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عنوان مقاله:
High throughput deep sequencing revealed different molecular mechanisms in cereals are mediated by miRNAs

محل انتشار:
هشتمین همایش بیوانفورماتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 1

نویسندگان:
بهنام بخشی - *ابخش تحقیقات زراعی و باغی، مرکز تحقیقات و آموزش کشاورزی و منابع طبیعی سیستان، سازمان تحقیقات، آموزش و ترویج کشاورزی، زابل، ایران*

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خلاصه مقاله:
In the current study cereal (including wheat, barley and rice) miRNAs have been investigated using small RNA extraction, high throughput deep sequencing and bioinformatics analysis. In this study 28175274, 28404511 and 27515162 miRNA reads have been observed for wheat, barley and rice, respectively. 53%, 60% and 76% of these reads were matched with their genomes, respectively.1814 reads of known miRNAs and 105 reads of novel miRNAs have been identified for wheat. Likewise, 782 reads of known miRNAs and 131 reads of novel miRNAs have been explored for barley. Furthermore, 338 reads of known miRNAs and 31 reads of novel miRNAs have been recognized for barley. MiR156 and Novel_1290 (in wheat), miR168 and Novel_1290 (in barley) and miR166 and Novel_1290 (in rice) were the most frequent miRNAs in the investigated cereals. Thus different frequent miRNAs are involved in cereals. Furthermore, differential expression of cereal miRNAs has been observed for many of expressed miRNAs. Additionally, target prediction and gene ontology analysis indicated that although some of miRNAs are involved in same pathways among cereals but could regulate them through another ways that could led to different molecular .mechanisms through differentially expressed miRNAs

کلمات کلیدی:
microRNAs, Next Generation sequencing, Wheat, Barley, Rice

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