

The 15 versions of the gene may represent duplicated copies of genes similar to those which control beta-glucan in barley, or additional genes in oats that are not present in barley.



RESULTS

Despite the identification of many copies of beta-glucan-like genes in oat, gene sequence differences were not detected between high and low beta-glucan lines. This means that the development of markers to associate those beta-glucan gene copies with beta-glucan content is not possible.

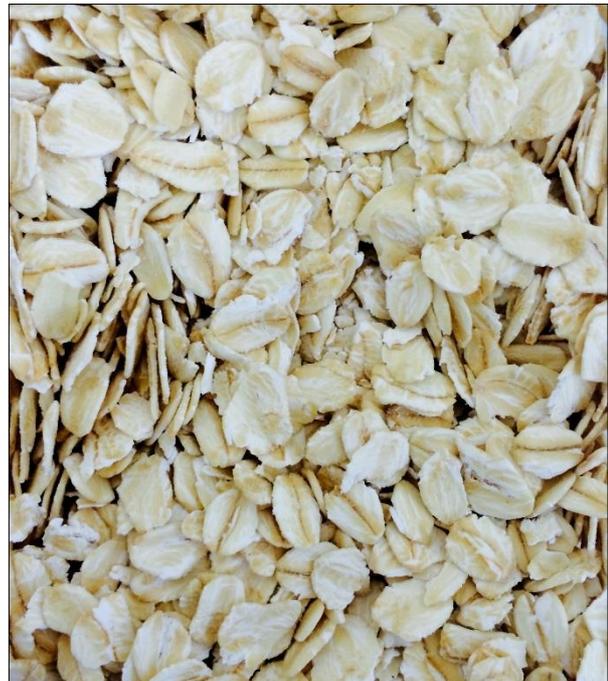
The results suggest that an approach based on transferring knowledge from one species (barley) to another (oat) will only partially assist in identifying markers to be used for selection in breeding.

Despite being unable to identify molecular markers because of the difference in genes from oat to barley, the project has provided important knowledge which guides the next steps in this area of research.

The next steps should include the screening of mapping populations to determine the genetic location of genes which control grain beta-glucan in oat, and further investigation into underlying biological differences between high and low beta-glucan lines, such as cell wall structure and composition. Screening of oat germplasm to identify alternative sources of high beta-glucan would also complement these approaches.



Researcher Dr Tim Sutton



VALUE FOR GROWERS

This project has been important in providing the foundation for future direction of research. Work will be ongoing to enable the cost efficient selection of high beta-glucan oats to provide South Australian growers with a competitive advantage.

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