



Category: Plant Genomics

Identification of isoforms of microRNAs in wheat (*Triticum aestivum* L.) and their role in leaf rust pathogenesis

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Abstract

Bread wheat, a type of grass under genus *Triticum* and species *aestivum* covers the largest land area when production of cereal crops is considered. Being an allohexaploid ($2n=6x=42$; AABBDD), its genome is contributed by three progenitors and is evolutionarily rich. Rust in leaves, caused by *Puccinia triticina*, severely affects grain quality. MicroRNAs are considered as major components of gene silencing and so have deep role to play during stress. Post transcriptional modification of miRNAs which generates isomiRNAs significantly affects target specificity especially when the modification occurs in 5' end.

A total of four small RNA libraries were prepared through next-generation Illumina sequencing techniques from leaves of two wheat Near Isogenic Lines (NILs), HD2329 (susceptible) and HD2329 + LR24 (resistant). Prior to this, one set of the two NILs was mock inoculated and considered as control (with sRNA library code named SM-mi and RM-mi) while other was treated with urediniospores of leaf rust fungus (with sRNA library code named SPI-mi and RPI-mi). Clean reads in all four libraries were previously used for prediction of 559 novel miRNAs and in the current study it was used to detect isoforms of these miRNAs. A total of 237 isoforms were detected for 41 miRNAs. These isoforms included both 5' and 3' modifications of miRNAs. There were 27 miRNAs with 5' modifications and five miRNAs with 3' modifications while nine miRNAs showed both types of modifications.

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