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Identification gene fertility Rf1 in collection samples of Sorghum bicolor (L.) Moench on southern Russia

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Abstract: Grain sorghum is one of the major crops used for various purposes, including animal and human nutrition. The most relevant strategy for create new sorghum hybrids is the use of lines with cytoplasmic male sterility (CMS). However, the process of creating sterile lines and lines that restore fertility is very laborious and time-consuming. The breeders need to know the genotype of the original parental forms of sorghum by the presence of the main genes that control fertility to speed up breeding work. One of these is the Rf1 gene. Our study aimed to identify alleles of the Rf1 gene in collection samples of grain sorghum (Sorghum bicolor (L.) Moench) adapted to the arid conditions of southern Russia. The studies carried out on southern Russia (FSBSI “ARC “Donskoy”, Zernograd, Russia) in 2018-2019. The presence of alleles of the Rf1 fertility gene using the Xtxp18 SSR marker by PCR analysis in collection samples of grain sorghum (313 pcs.) was studied. A crossed some samples with two sterile lines - "Demetra S" and "Dzhetta S" (developed in FSBSI "ARC "Donskoy") were doing in 2019. The assessment of the fertility of self-pollinated lines was carried out in the field using a 3-point scale. The polymorphism of the Xtxp18 marker, a wide allelic diversity of the Rf1 gene in collection samples of sorghum and the association of the identified Rf1 alleles with the fertility and sterility of self-pollinated hybrids of grain sorghum as a result of the study was performed. This result will make it possible to deepen understanding of the influence of the Rf1 gene alleles on the level of fertility of sorghum plants in the future, as well as to accelerate the breeding process to create sterile lines and their fertile analogues for further obtaining commercial hybrids.

Keywords: Sorghum bicolor; Rf1; fertility; PCR; allele identification

Results and Discussion

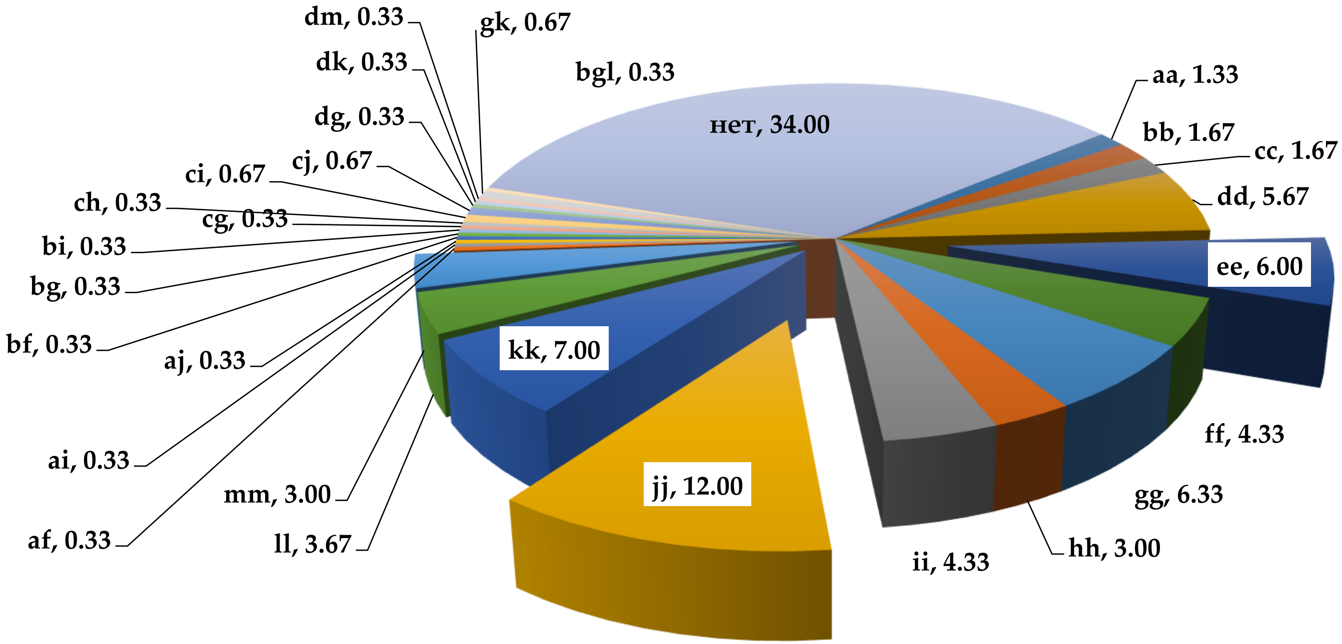

Figure 1. Percentage distribution of grain sorghum samples by the presence of Rf1 gene alleles: **aa** – 266 bp, **bb** – 262 bp, **cc** – 258 bp, **dd** – 248 bp, **ee** – 238 bp (associated with rf1), **ff** – 236 bp, **gg** – 232 bp, **hh** – 230 bp, **ii** – 228 bp, **jj** – 220 bp (associated with Rf1), **kk** – 210 bp, **ll** – 200 bp, **mm** – 190 bp, **af** – 266 bp + 236 bp, **ai** – 266 bp + 228 bp, **aj** – 266 bp + 220 bp, **bf** – 262 bp + 236 bp, **bg** – 262 bp + 232 bp, **bi** – 262 bp + 228 bp, **cg** – 258 bp + 232 bp, **ch** – 258 bp + 230 bp, **ci** – 258 bp + 228 bp, **cj** – 258 bp + 220 bp, **dg** – 248 bp + 232 bp, **dk** – 248 bp + 210 bp, **dm** – 248 bp + 190 bp, **gk** – 232 bp + 210 bp, **bgl** – 262 bp + 232 bp + 200 bp, **NA** – null-allele.

Results and Discussion

The identified fertile and sterile hybrid combinations of grain sorghum.

♂ Alleles	Number of combinations	Number of fertile and sterile lines[1]	
		♀ Demetra S	♀ Dzhetta S
NA	33	31.5 F : 1 FS : 0.5 S	32 F : 1 S
b	2	2 F	2 F
c	3	1 F : 2 S	1 F : 2 S
d	3	3 F	3 F
e	2	1 F : 1 S	2 F
g	2	1.5 F : 0.5 S	2 F
i	1	1 F	1 F
j	3	2 F : 1 S	3 F
k	1	1 F	1 F
l	1	0.5 F : 0.5 S	1 F
m	2	2 F	2 F

[1] F – fertile lines, FS – semi-sterile line, S – sterile lines.

Results and Discussion

We identified 36 samples of grain sorghum with the j allele associated with fertility, 18 samples with the e allele associated with sterility, as well as samples with previously unknown alleles, which we temporarily named k - 22 samples, l - 11 samples, and m - 9 samples.

Sterility in 2 repetitions was revealed in crossing combinations Demetra S/ZSK 1530/15, Dzhetta S/Zernogradskoe 204w4, Demetra S/LBK 28, Demetra S//Svetloje/Belozernoje 100, Dzhetta S//Svetloje/Belozernoje 100, hence their paternal forms are sterility fixers and can be used in further breeding work.

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Thank you for attention!!!