Building a Reference Transcriptome for the Hexaploid Hard Fescue Turfgrass (*Festuca brevipila*) Using a Combination of PacBio Isoseq and Illumina Sequencing

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Abstract

Background: Hard fescue (*Festuca brevipila* Tracey, $2n=6x=42$) is a cool season turfgrass with a fine leaf texture that performs well under low-input management. Breeding and genetics studies of *F. brevipila* have been limited due to the complexity of its hexaploid genome. To advance our knowledge of *F. brevipila* genomics, we used PacBio isoform sequencing to develop a reference transcriptome for this species.

Results: Here, we report the *F. brevipila* reference transcriptome generated from root, crown, leaf, and seed head tissues. We obtained 59,510 full-length transcripts, of which 38,595 were non-redundant full-length transcripts. The longest and shortest transcripts were 11,487 and 58 bp, respectively. To test the polyploid origin of *F. brevipila*, we sequenced three additional transcriptomes using closely related species on an Illumina platform. The results of our phylotranscriptomic analysis supported the allopolyploid origin of *F. brevipila*.

Conclusions: Overall, the *F. brevipila* Pacbio Isoseq reference transcriptome provided the foundation for transcriptome studies and allowed breeders for gene discovery in this important turfgrass species.

Full-text

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