



Studying polymorphism of the gene *CslF6* associated with β -D-glucan biosynthesis in diploid oat accessions of *Avena strigosa* Schreb. from the VIR collection

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(What appears below is a summary and translation of the original work)

Background:

Oat is one of the most widespread and important cereal crops in global agricultural production. Searching for new high-yielding and high-quality genotypes remains relevant, especially in the context of global climate change, as most local oat varieties may become economically ineffective.

Materials and methods:

The materials for this study included 50 local varieties of the diploid cultivated oat species *Avena strigosa* Schreb. from the VIR collection that had diverse geographical origins. These accessions were grown under field conditions at the Pushkin and Pavlovsk Laboratories of VIR in 2023–2024. The field testing of the oat collection was carried out following the guidelines for the study of material in the VIR collection; biochemical indicators were assessed using conventional techniques. Molecular genetic research methods (DNA isolation, polymerase chain reaction, and Sanger sequencing) were applied to oat accessions contrasting for β -glucan content. The allelic state of the key gene for the biosynthesis of β -glucan, *CslF6*, was identified for each accession.

Results and discussion:

Oat is one of the grain crops with a high amount of healthy dietary components. Oat grains contain large amounts of protein, oil, and polysaccharides (β -glucans). The β -glucan content varies among different oat species. The average content of β -glucan in accessions from the VIR collection is: *A. sativa* L. – 3.60%, *A. byzantina* Koch – 3.40%, *A. abyssinica* Hochst. – 2.46%, and *A. strigosa* Schreb. – 2.97%.

The mechanism of biosynthesis of oat β -glucans has not been fully elucidated. This is because of the complex structure of the oat genome. The *Csl* (*Cellulose synthase-like*) gene family is one of

those associated with the biosynthesis of soluble polysaccharides. The coding region of the *CslF6* gene in diploid *A. strigosa* accessions from the VIR world collection was studied by the authors (Figure 1).

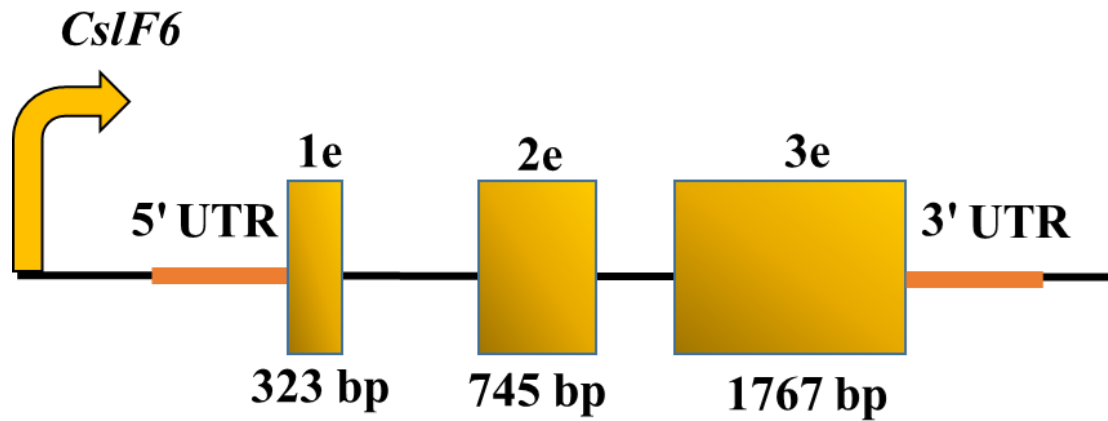


Figure 1. Structure of the *CslF6* gene of *Avena strigosa* (5517 bp)

The collection of *A. strigosa* is represented by three subspecies: *A. strigosa* subsp. *strigosa* (Schreb.) Thell. (covered sandy oats, with a long, narrow grain), *A. strigosa* subsp. *brevis* Husn. (short sandy oats), and *A. strigosa* subsp. *nudibrevis* (Vavilov) Kobyl. et Rod. (naked sandy oats). The allelic state of the *CslF6* gene was analyzed in eight of the 50 studied local varieties that contrasted for β -glucan content (Table 1).

Table 1. The *Avena strigosa* Schreb. accessions used in the evaluation

Nº VIR catalogue	Origin	Subspecies and variety of <i>Avena strigosa</i> Schreb.	Accession name	Special aspects
5199	Spain	subsp. <i>strigosa</i> var. <i>strigosa</i>	`Local`	The grain is covered, elongated, and the lemma is gray
9286	Ukraine	subsp. <i>strigosa</i> var. <i>strigosa</i>	`Local`	The grain is covered, elongated, and the lemma is gray
2167	Germany	subsp. <i>brevis</i> var. <i>semiglabra</i>	`Local`	The grain is covered, short, and the lemma is gray
4480	UK	subsp. <i>brevis</i> var. <i>candida</i>	`Local`	The grain is covered, short, and the lemma is gray
5278	Portugal	subsp. <i>brevis</i> var. <i>nigricance</i>	`Local`	The grain is covered, short, and the lemma is black



5288	Portugal	subsp. <i>brevis</i> var. <i>candida</i>	`Local`	The grain is covered, short, and the lemma is white
4968	UK	subsp. <i>nudibrevis</i>	`Pilcorn Oat`	Naked grain
14674	Turkey	subsp. <i>nudibrevis</i>	`Kleiner Nackhafer`	Naked grain

A biochemical evaluation of this set of accessions of sandy oat showed their diversity in the content of biochemical components. Biochemical analysis revealed accessions of *A. strigosa* that had high protein content (above 17%), starch (above 53%), oil (above 7%), and β -glucan (above 5%). High protein accessions included VIR-5278 from Portugal and accessions of the naked subspecies *nudibrevis*, including VIR-4968 from Great Britain and VIR-14674 from Turkey. The naked accessions differed from the others in their higher contents of starch (53.6% and 53.87%), oil (7.05 and 5.27%), and β -glucan (5.25 and 5.75%). Details are in Table 2 of the original article.

The sequencing of *CslF6* gene fragments and alignment to the reference genome of *A. strigosa* (NCBI GeneBank: MN453302.1) in the UGENE program did not reveal mutations in the coding part of the gene. This suggests that the change in the content of oat β -glucan may be associated with changes in other genes of the *Csl* family, which currently remain unannotated in *A. strigosa* (Schreb.). Further study of the genetic and epigenetic regulation of β -glucan synthesis will not only allow the creation of new oat varieties with increased content of soluble polysaccharides, but will also generally supplement the existing knowledge of plant biology.

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