

Natural variation of *E1-E4*, *E9*, *GmFT5a* genes
in 180 soybean accessions adapted to Novosibirsk regions

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Motivation and Aim: *E1-E4* genes have the major effect on maturity time and provide soybean adaptation to wide range of latitudes. Also, some variations in flowering time are associated with the *E9* and *GmFT5a* genes. The natural variation of the *E1-E4* genes has been widely studied in different germplasm collections of China, Europe, America, India, but not in Russia. The Novosibirsk district is a unique region for soybean production, because in the past there were no adapted varieties for cultivation in this region. At present, in Siberian Research Institute of Forages has bred and selected accessions that are able to fully maturity in such a northern cold region. Which alleles of the *E1-E4*, *E9* and *GmFT5a* genes provide adaptation to these conditions is unknown. Thus, the aim of our study is to reveal which alleles of this genes provide soybean adaptation and variation of maturity time in the Novosibirsk conditions.

Methods and Algorithms: Soybean accessions for DNA extraction were provided by Siberian Research Institute of Forages (172) and by EFKO (8) company. The 180 accessions were grown in the experimental field of the Siberian Research Institute of Forages (55°) under natural daylength conditions. The date of the emergence (VE), the first flower appearance (R1) and full maturity (R8) was recorded as the average between of three replicates. We used previously developed molecular markers to determine the alleles of the *E1-E4*, *E9* and *GmFT5a* genes. The box-plot were plotted in R 4.1.

Results: We found the high frequency of recessive alleles of *E1-E4* genes (Table 1). All accessions carry the dominant allele *E9*, which reduce the flowering time. For the *GmFT5a* gene, only three cultivars Kassidy, Pripyat and Aktai carry the *GmFT5a-H4* haplotype which associated with early flowering.

Table 1. Defined alleles of genes *E1-E4*

<i>E1</i>	<i>n</i> *	%	<i>E2</i>	<i>n</i>	%	<i>E3</i>	<i>n</i>	%	<i>E4</i>	<i>n</i>	%
<i>e1-nl</i>	112	62,2	<i>e2</i>	168	93,3	<i>e3-fs</i>	122	67,7	<i>e4-SORE-1</i>	93	51,6
<i>e1-as</i>	58	32,2	<i>E2</i>	12	6,6	<i>e3-tr</i>	38	21,1	<i>e4-kes</i>	46	25,5
<i>E1</i>	2	1,1				<i>e3-ns</i>	10	5,5	<i>E4</i>	41	22,7
<i>e1-fs</i>	1	0,55				<i>E3-Ha</i>	8	4,4			
						<i>e3**</i>	2	1,1			

* – number of accessions, ** – mix of haplotypes *e3-fs* and *e3-tr*

In field conditions, 10 varieties did not reach full maturity and were dropped out from further analysis. Almost all of these cultivars carry dominant alleles *E3* or *E4*. Recessive

alleles of the *E1-E4* genes, which reduce the maturity time, have a very high frequency in studied soybean population (see Table 1). Accessions with *e1-nl/e2/e3/e4* and *e1-as/e2/e3/e4* genotype have the earliest flowering time (Fig. 1a) and maturity (see Fig. 1, b). Accessions carrying dominant alleles *E3* or *E4* genes have the latest flowering time (see Fig. 1, a) and maturity time (see Fig. 1, b).

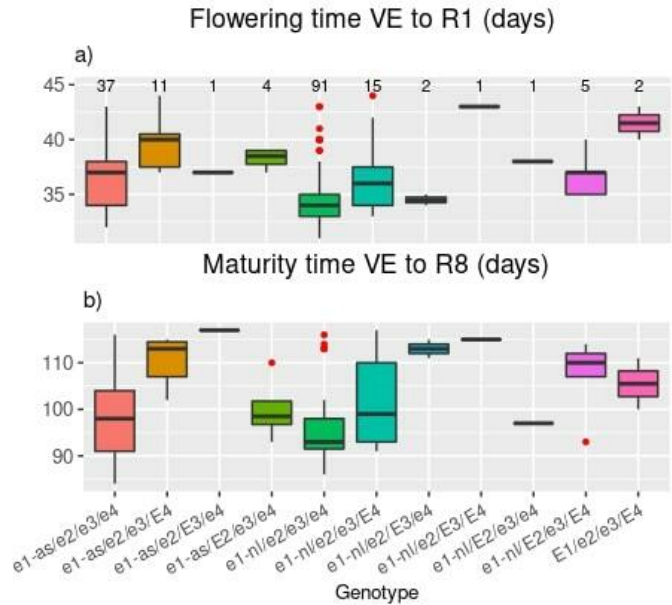


Fig. 1. a) Flowering time (VE to R1) of 170 cultivars of different *E* genotype, the numbers under boxes are the number of cultivars in each *E* genotype. b) Maturity time (VE to R8) of 170 cultivars of different *E* genotype

Results: Recessive alleles *E1-E4* predominate in the studied accessions that proves their key role in soybean adaptation to northern latitudes according with previous studies [1]. Rare for foreign soybean collections *e1-nl*, *e3-fs* and *e4-kes* alleles were identified in a large number of accessions. Three cultivars carry the rare *GmFT5a-H4* allele and can be used as a source of this rare allele in breeding. Different flowering time between genotypes (*e1-nl/e1-as*)/*e2/e3/e4* and (*e1-nl/e1-as*)/*e2/e3/E4* can be explained by the influence of the *E4* gene on flowering time. In previous studies *E4*, under natural conditions, effects on the post-flowering development [2], possibly in the Novosibirsk conditions, *E4* also effects on flowering time, as in experiments with 20-hour artificial daylight [3]. For the Novosibirsk region, varieties with the shortest maturity time are required. Accessions with genotypes *e1-nl/e2/e3/e4* and *e1-as/e2/e3/e4* have the earliest maturity time, so these genotypes can be used as a “molecular model” in soybean breeding to create varieties adapted to Novosibirsk conditions.

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