer et al., 2001). The soybean is an autogamous crop with a small percentage of natural cross-pollination, and pollen transmission is the most difficult way soybean breeders adopt. But we hope that the answer for effective pollen transmission may open the window for soybean hybridization in the coming time, which would be a noteworthy development toward the rise of soybean yield (Liu et al., 2020b). 'MACS-1188' and 'Pant Soybean-19' are the cultivars developed by the hybridization method. The modified hybridization techniques would lead to more efficient and high-yielding cultivars in soybean crops. The conventional way to breed soybean cultivars is shown in Figure 3.

Figure 2. The main breeding targets in soybean are yield, quality improvement and diseases resistance

It has been stated that the development of hybrid vigor in soybean does occur and that hybrid soybean

Figure 3. The conventional way to develop high yielding soybean cultivars
Use of fertilizers

To attain a significant point in soybean yield and quality, the use of highly effective fertilizers is one of the main agronomic approaches (Onyenali et al., 2020). A field experiment was conducted to examine the effect of organic fertilizers on soybean yield and quality. Organic fertilizers significantly improved the yield and quality of soybeans compared to the control one (Onyenali et al., 2020). It is significant to recognize better the effects of the use of long-period fertilizer on crop yield, soil features and nitrogen (N) use efficacy in a replacement crop farming system under the circumstances of recurrent soil disruption. Hua et al. (2020) studied the effects of manure application on the yield of 40 years of soybean and maize crop rotation. Their outcomes presented that long period use of organic fertilizer could efficiently increase N use efficiency by enhancing soil organic manure and refining soil fruitfulness, thus leading to a rise in crop yield. Likewise, the application of N was added in the soil to examine its effects on soybean grain yield. N was applied at a concentration of 75 kg ha\(^{-1}\) (Table 2). A noteworthy association was found between photosynthesis and grains yield at developmental stages. This study directed that the use of N is essential to increase soybean harvest across the Sanjiang River Plain in PR. China (Gai et al., 2017). The use of nitrogen fertilizer to increase soybean was reviewed by Ohyama et al. (2016), and they have concluded that large application of N with a low release rate encouraged the growth and seed yield as well as the quality of soybeans without discouraging the nitrogen fixation process (Ohyama et al., 2017).

The use of fertilizer not only affects soybean yield but also influences its quality. Late season nitrogen was applied to the soybean field to investigate its effects on yield and protein concentration. N at the rate of 202 kg ha\(^{-1}\) was applied to the field, and results showed that late-season N could significantly improve the soybean yield and quality. However, they have stated that a new study is essential to examine maintainable management approaches that increase N accessibility to late-season soybean (Chiluwal et al., 2021). The yield and quality of soybeans were affected by integrated fertilizer management and application of zeolite. Amiri et al. (2021) showed that applying zeolite 12 Mg ha\(^{-1}\) significantly improved the soybean yield and quality. The research proves that altering soil with these ordinary fertilizer’s composts could be a capable plan to increase soybean yield and quality. The use of sulfur as a fertilizer is highly recommended for soybean production. The impact of S application (168 kg S ha\(^{-1}\)) on soybean yield and crude protein was studied. Adding S did not alter the CP of soy seed; however, the S contents were slightly higher (Letham et al., 2021).

Zinc fertilizer also plays a major role in soybean yield and quality. In an experiment, zinc at the concentration of 4500 g ha\(^{-1}\) was added to the soybean field, and significant effects were observed on soybean yield and quality (Aytaç et al., 2007) (Table 2). Limestone and copper were applied to the soybean field, and their effects were studied on soybean quality, soil fertility, and nutritional status. Limestone at the concentration of 5.0 Mg ha\(^{-1}\) and Cu at the concentration of 16 mg kg\(^{-1}\) were applied. They have significantly increased the number of grains per pod (Santos et al., 2020). Biochar at a concentration of 5.0 t ha\(^{-1}\) was added to the soil. Its effects on soybean yield and quality were studied. Results showed that using this treatment can reduce the use of ammonium sulfate and increase the soybean yield (Alam et al., 2020). These findings showed that fertilizer application is a vital step towards higher soybean yield achievement. The integrated use of fertilizers would be a promising approach for higher yield in soybean (Bhat et al., 2016). However, further studies are required for a more in-depth analysis of fertilizer role in soybean yield and quality improvement.
Table 2. Significant effects of fertilizers on soybean yield and quality improvement

| Crop  | Fertilizer | Concentration | Trait improvement | References                        |
|-------|------------|---------------|-------------------|-----------------------------------|
| Soybean | Zinc       | 4500 g ha⁻¹  | Yield and quality | (Aytaç et al., 2007)             |
|        | N          | 75 kg ha⁻¹    | Grain yield       | (Gai et al., 2017)               |
|        | Potassium (K) | K150 kg ha⁻¹  | Yield             | (Shahkoomahally and Shahkoomahally, 2017) |
|        | Nitrogen   | 668.5 kg ha⁻¹ | Yield             | (Hua et al., 2020)               |
|        | Limestone  | 5.0 Mg ha⁻¹   | Grains number per pod | (Santos et al., 2020)           |
|        | Copper     | 16 mg kg⁻¹    | Grains number per pod | (Santos et al., 2020)           |
|        | Biochar    | 5.0 t ha⁻¹    | Yield             | (Alam et al., 2020)             |
|        | Nitrogen (N) | 202 kg ha⁻¹   | Yield and protein | (Chiluwal et al., 2021)         |
|        | Zeolite    | 12 Mg ha⁻¹    | Yield and quality | (Amiri et al., 2021)            |
|        | Sulfur     | 168 kg S ha⁻¹ | Yield and crude protein | (Letham et al., 2021)         |

Early sowing
The sowing date is particularly important in soybean yield and quality because it affects the formation of vegetative and reproductive parts (Nico et al., 2019) and, ultimately, final biomass. The early planting of soybean cultivars showed improved growth and quality (Divito et al., 2016). Earlier research studies showed that sowing date is a serious management choice that disturbs soybean development, growth features and, grain yield (Zhang et al., 2010b). Until the end of the last century, little research was published on soybeans due to a lack of proper knowledge and germplasm. However, research work on soy crops was significantly improved in all aspects at land grants associations institutes (Khan et al., 2020). Research showed that the soybean crop planted early in May yielded more pods than the late-planted crop (Lueschen et al., 1992). Different types of cultivars have different yield trends. The determinate type of soy cultivars exhibited higher yield when planted in May than indeterminate types sown later (Robinson et al., 2009).

Another research study showed that sowing in April showed a higher yield than cultivars planted in May (Robinson et al., 2009). Likewise, soybean genotypes planted in April or early May recorded higher yield percentage. The grains yield data was collected for early sowed genotypes. Analysis showed that early sowing genotypes have more grains than late sowing genotypes (Egli and Cornelius, 2009). The studies reported the subsequent increase in seed yield from a given area. Lakpale and Tripathi (2012) showed that growth factors, yield features, and grain yield of soybean genotypes were recorded maximum, and soybean oil content was considerably changed by managing soybean genotypes sowing date and time. Sowing in early July yielded 72% more grains yield than that of delayed sowing.

Similarly, the early sowing date improved the grain protein of soybean by 5% compared to late sowing (EL Toum et al., 2020). Jarecki and Bobrecka-Jamro (2021) assessed the influence of sowing dates on soybean yield and quality by growing soybeans in dissimilar sowing intervals. They have determined that early sowing time increased the pod’s number per plant and 1000 seed weight. All of these above findings showed that soybean yield and quality can be improved significantly by adjusting the sowing date.

Use of hormones
Hormones like gibberellins, cytokinin, and auxins promote the plant growth and yield and are important plant growth-promoting factors. Phytohormones can cause physiological and morphological modifications that rely on their application rate, tissue sensitivity, and crop species. Plant growth hormones can encourage, hinder, or change plants’ physiological procedures depending on the application rate (Santer and Estelle, 2009). Llanes et al. (2019) studied the effect of different plant hormones on the growth and yield of soybeans. The foliar application of gibberellic acid significantly improved the yield of soybeans. The effect of auxin and cytokinin on pod set in soybean was studied, and results indicated that auxin had positive effects on soybeans pod setting rate (Nonokawa et al., 2007). The CK has a key role in facilitating the nodule development in soybean. The treatment of seeds with cytokinin increased yield and nitrogen usage in soil
(Kempster et al., 2021). The plant growth regulator and its effect on soybean yield were studied by Klumpp (2018). The application of growth regulator auxin had positive effects on soybean yield. This yield benefit was due to soybean plants yielding maximum nodes to develop extra seeds and pods, leading to a higher yield.

The use of hormones or growth regulators during the soybean pod initiation stage exhibited a weighty effect on PH, branches per plant and seed yield. Findings showed that soybean seed yield was recorded highest by spraying 2,3,5-triiodobenzoic acid at a concentration of 50ppm in an area of 21.24 q/ha (Solanke et al., 2018). Salicylic acid (SA) is an endogenous signaling hormone. It has numerous roles, particularly in sprouting and growth, interference with root immersion, condensed leaf abscission and transpiration (Ashraf et al., 2010; Hayat et al., 2010). Abscisic acid and its role in soybean yield were studied in an experiment. The ABA hormone at a concentration of (300 mg/L) was used as a foliar spray at the V7 and R2 phonological phases, whereas GA3 (300 mg/L) was used at R2 and seven days later. Results showed that plants treated with ABA have more roots and shoots and ultimately a higher yield (Travaglia et al., 2009). The use of SA also considerably improved the root dry weight parameter. SA also increased soybean seed dry weight (Khan et al., 2003). Pod shattering rate is one of the main determinants of soybean yield. Using two different genotypes of the soybean crop, researchers Taniguchi et al. (2018) studied the association between plant growth facilitated by gibberellin and pod setting ratio. After flowering, the plant growth rate was meaningfully improved in Fukuyutaka and lower in the Kariyutaka genotype. Hence, it is proven that soybean yield and quality can be increased by using plant growth hormones. More studies are needed to understand the critical role of these growth regulators behind higher-yield and good-quality soybeans.

**Molecular tools to enhance soybean yield and quality**

**QTL for soybean yield improvement**

Enhancement of soybean yield plays a significant role in meeting the high demand for protein in China and other countries. Different studies were conducted to improve the soybean yield and quality, and many significant QTL were identified for these yield and quality traits (Prince et al., 2020). The soybean yield is the ultimate product of any breeding program, and identification of genomic regions for this trait can increase yield by MAS selection. Zhao et al. (2021) used 175 recombinant lines (RILs) to estimate yield and quality traits. They have conducted field trials for consecutive years. The QTL qGY6.2 identified for yield was marked as a major QTL and significantly contributed towards yield improvement, as shown in Table 3. In another experiment, the RIL population was evaluated for QTL mapping, and 13 yield-related QTL were identified. Some of the genomic areas displayed pleiotropic influences on yield characters. They further recognized candidate genes for these areas. These results laid the foundation for developing high-yielding soybean cultivars with outstanding characters (Su et al., 2019).

Likewise, two mapping populations, SD02-911 × SD00-1501 and SD02-4-59 × A02-381100, were phenotype for QTL mapping and 12 QTL for seed yield were identified on different chromosomes. Further analysis evidenced that these QTL were leading regions towards higher yield in soybeans (Wang et al., 2014). Zhang et al. (2010a) worked on a RIL population from ‘Nannong 94-156’ and ‘Bogao’ and detected two QTL gpn11 and gpn20, which regulated the number of pods per plant which ultimately led to the higher yield in soybeans. A large number of QTL, qPH13a, qNN19a, PH19b-2 related to plant height and pod number per plant were identified in a study using RIL population, signifying that plant height and pod number are important traits for a higher soybean yield (Liu et al., 2017a). 100-seed weight (HSW) is one of the most powerful yield-related traits studied by researchers. Qi et al. (2020) conducted GWAS for HSW of soybean cultivars by using 144 FW-RILs populations based on data collected from 20 diverse environments. The study identified 118 QTL out of them 2 QTL, qHSW2 and qHSW3 for HSW were major regions and identified potential alleles behind the expression of these QTL. A QTL mapping was done based on 944 RILs population resulted from a five-parent half-diallel crossing plan.
They recognized five to eight QTL for each of the four key agronomic characters, and some showed a substantial amount of genotypic modification. Two main QTL, \( q_{SY1} \) and \( q_{SY2} \), were significant QTL controlling seed yield in soybean cultivars (Zhu et al., 2021). These findings contributed to understanding the gene network controlling important yield-related traits in soybeans. Seed weight is a significant soybean yield constituent and influences the quality of soya foods. 112 RILs were used to map the QTL linked to soybean seed weight contributing to the yield. The QTL, \( q_{SW1} \) and \( q_{SW20} \) were mapped on chromosomes 1 and 20, highlighting the genetic mechanism behind the yield increment in soybeans (Wu et al., 2018). Yield-related components also play a key role in yield enhancement, and plant breeders identified QTL for these traits. Li et al. (2020) used 208 CSSL populations and identified 24 QTL for plant height located on different chromosomes. \( q_{PH-m-1} \) and \( q_{PH-o-2} \) were detected for PH, and they strongly influence the soybean yield.

PH is a significant feature in soybean, as taller plants may have a greater yield (Xue et al., 2019). Thirty-six regions governing PH were identified at numerous developmental phases and showed uneven effects (Xue et al., 2019). 1000 seed weight is a key contributor to soybean yield, and many previous studies have identified QTL for this trait. Previously a QTL, \( sw_{HCA2-1} \) for 1000-seed weight was identified by Han et al. (2012), \( qSw_{17-1} \) by Kato et al. (2014) and \( qSWT_{13-1} \) by Yan et al. (2014) as shown in Table 3. The two major genes, \( CHS7 \) and \( CHS8 \) involved in isoflavonoid synthesis in soybean (Yi et al., 2010). Likewise, \( FKKI \) and \( G1 \) regulate soybean photoperiod (Li et al., 2013). Hence, it is mandatory to identify the putative genomic regions and transfer them into candidate cultivars via MAS to increase soybean yield. More studies are required to understand the soybean genetic architecture behind the high-yielding attitude.

| Crop | QTL          | Chromosomes | Trait  | References                  |
|------|--------------|-------------|--------|-----------------------------|
| Soybean |            |             |        |                             |
|       | \( qpn_{11} \) | 11          | PNP    | (Zhang et al., 2010a)       |
|       | \( qpn_{20} \) | 20          | PNP    | (Zhang et al., 2010a)       |
|       | \( sw_{HCA2-1} \) | 2          | 1000-SW | (Han et al., 2012)          |
|       | \( qSw_{17-1} \) | 7          | 1000-SW | (Kato et al., 2014)         |
|       | \( qYIE-B2 \) | 2           | Yield  | (Wang et al., 2014)         |
|       | \( qSWT_{13-1} \) | 13        | 1000-SW | (Yan et al., 2014)          |
|       | \( qYIE-D2-1 \) | 2           | Yield  | (Wang et al., 2014)         |
|       | \( qPH13a \) | 13          | Yield  | (Liu et al., 2017a)         |
|       | \( qNN_{19a} \) | 19          | Yield  | (Liu et al., 2017a)         |
|       | \( qHSW_{6-1} \) | 6           | HSW    | (Hacisalihoglu et al., 2018) |
|       | \( qHSW_{6-2} \) | 6           | HSW    | (Hacisalihoglu et al., 2018) |
|       | \( qSW_{1} \) | 1           | SW     | (Wu et al., 2018)           |
|       | \( qSW_{20} \) | 20          | SW     | (Wu et al., 2018)           |
|       | \( qPH_{28-A1} \) | 1          | PH     | (Xue et al., 2019)          |
|       | \( qPH_{70-G-1} \) | 1          | PH     | (Xue et al., 2019)          |
|       | \( qGY_{1} \) | 1           | Yield  | (Su et al., 2019)           |
|       | \( qGY_{16} \) | 16          | Yield  | (Su et al., 2019)           |
|       | \( qHSW_{2} \) | 2           | HSW    | (Qi et al., 2020)           |
|       | \( qHSW_{3} \) | 3           | HSW    | (Qi et al., 2020)           |
|       | \( qPH-o-1 \) | 1           | PH     | (Li et al., 2020)           |
|       | \( qGY_{6-2} \) | 6           | Yield  | (Zhao et al., 2021)         |
|       | \( qSHR_{3} \) | 3           | Yield  | (Zhao et al., 2021)         |
|       | \( qSY_{1} \) | 1           | SY     | (Zhu et al., 2021)          |
|       | \( qSY_{2} \) | 2           | SY     | (Zhu et al., 2021)          |
|       | \( qBHW_{4-1} \) | 4          | 1000-SW | (Huang et al., 2021)        |
**QTL for soybean quality improvement**

Being an important oil crop globally, soybean yield and quality improvement are always key objectives for plant breeders. In an experiment, a total of 20 QTL governing linoleic acid, oil and palmitic acid were identified, varying in their expression (Silva et al., 2021). Enhancing the content of soybean storage protein while increasing the ratio of glycinin to β-conglycinin is of great importance for soybean breeding plans and soybean food products. In an experiment, 35 QTL and five major significant genomic areas were detected using the RIL population. The two significant QTL, q11S-6-2 and qSGC-6-2 improved the glycinin and conglycinin contents in soybean (Ma et al., 2016). Oil and protein contents were significantly improved to attain better soy quality. Two major QTL, qOC1, I and qPC2 controlling oil, and protein contents were detected on chromosomes 1 and 2 (Liang et al., 2010).

Likewise, Zhang et al. (2018) used 313 diverse soybean accessions and genotyping was done with high-quality SNP and identified QTL, qPA5 and qOC5 controlling palmitic acid and oil content in soybean accessions. These findings suggested that the genetic mechanism of soybeans could be understood more clearly by using high-resolution mapping populations. To improve the fatty acid contents in soybeans, a study was conducted and QTL mapping was done to identify the QTL regulating the fatty acid contents. In total, 18 QTL were mapped on different chromosomes explaining varying ranges of phenotypic variance. The study suggested that these major and minor QTL should be used to improve fatty acid contents in soybeans (Zheng et al., 2006). Zhang et al. (2021) conducted a genome-wide association study to identify the QTL for protein contents and water-soluble proteins. A total of 211 diverse genotypes were used for this study. The QTL, qPC-15-I and WSPC-8-I were potent QTL, which enhanced the required quantity of proteins. The best way to improve soy quality is to map the major regions across various populations. Wang et al. (2020b) identified the 14 new QTL, qHC8, which improved the hexanal contents in soybean. The first GAWS study identified many novel QTL and many genes behind these regions. An experiment detected the QTL controlling the soymilk off-flavor on many chromosomes. The QTL, qOC18 identified on chromosome 18, was a highly valuable region because it enhanced the soy 1-octen-3-ol content, which improved the soybean milk flavor (Xia et al., 2019).

Seed size and shape also contribute to soybean quality features, as better size and shape would attract the consumers to buy more products. Many studies have been conducted to identify the hotspot regions for soybean seed size and seed shape traits. In one attempt, RILs were evaluated, and QTL mapping was conducted to identify the QTL for these significant traits. Two QTL, qSL-13-3 and qSL-13-4 (Table 4), were detected on chromosome 13, governing the seed size and shape in soybean. Hence, overall, these studies showed that soybean yield and quality improvement are significant targets for any plant breeding program. Many studies have been done on this, but major genes have not been cloned up to now. There is a current need to conduct studies using diverse populations to kick off the significant variation for attaining targeted results. The use of ideal and high-resolution mapping populations would yield important results for soybean improvement. The global food supply chain is presented in Figure 4.
Figure 4. The global food supply chain represents the flow of food from the source to the final consumer in the ecosystem.

| Crop  | QTL          | Chromosomes | Trait                | References                      |
|-------|--------------|-------------|----------------------|---------------------------------|
| Soybean | qOC1         | 1           | Oil content          | (Liang et al., 2010)            |
|       | qPC2         | 2           | Protein content      | (Liang et al., 2010)            |
|       | q11S-6-2     | 6           | Conglycinin          | (Ma et al., 2016)               |
|       | qSGC-6-2     | 6           | Glycinin content     | (Ma et al., 2016)               |
|       | qPA5         | 5           | Palmitic acid        | (Zhang et al., 2018)            |
|       | qOC5         | 5           | Oil content          | (Zhang et al., 2018)            |
|       | qOC18        | 18          | Soymilk off-flavor   | (Xia et al., 2019)              |
|       | qSL-13-3     | 13          | Seed size            | (Hina et al., 2020)             |
|       | qSL-13-4     | 13          | Seed size            | (Hina et al., 2020)             |
|       | qHC8         | 8           | Hexanal contents     | (Wang et al., 2020b)            |
|       | qPA5-02      | 2           | Oil content          | (Silva et al., 2021)            |
|       | qOle-02      | 2           | Oil content          | (Silva et al., 2021)            |
|       | qPC-15-1     | 15          | Protein              | (Zhang et al., 2021)            |
|       | WSPC-8-1     | 8           | Water-soluble proteins | (Zhang et al., 2021)        |

Role of CRISPR/Cas9 in soybean genetic improvement

CRISPR/Cas9 based targeted genome editing in soybean

After completing soybean genome sequencing, the major challenge faced by the researchers was to identify the role of thousands of soy genes individually (Bai et al., 2020). The transgenic technique for a comprehensive understanding of the soybean genomic model is valuable, but it has several limitations in practical use. During the last few years, the transformation of soybeans using Agrobacterium has been widely increased because of its simplicity, low cost and fewer rearrangement errors.

In 2011, a genome-editing tool generated heritable mutants in two homologous genes DCL4 and DCL4b (Curtin et al., 2011). TALENs tool was first applied in soybeans to alter two fatty acid genes FAD2-1A and FAD2-1B, for fatty acid composition and produced an extraordinary oleic acid soybean genotype (Haun et al., 2014). Five research teams working on soybeans in 2015 effectively assessed the alteration efficacy.
of CRISPR/Cas9 tool in endogenous soybean gene in hairy roots, left a layout for using the Cas9 system to investigate soybean gene (Michno et al., 2015; Sun et al., 2015). Afterward, Du et al. (2016) associated the competence of TALENs and Cas9 in manipulating two genes, *GmPDS11* and *GmPDS18*, in hairy roots of soybeans. Results exhibited that CRISPR/Cas9, particularly CRISPR/Cas9 with GmU6-16g-1 promoter, was much more effective than TALENs in simultaneous editing of two main alleles. In an experiment, homozygous mutants acquired by CRISPR/Cas9 facilitated mutation in the *GmFT2a* gene and delayed soybean flowering time (Cai et al., 2018). They altered *GmFT5* by Cas9 method and crossed it with ft2 mutants, which had a flowering period 31 days later than the wild type, yielding more pods and ultimately higher yield (Cai et al., 2020). Likewise, the knockout of the *GmSPL9* gene resulted in different mutants, which showed altered nod numbers and pod numbers (Bao et al., 2019). In addition, soybean seed oil quality (Al Amin et al., 2019), the beany taste of soybean seed (Wang et al., 2020a), and contents of isoflavone, as well as diseases resistance (Zhang et al., 2020), have been enhanced by CRISPR/Cas9 tool. The above research findings confirmed the great prospective of genome editing tools to back soybean enhancement. Many other novel genomic editing methods have been developed besides CRISPR/Cas9, such as CRISPR/Cas12a, base editing systems and other CRISPR/Cas alternatives.

Nonetheless, to our awareness, most of them have not yet been deployed in soybeans, excluding only one study that claims the use of Cas12a-RNP in protoplast of soybean to facilitate gene manipulation (Kim et al., 2017). Due to the unavailability of the latest stories on effective soybean redevelopment from protoplast, RNP-based genome alterations may not be a favored choice for future soybean research (Kim et al., 2017). The list of genes knockout by CRISPR/Cas9 is shown in Table 5. Therefore, CRISPR based genome editing could be potentially used in soybeans to develop high-yielding genotypes to ensure global food security. The use of this technique would lead to a green revolution in soybean yield and breeding and the products would be highly accepted in the society.

**Table 5.** List of different genes knockout by CRISPR/Cas9 in soybean

| Crop   | Gene          | Trait                        | References                  |
|--------|---------------|------------------------------|-----------------------------|
| Soybean| *GmSPL9*      | Plant stature                | (Bao et al., 2019)          |
|        | *GmFAD2–1B*   | Low linoleic acid           | (Do et al., 2019)           |
|        | *GmFT2a/5a*   | Early flowering             | (Han et al., 2019)          |
|        | *GmF3H1*      | Hairy roots                 | (Zhang et al., 2020)        |
|        | *GmFT5a*      | Regional adoptability for high yield | (Cai et al., 2020) |
|        | *GmPLAs*      | P efficiency                | (Xiao et al., 2021)         |
|        | *GmAMS1*      | Male sterile lines          | (Chen et al., 2021)         |
|        | *MS1*         | Male fertility              | (Fang et al., 2021)         |
|        | *GmFATB1*     | Reduced saturated fatty acid | (Ma et al., 2021)           |
|        | *GmKIX8-1*    | Increase seed weight        | (Nguyen et al., 2021)       |
|        | *NBS-LRR*     | Disease’s resistance        | (Nagy et al., 2021)         |
|        | *GmAAGGED1*   | Higher yield                | (Cai et al., 2021)          |
|        | e FAD2        | Fatty acids                 | (Xiao et al., 2022)         |

**Genome by sequencing (GBS) and its importance in soybean**

In the past times, soybean genome sequencing progress yielded numerous NGS-based condensed representation genotyping stages. These comprise condensed representation libraries, DNA sequencing, GBS, reduction of complication in polymorphic arrangement, reduction of the genome in restriction-site protection, and altered methods (Andrews et al., 2016). GBS is the most influential, modest, high-throughout, and profitable system for locating SNP markers (Happ et al., 2019). GBS is an improved RAD-seq system based on NGS and is a highly multiplexed and simple technique.
Most recently, cost-effective use of GBS has made it more easy and feasible in soybeans compared with WGRS type method of soybean genotyping (Gutierrez-Gonzalez et al., 2019; Jiang et al., 2020). The GBS-based genotyping system has been regularly used in mapping genes and other molecular studies in soybeans. It has been validated as an effective system for high-resolution genetic diagraming and specific breeding practices in soybean crops (Getachew, 2019). Many different mapping populations have been sequenced using the GBS system, and various traits have been analyzed in soybeans. Moreover, GBS covers a much higher fraction of the genome than the SNP arrays currently available in soybean plants (Gorjanc et al., 2015). The SNP collections are characteristically established from a restricted sample of genotypes; however, GBS can predict genetic difference that is precise to a progeny. GBS system has the benefit that markers are developed using the progeny to be sequenced, thus reducing ascertainment prejudice. The flexibility, low price, and forecast precision of GBS make this a perfect method for GAB used in soybean at the present time. It would be increased soon because of its efficiency and low-cost nature.

Use of genetic engineering techniques in soybean

GE involves the manipulation of the host genome by any means, either natural or artificial (Shea et al., 2020). The most commonly used methods are Agrobacterium, particle bombardment, and protoplast transformation (National Research Council, 2004). The new genetic engineering technique is CRISPR/Cas9 (Editing, 2020). Genetic engineering works by introducing a gene of interest from one living organism to another. That gene expresses in the host organism and causes required changes (Shea et al., 2020). This technique is gaining a lot of attention due to its promising efficacy and effectiveness in improving agronomic traits of the crop (Arora and Narula, 2017; Wang et al., 2019). GE in soybeans was primarily completed in the late1990s (Aldemita and Hautea, 2018).

Meanwhile, this time, GE has been used regularly in soybeans. The GM soybean was planted on 90.7 million ha area in 2014 (Aldemita and Hautea, 2018). The main soybean which was developed was resistant to herbicides and called Roundup ready soybean (Shea et al., 2020). This soy cultivar permits farmers to use herbicides to destroy any weed in the field while not damaging the soybean (Shea et al., 2020). GE has been used to improve the protein quality of soybeans by changing biosynthetic response pathways (Falco et al., 1995; Liu, 2012). Moreover, GE has been used to change the contents of soybean oil by enhancing oleic acid contents, reducing linolenic acid contents, and slowing down the flowering duration in soybean (Cai et al., 2018). This can be completed via GE by knocking out specific genes accountable for the anti-nutritional factors. The transgene cultivars can raise public concerns about biosafety issues; however, different molecular techniques can be integrated to get more efficient cultivars (Alfonso, 2020).

Conclusions

We completed an organized review about soybean yield and quality improvement. Soybean yield and quality improvement have been attained by using conventional and molecular techniques. These factors have contributed to a comprehensive understanding of genetic factors for soybean yield and quality improvement. This compiled information could help to unfold the genetic architecture of soybean genetics and breeding. Being an important legume crop, efforts are still needed to conduct more novel research studies to enhance yield and quality. The studies should focus on the number of genes that play a key role in soybean domestication: yield, quality, and disease resistance. As the soybean crop faces numerous challenges, lack of fertile land, trade wars, lack of high-yielding cultivars, proper scientific research, there is a need to make a bright road map of proper scientific investigation for unfolding the genetic mechanism behind this. The detailed information presented in the current review gives a strong theoretical layout for future studies. As the use of
the latest novel gene-editing techniques like CRISPR/Cas9 is increasing day by day, soybean yield and quality are the most significant traits to be improved currently. The gaps between the studies should be identified and addressed properly. This will likely be useful for achieving the maximum soybean yield from a given area.

High yield and quality of soybean attract the consumers and offers a huge benefit to the producer. The lack of genes is the main issue in using genetic management methods to develop yield and quality characters in soybean. As previous uses of breeding methods and genome editing in soybeans mostly concentrated on transforming a few recognized genes, most novel genomic resources are still unknown. Use of novel genome editing tools and breeding methods and can speed up the process of soybean development. Luckily, the joint use of genome editing methods and conventional methods would be more fruitful for maximizing yield and quality. In addition, a CRISPR-based mutant library can be used to develop novel traits in soybean (Rasheed et al., 2021a). It is difficult to make a genome-wide mutant library in soybeans, but it is possible to build a small-scale library for certain purposes. We strongly believe that CRISPR/Cas9-based targeted mutagenesis would develop novel soybean traits. Exploring wild soybean resources and their domestication by CRISPR could help us to understand soybean’s genetic mechanism. CRISPR/Cas9 can mutate different recessive genes, and genetic diversity can be expanded to increase soybean yield and quality. Use of agronomic practices, like land management, use of growth hormones, irrigation, early planting of genotypes, and highly effective fertilizers could be more significant for yield and quality enhancement in soybean.

Authors’ Contributions

GY supervised the study, AR prepared the draft, ZZ, JJG, MI, MA reviewed the manuscript. WP and SFAG provided technical assistance. MB improved scientific figures. WJ supervised the study.
All authors read and approved the final manuscript.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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