GENETIC VARIATION OF SOYBEAN COLLECTION BASED ON MICROSATELLITE DNA MARKERS RELATED TO PLANT HEIGHT

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ABSTRACT

Soybean is a relatively new crop in Kazakhstan, and the development of new competitive cultivars with high productivity and quality is an important direction in the local breeding program. Previously, one of the major approaches for the development of new cultivars was breeding projects based on the evaluation of key morphological traits, including flowering time and plant height (PH). However, with the development of soybean genetics new molecular tools have emerged, including the development of DNA microsatellites, or simple sequence repeats (SSRs). In this study, a collection of hundred accessions grown in the southeast of Kazakhstan in 2020–2021 was assessed using eight agronomic traits, including plant height (PH), the height of lowest pod, number of lateral branches, number of fertile nodes, number of seeds per plant, thousand seeds weight, yield per square meter (YP2), and maturity group. The assessment of field trials showed a wide range of variability in agronomic traits and suggested that PH is significantly correlated with all studied traits, including YP2. The collection was genotyped using eight SSRs associated with PH. The results suggested that three SSRs (Satt244, Satt288, and Satt371) were the most polymorphic, and five out of eight SSRs were associated with six important agronomic traits, including flowering time, PH, and yield per square meters. Obtained results can be efficiently used in soybean breeding based on a marker-assisted selection approach.

Key words: soybean, plant height, agronomical traits, yield, SSR markers, correlation, genetic diversity.

INTRODUCTION

Soybean is one of the main legume crops in many countries around the world. Due to its biochemical composition, soybean seeds are a major source of both food and animal feed. Soybean is the only plant that contains a complete protein. Mature soybean seed contains about 19% oil, 34% protein (essential and non-essential amino acids), 30% carbohydrates (21% insoluble carbohydrates (fiber), 9% soluble carbohydrates), 17% moisture, slag, and shell [1]. Therefore, soybean has a wide range of industrial uses and makes a substantial contribution to the world economy [2].

According to the World Soybean Production website, as of February 2021, the global soybean production is 361.00 million tons [3]. In Kazakhstan, commercial soybean cultivation began in 1986, on an area of fewer than 10 hectares [4]. Now there is a trend towards an annual increase in soybean acreage with the expansion of other arable areas in several regions of the country. According to the Committee on Statistics of the Republic of Kazakhstan for 2021, the area under oilseeds in the country amounted to 3.1 mln ha, where 0,2 mln ha of which are occupied by soybean [5].

In order to improve the yield of soybean, it is important to study the morphological, genetic, agronomic, and other traits of cultivars from wide and various collections. There are many major morphological and productivity traits of soybean, including plant height (PH), the height of lowest pod (HLP), number of lateral branches (NLB), number of fertile nodes (NFN), number of seeds per plant (NSP), thousand seeds weight (TSW), yield per plant (YP), and maturity group (MG) [6]. Soybean cultivars are divided into maturity groups depending on their response to the photoperiod. Today, there are 13 main groups in the range from MG 000 to MG X, which include cultivars that ripen in 75–80 days to late-ripening cultivars with a growing season of more than 200 days [7].

These groupings were based on adaptation at certain latitudes. Kazakh cultivars of different maturity groups, as well as foreign ones, were studied in the conditions of the South-East of Kazakhstan [8]. Under these conditions, cultivars in the mid-late and middle season ripening group have the highest yield.

According to Li Z. et al (2018), the plant height is regulated by the GmDW1 gene, mapped on Ch.8 [9]. This gene encodes the ent-kaurene synthase enzyme, involved in the gibberellin's biosynthetic pathway in soybean. Mutations in the GmDW1 gene cause dwarfism genotypes in plants, which are characterized by reduced plant height and shortened internodes. The semi-dwarf cultivars are high-yielding and more resistant to lodging and convenient for mechanized harvesting [10, 11].

The molecular studies of the genetic diversity of the important agronomic traits can be helpful in the characterization of cultivars for different breeding programs. One of the effective tools for genetic diversity issues is microsatellite molecular markers associated with the traits. Microsatellite markers are one of the classes of DNA markers based on the polymerase chain reaction. They have several advantages, such as a high level of polymorphism, and co-dominant inheritance, they can be easily detected using a polymerase chain reaction (PCR), and information about their localization is usually known. There are many SSR markers that are shown to be associated with genes and QTLs (quantitative trait loci) for plant height and growth type in soybean [12–17 Polymorphic markers SSR_18_1821, SSR_18_1822, and SSR_18_1825 were effectively used to search for recombinants in the region closest to the Dt2 gene [12]. Eight microsatellite markers (Sat_308, Satt153, Satt244, Satt288, Satt309, Satt371, Satt460, and Satt600) are known to be associated with QTL for plant height [13–15]. Also, Satt153 was localized on chromosome 10 (linkage group O) as the E2 gene. Recently, it was discovered that the E2 locus plays an important role in con-

trolling plant height [16]. Satt244 is located on chromosome 16 (linkage group J) as the GmAP1 gene, which is a MADS-box transcription factor that determines the flower meristem and petal and sepal differentiation on chromosome 16 (linkage group J) [17]. Earlier it was reported that GmAP1 takes part in metabolic pathways that affected plant height by regulating the genes related to these pathways: DW1, GA1, GR2, GR8, GA3ox_13G, and GA20ox_14G [17]. Satt309 and Satt288 are located on the same chromosome 18, as the Dt2 gene, which controlled stem growth habits in soybean [18]. Types of stem growth in soybean are regulated by epistatic allele interactions at the two Dt loci (Dt1 and Dt2) [22]. They are known to have a significant impact on the final number of main stem nodes. The Dt1 gene is located in the linkage group L (chromosome 19) [23]. It was shown that Dt1, designated as GmTfl1 or GmT-FL1b, is an orthologue of TERMINAL FLOWER1 (TFL1), a flowering suppressor gene in Arabidopsis thaliana that predominantly encodes a signaling protein and is expressed in shoot apical meristems [24]. Previously, it was found that Dt1 has an epistatic effect on Dt2 [18].

There are several reviews and articles on genetic diversity studies of soybean collections from Kazakhstan and other countries using SSR and other markers [26–33], including those associated with photoperiod, flowering time, seed maturation [26], and fungal diseases [27, 28]. While soybean accessions were studied on susceptibility to fungal diseases and flowering time in relation to SSR markers [26–33], characterization of world collection including Kazakhstan's commercial cultivars and breeding material by specific markers associated with plant height has not been carried out. Thus, the purpose of this study was the evaluation of the world soybean collection, including Kazakhstan's accession, using informative molecular markers associated with plant height as well as other important yield-related traits.

MATERIALS AND METHODS

Plant material and field evaluation

The object of this study was the world soybean collection represented by 100 samples from different origins, including 19 released cultivars and prospective lines from Kazakhstan [33]. The collection consists of the soybean samples originated from 5 geographic regions, including Eastern Europe (n = 56), Western Europe (n = 6), East Asia (n = 3), North America (n = 16), and Kazakhstan (n = 19). Cv. 'Zhansaya' was used as a check cultivar Almaty Region. Field trials were carried out on the experimental plots of the Kazakh Research Institute of Agronomy and Plant Industry (KRIAPI) in 2020 and 2021. The soybean collection was grown in two randomized replicates on one-meter plots [34]. The field data covered the following 8 major agronomic traits: plant height (PH), the height of lowest pod (HLP), number of lateral branches (NLB), number of fertile nodes (NFN), number of seeds per plant (NSP), thousand seeds weight (TSW) and yield per square meter (YP2) and maturity group (MG).

DNA extraction and SSR genotyping

Isolation of total DNA was performed according to Dellaporta et al. (1983) [35]. The concentration of total DNA was determined spectrophotometrically using Nanodrop (USA). For PCR, the initial DNA was adjusted to a concentration of 50 ng/μl.

Genotyping of soybean collection was performed using eight SSR markers, linked to QTLs for plant height (www.soybase.com). The selected eight SSR loci are genetically located in the vicinity of mapped QTLs associated with PH (Fig. 1).

All PCR reactions were performed in a 20 μl volume in the Veriti® 96-Well Thermal Cycler (Applied Biosystems, USA). The master mix for SSR amplification included 20 ng
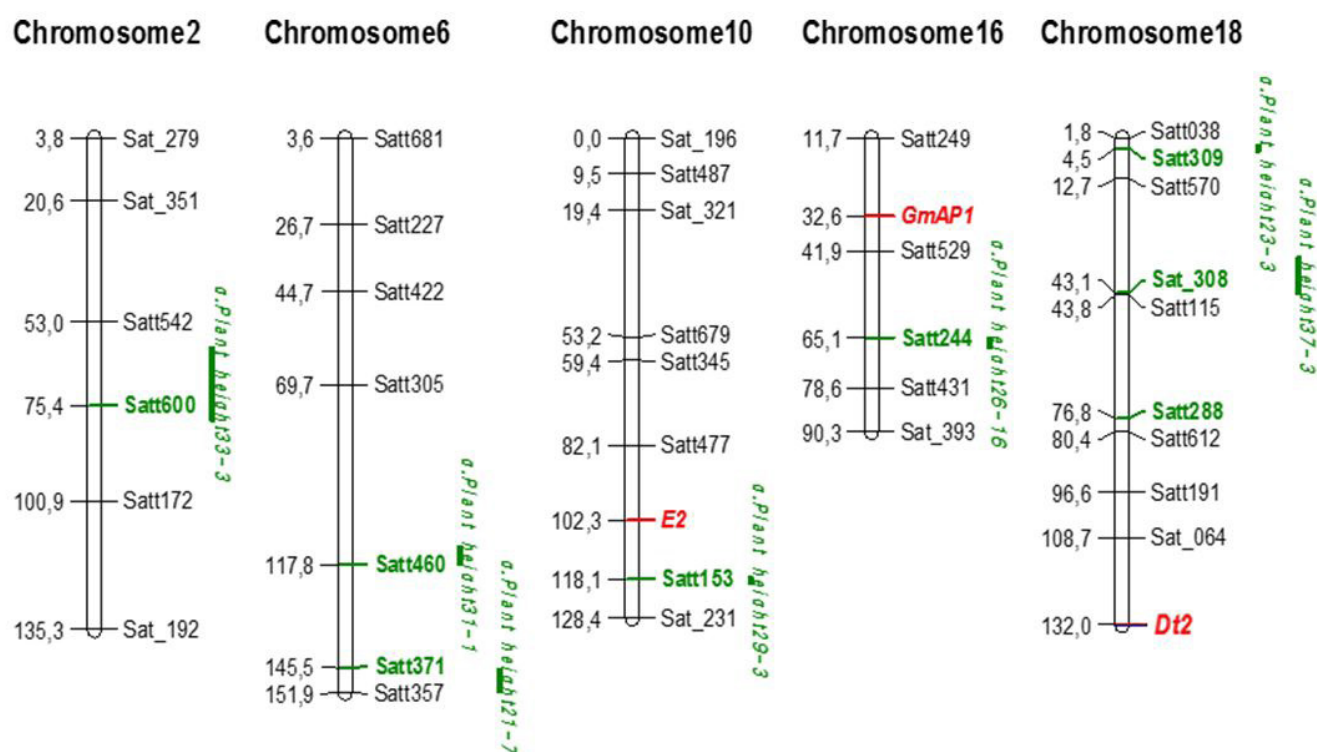

Figure 1. The location of eight SSR markers associated with previously mapped quantitative trait loci of plant height [36]
The list of SSR markers used for the analysis is presented in Table 1

of genomic DNA, 1 mM of each dNTP, 1.2 mM MgCl2 in the 1× Taq Buffer, 2mM of each primer, and 1U Taq DNA polymerase. PCR, including preliminary denaturation of total DNA at 94 °C for 1 min, followed by 30–35 cycles (94 °C — 1 min, 50–60 °C –30–60 sec, 72 °C — 1 min) and elongation at 72 °C — 7 min.

Table 1. The list of SSR markers used in the study

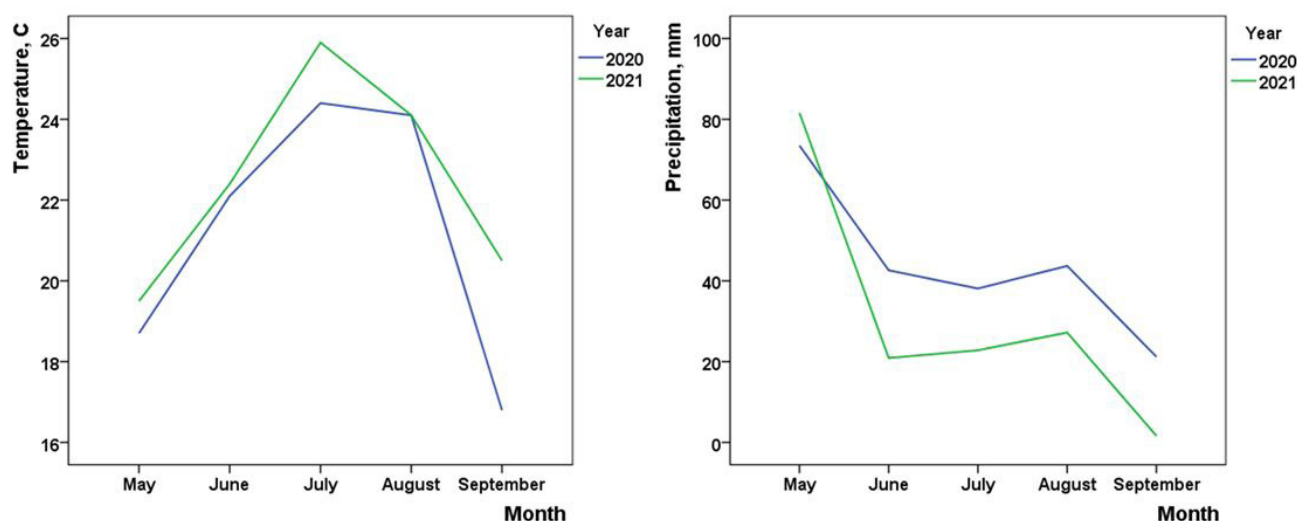| Marker	Chromosome	Linkage Group	Forward sequence 5' – 3	Reverse sequence 5' – 3	Motif
Sat_308	Gm18	G	GCGTTGGCAATTCAGGA-TATATTTAAGATTT	GCGGCTGCGTTTTTATTCAAACTTGTT	(AT)19
Satt153	Gm10	O	GGGTTATATCAGTTTTTCTTTTTGTT	CCATCCTCGTTAGCATCTAT	(TTG)4
Satt244	Gm16	J	GCGCCCCATATGTTTAAATTATAT-GGAG	GCGATGGGGATATTTTCTTTATTATCAG	(AAT)27
Satt288	Gm18	G	TCATAACGTAAGAGATGGTA-AAACT	CATTATAAGAAAACGTGCTAAAGAG	(TAA)17
Satt309	Gm18	G	GCGCCTTCAAATTGGCGTCTT	GCGCCTTAAATAAAACCCGAAACT	(ATA)13
Satt371	Gm6	C2	TGCAAACTAACTGGATTCACTCA	GAGATCCCGAAATTTTAGTGTAACA	(TAA)11
Satt460	Gm6	C2	GCGCGATGGGCTGTTGGTTTTTAT	GCGCATACGATTTGGCATTTTTCTATTG	(AAT)8t(ATA)17
Satt600	Gm2	D1b	GCGCAGGAAAAAAAAAC-GCTTTTATT	GCGCAATCCACTAGGTGTTAAT	(TTA)15(TTG)18

Figure 2. Temperature ranges and precipitation amount during the vegetation period at the experimental station of the Kazakh Research Institute of Agriculture and Plant Industry (KRIAPI, southeast of Kazakhstan) in years 2020 and 2021.

PCR products were detected using 6% polyacrylamide gels (Amresco, Solon, OH) in 0.5× tris-EDTA-borate buffer (TBE). Gels were stained by ethidium bromide, and the images were recorded with a Bio-Rad Image System (Bio-Rad, Hercules, CA). DNA molecular weight markers (100 bp ladder, Fermentas) were used to define allele sizes.

Statistical and population analysis

Statistical analysis of the field data was performed using SPSS 22.0 (https://www.ibm.com/analytics/data-science/predictive-analytics/spss-statisticalsoftware) software. Population analysis was done using GenAlEx 6.5 (Peakall et al., 2012) [37], it includes estimates of heterozygosity and genetic diversity, F-statistics, Nei genetic distance, polymorphism information content (PIC) index, population distribution, and relatedness.

RESULTS

Phenotypic evaluation

The studied collection consisted of 100 accessions that were phenotyped for two years (2020 and 2021), in conditions of the southeast region of Kazakhstan (Fig.2.). In this region, in comparison to 2021, the climatic conditions in 2020 were more favorable for plant growth. This happened due to the 65 mm more amount of precipitation, than in 2021 (Fig. 2), which is presumably impacted on the performance of studied traits.

Average data of two-year trials revealed that genotypes from Kazakhstan have the highest PH (68.4 ± 21.8 cm) in the studied collection, at the same time lowest PH showed genotypes from Eastern Europe (48.5 ± 16.3 cm). In 2020 the highest PH (103, 107, 113 cm) was observed in samples from Kazakhstan 362/2, Zara, and Rosa, respectively. In 2021 the cultivar Zhalpaksay from Kazakhstan showed the highest PH (102.2 cm ±2.3), whereas in 2020 it was 80.3 cm ± 2.3 (Fig. 3).

For the local genotypes, the two-year average plant height was 68.4 ± 21.8 cm, with means of 80.0 ± 16 cm and 57.0 ± 21.3 cm in 2020 and 2021, respectively. The standard culti-
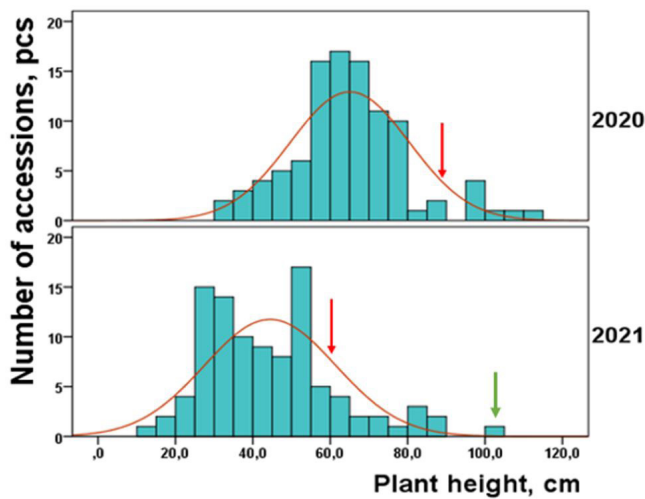
Figure 3. Plant height distribution of 100 soybean accessions.

The red arrow indicates the position of the standard cv. "Zhansaya"

The green arrow indicates the position of the cv. "Zhalpaksay"

var Zhansaya showed an average PH of 87.2 cm in 2020 and 59.8 cm in 2021 (Fig. 3), and the average PH for this cultivar over two years was 73.5 ± 19 cm.

The assessment of YP suggested that it was 8.0 ± 3.4 g in 2020 and 5.6 ± 3.9 g in 2021. (Fig. 4).
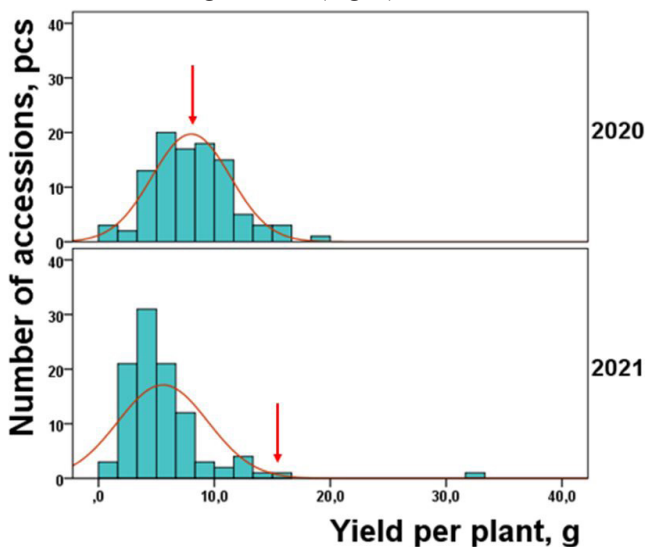

Figure 4. Diagram of yield per plant distribution in 100 soybean samples

The arrow indicates the data for the standard cv. Zhansaya

Average data of two years showed, that the most productive genotypes were from Kazakhstan (8.4 ± 3.7 g) and the less were from Eastern Europe (6 ± 2.1 g). The highest YP in 2020 was revealed in the cultivar Dawson from North America (18.4 g) in 2020 and line 350/1 from Kazakhstan (31.8 g) in 2021. The cultivar Zhansaya had an average yield of 11.6 ± 4.5 g for two years of study (7.3 g in 2020 and 15.9 g in 2021) (Fig. 4).

Correlation analysis of the studied traits

Pearson correlation based on the average values of two years of field trials showed that PH had a significant positive relationship between all the traits (P < 0.05) (Fig. 5).

The YP, as expected, was highly correlated with major yield components, including NSP, NFN, and PH (Fig. 5). The
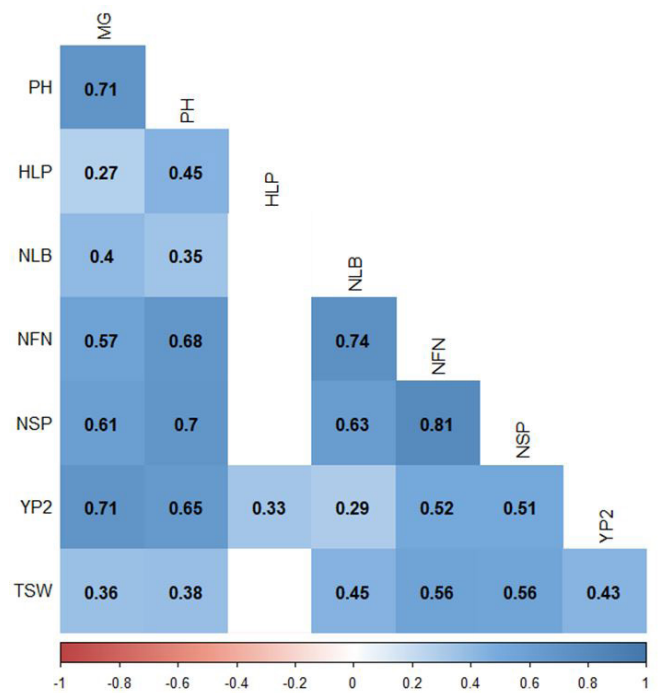
6

Figure 5. The Pearson correlation analysis of the two-year average values

The intensity of colors indicates relationship strength according to the scales given on and bottom side of the plot (the darker color – the higher significance)

PH was highly significantly correlated with NSP and NFN. No correlation was found between HLP and traits NLB, NFN, NSP, and TSW.

Microsatellite analysis of soybean collection

Assessment of the genetic diversity level of SSR loci associated with plant height

Microsatellite analysis of soybean collection was conducted using eight SSR markers, associated with plant height (Table 1).

Figure 5 is showing a fragment of the electrophoretic analysis of SSR of soybean accessions using Satt309. In total, 13 accessions were detected to carry allele Satt309–147 (Fig. 6) that according to Reinprecht Y. et al. (2006) [38] is associated with tall PH.
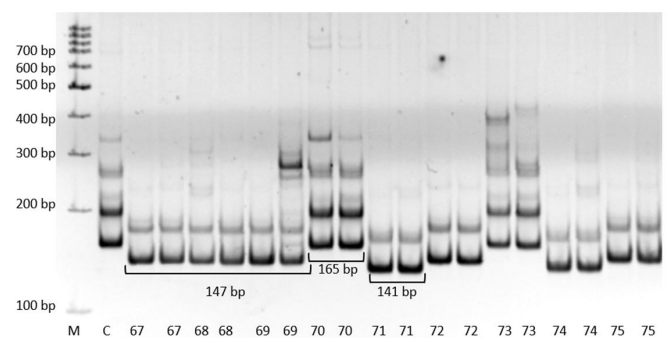

Figure 6. Electropherogram of PCR products amplified with primers Satt309

M – DNA molecular weight marker (100 bp ladder, Fermentas), C – check cultivar Zansaya, 67–75 – soybean cultivars and lines: 67 – Kalmit, 68 – Sepia, 69 –186/1, 70 – Dawson, 71 – Amphor, 72 – Krasivaya mechta, 73 – Zara, 74 – Almaty, 75 –Prikorpat'ska 81

In total 37 alleles were identified for eight SSR markers, with an average number of 3,08 alleles per marker (Table 2).

Table 2. Mean genetic diversity indexes in 5 soybean origin groups based on 8 SSR markers

Marker	Na	Ne	Nei	PIC
Satt244	3,8 ± 1,16	2,59 ±0,51	0,51 ± 0,14	0,78
Satt309	2,2 ± 0,37	1,54 ± 0,18	0,31 ± 0,09	0,41
Satt371	4,0 ± 0,55	3,11± 0,46	0,63 ± 0,09	0,78
Satt288	5,0 ±0,95	2,50 ±0,31	0,57 ± 0,06	0,76
Satt460	2,2 ± 0,37	1,44 ± 0,15	0,27 ± 0,08	0,31
Satt600	2,4 ± 0,40	1,47 ± 0,12	0,29 ± 0,07	0,37
Sat_308	1,8 ± 0,37	1,22 ± 0,09	0,16 ± 0,07	0,29
Satt153	3,2 ± 0,66	1,99 ± 0,32	0,43 ± 0,12	0,6
Mean	3,08	1,98	0,40	0,54

Na — no. of different alleles; Ne = no. of effective alleles; Nei — Nei's diversity index; PIC — polymorphic information content

The number of alleles per locus varied from 1,8 (Sat_308) to 5 (Satt288). At the same time, the number of effective alleles varied from 1,22 to 3,11 with an average value of 1,98. Nei's genetic diversity index averaged 0,40. The average value of PIC in the analysis was 0,54, and four SSRs were above this value. Satt244, Satt288, and Satt371 were the most informative SSRs with the highest PIC values.

For five origin groups of accessions Nei's genetic diversity index averaged 0,44 (Table 3). Accessions from Kazakhstan had the highest Nei's index values (0,53).

Table 3. Mean genetic heterozygosity indexes in five studied soybean groups

Origin groups	N	Na	Ne	Nei
Eastern Europe	56	4,58 ± 0,51	2,59 ± 0,36	0,52 ± 0,07
Western Europe	6	2,58 ± 0,29	2,09 ± 0,19	0,47 ±0,05
East Asia	3	1,42 ± 0,15	1,32 ± 0,12	0,17 ± 0,06
North America	16	3,58 ± 0,45	2,49 ± 0,33	0,52 ± 0,06
Kazakhstan	19	3,83 ± 0,42	2,46 ± 0,26	0,53 ± 0,06
Mean		3,20 ± 0,22	2,19 ± 0,13	0,44 ± 0,03

Note: N — number of samples; Na — number of different alleles; Ne = number of effective alleles; He — expected heterozygosity index

Principal coordinate analysis of 100 soybean samples based on 8 SSR markers associated with plant height

The PCoA analysis based on Nei's data showed that Coordinate 1 separated genotypes of Kazakhstan from the remaining four groups. The samples from Eastern and Western Europe were further clustered separately from the samples of East Asia and North America using the Coordinate 2 (Fig. 7).
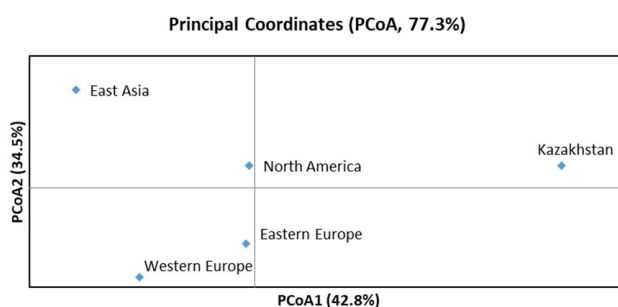

Figure 7. Principal Coordinate Analysis of five soybean groups based on eight SSR markers associated with plant height

The samples from Western Europe and Eastern Europe appeared to be the closest groups, while the samples from East Asia and Kazakhstan were genetically more distant from the other three groups.

4. Association of SSR and agronomic traits using t-test

The results of genotyping 100 soybean accessions using eight SSRs analyzed using average values in six agronomic traits. All 100 accessions were grouped according to the allele status for each trait, and averages in all groups were analyzed using the t-test within each trait (Table 4).

Table 4. The results of the t-test with average data of main agronomic traits and effective alleles of eight SSR markers

Trait	Satt244	Satt309	Satt371	Satt288	Satt460	Satt600	Sat_308	Satt153
MG	***		**			**		***
PH	***		**	**				
NFN			**	*				
NSP			*	**			*	
TSW				**				
YP2	***							

Notes: *** — P<0.001, ** — P<0.01, * — P<0.05. Morphological characters: maturity group (MG), plant height (PH), number of lateral branches (NLB), number of fertile nodes (NFN), yield components: number of seeds per plant (NSP), thousand seeds weight (TSW) and yield per plot (YP2)

The assessment of the results using the t-test suggested

that Satt244 was the only marker significantly associated with YP (Table 3). Satt244 was also significantly associated with MG and PH, confirming the importance of this SSR for the evaluation of agronomic traits. Interestingly, four SSRs were statistically related to the MG (Table 3). Along with Satt244, Satt288, and Satt371 were related to the performance of the PH, as the two last SSRs were additionally associated with NFN and NSP. Finally, Satt288 was also related to the performance of the TSW. In this study, it was found that Sat_308, Satt309, and Satt600 had no relationships with all studied traits.

DISCUSSION

The assessment of the five groups of soybean from different regions of the world showed that the averages of the PH ranged from accessions in Eastern Europe (48.5 ± 16.3 cm) to accessions in Kazakhstan (68.4 ± 21.8 cm). Apparently, the breeding activities in Kazakhstan are associated with the selection of tall plants [39]. For instance, the standard cultivar Zhansaya in the previous report showed variability from 77.1 cm (2018) to 99.6 cm (2017) [40]. In this study, the Zhansaya showed the average PH as 87.2 cm in 2020 and 59.8 cm in 2021, suggesting that the year 2021 was more stressful for the soybean. The PH data was coherent with YP performance, as the average YP for the entire collection was 8 ± 3.4 g in 2020 and 5.6 ± 3.9 g in 2021. According to a previous study, the optimal PH in the southeast of Kazakhstan was (95–105 cm) [41]. In 2020, seven cultivars, Dawson, Podyarka, Sepia, 362/2, Zara, Rose, Misula, were in this range. In 2021, only one cultivar (Zhalpaksay) fitted this range (Fig. 3). The correlation analysis confirmed that YP was positively correlated with the PH (P<0.001, Fig. 5), confirming the importance of the PH the soybean production. The assessment of the YP in five groups expectedly showed that the genotypes from Kazakhstan were the most productive (8.4 ± 3.7 g), while the genotypes from Eastern Europe showed the lowest YP (6 ± 2.1 g) among the studied groups.

The application of eight SSR markers associated with PH indicated their high polymorphism level, as the PIC average value for all SSRs was 0.54. The polymorphism level of three SSRs (Satt244, Satt288, and Satt371) was particularly high in the studied collection, suggesting the superior importance of these markers in PH assessment for genetic structure analysis and marker-assisted selection. The application of Nei's heterozygosity index showed that the genetic diversity of accessions from Kazakhstan was high (0.53) and comparable with the variation in samples from Eastern Europe and North America (0.52; Table 3). The PCoA analysis showed that Coordinate 1 is clearly distinguished from four other groups (42.8%), and Coordinate 2 further separated Western and Eastern Europe from Eastern Asia and North America (Fig. 7). Interestingly, the closest group of samples to soybean bred in Kazakhstan was a group of accessions from Northern America. However, it is easily can be explained by the fact that many USA commercial cultivars were used in the breeding activities of Kazakhstan. This fact can be confirmed by the analysis of the list of local commercial cultivars that includes such cultivars as Misula, Kazakhstanskaya 2309, Zhalpaksai. Nevertheless, the plot in Fig. 6 indicated that the soybean samples from Kazakhstan were genetically distant from the other studied groups.

The association of eight SSR markers with seven agronomic traits was evaluated using a two-tailed t-test (Table 3). The conducted analysis showed that five out of eight markers were statistically significant with at least one of the analyzed agronomic traits. Particularly, the results showed that four SSRs were associated with the MG, three SSRs with PH and NSP, and two SSRs with NFN (Table 3). Notably, the Satt224 (one of the two most polymorphic SSRs) was associated not only with PH and MG but also with YP2 (p<0.001). Another highly polymorphic marker Satt288 was associated not only with PH, NFN, and NSP but also with TSW (p<0.01). Hence, obtained results from the study of eight SSRs associated with the PH and other important agronomic traits can be efficiently used in the discrimination of soybean accessions and can be useful in local breeding projects.

CONCLUSIONS

The collection of 100 soybean accessions with different geographic origins was analyzed using eight major agronomic traits, including MG, PH, HLP, NLP, NFN, NSP, TSW, and YP2, in conditions southeast Kazakhstan. The correlation indices indicated that PH is significantly positively correlated with the remaining seven traits, including YP2 (P<0.001). Additionally, the collection was genotyped using eight SSRs associated with PH. It was determined that three of those microsatellites were highly polymorphic (Satt244, Satt288, and Satt371) and informative in sample discrimination. Also, the application of the t-test suggested that five out of eight studied SSRs were related to six different traits. Particularly, it was shown that Satt224 was highly significantly associated with both PH and YP2. It was concluded that five out of eight studied SSRs were not only helpful in sample discrimination but also in breeding via the marker-assisted selection approach.

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ГЕНЕТИЧЕСКОЕ РАЗНООБРАЗИЕ КОЛЛЕКЦИИ СОИ НА ОСНОВЕ МИКРОСАТЕЛЛИТНЫХ ДНК-МАРКЕРОВ, СВЯЗАННЫХ С ВЫСОТОЙ РАСТЕНИЯ.

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АБСТРАКТ

Соя является относительно новой культурой в Казахстане, и создание новых конкурентоспособных сортов с высокой продуктивностью и качеством является важным направлением местной селекции. Ранее одним из основных подходов к созданию новых сортов были селекционные методы, основанные на оценке ключевых морфологических признаков, включая время цветения и высоту растений (PH). Однако с развитием генетических исследований сои появились новые молекулярные инструменты, в том числе разработка микросателлитов ДНК или простых повторяющихся последовательностей (SSR). В данном исследовании коллекцию из ста образцов, выращенных на юго-востоке Казахстана в 2020–2021 гг., оценивали по восьми агрономическим признакам, включая высоту растения (PH), высоту прикрепления нижнего боба, количество боковых ветвей, количество продуктивных узлов, количество бобов с растения, масса тыс. семян, урожайность с квадратного метра (YP2), группа спелости. Оценка полевых испытаний показала широкий диапазон изменчивости агрономических признаков и позволила предположить, что PH достоверно коррелирует со всеми изучаемыми признаками, включая YP2. Коллекцию генотипировали с использованием восьми SSR, ассоциированных с PH. Результаты показали, что три SSR (Satt244, Satt288 и Satt371) были наиболее полиморфными, а пять из восьми SSR были связаны с шестью важными агрономическими признаками, включая время цветения, PH и YP2. Полученные результаты могут быть эффективно использованы в селекции сои на основе маркерориентированного подхода.

Ключевые слова: соя, высота растения, агрономические признаки, урожайность, SSR маркеры, корреляция, генетическое разнообразие.

ӨСІМДІК БИІКТІГІМЕН БАЙЛАНЫСТЫ МИКРОСАТЕЛЛИТТІ ДНҚ-МАРКЕРЛЕРІНІҢ НЕГІЗІНДЕ СОЯ КОЛЛЕКЦИЯСЫНЫҢ ГЕНЕТИКАЛЫҚ АЛУАНТҮРЛІЛІГІ

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ТҮЙІН

Соя Қазақстанда салыстырмалы түрде жаңа дақыл болып табылады және өнімділігі мен сапасы жоғары бәсекеге қабілетті жаңа сорттарды дамыту жергілікті селекцияның маңызды бағыттарының бірі. Осыған дейін жаңа сорттарды шығарудың негізгі тәсілдерінің бірі морфологиялық белгілерге, оның ішінде гүлдену уақыты мен өсімдік биіктігін (PH) бағалауға негізделген селекция әдістері болды. Дегенмен, сояның генетикалық зерттеулерінің дамуымен жаңа молекулалық құралдар пайда болды, соның ішінде ДНҚ микросателлиттерінің немесе қарапайым қайталанатын тізбектердің (SSR) дамуы. Бұл зерттеуде 2020–2021 жылдары Қазақстанның оңтүстік-шығысында өсірілген жүз үлгіден тұратын коллекция сегіз агротехникалық белгілері бойынша бағаланды, оның ішінде өсімдік биіктігі (PH), төменгі бұршік бекіну биіктігі, бүйірлік бұтақтар саны, өнімді түйіндер саны, өсімдіктегі бұршақ саны, мың дән салмағы, бір шаршы метрден алынатын өнім (YP2), пісу тобы. Далалық сынақтарды бағалау агрономиялық белгілердің кең ауқымды өзгергіштігін көрсетті және PH барлық зерттелген белгілермен, соның ішінде YP2-мен айтарлықтай корреляцияның бар екендігін. Коллекция PH белгісімен байланысқан сегіз SSR көмегімен генотиптелді. Нәтижелер үш SSR (Satt244, Satt288 және Satt371) полиморфтылығы жоғары және сегіз SSR-дың бесеуі гүлдеу уақыты, PH және YP2 сияқты алты маңызды агротехникалық белгілермен байланысты екендігін көрсетті. Алынған нәтижелерді маркер-бағытталған тәсіл негізінде сояны өсіруде тиімді пайдалануға болады.

Түйінді сөздер: соя, өсімдік биіктігі, агрономикалық белгілері, өнімділік, SSR маркерлер, корреляция, генетикалық алуантүрлілік.