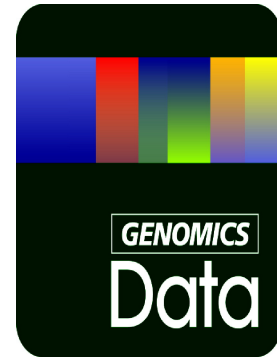


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Transcriptome of barley under three different heavy metal stress reaction

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Data in Brief

Title:

Transcriptome of barley under three different heavy metal stress reaction

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Keywords

Barley; RNA-Seq; Transcriptome; Heavy metal; Copper; Zinc; Cadmium

Abstract

In the present study, we used Illumina sequencing technology (HiSeq 2000) to sequence the transcriptome of barley (*Hordeum vulgare* L., cv. Morex) under three different heavy metal stress conditions: copper, zinc and cadmium. For each of those metals, the concentration causing a 50% inhibitory effect for root growth (EC₅₀) was determined. We sequenced the total RNA of both roots and shoots from barley with and without heavy metal treatments in three replicates. Raw reads of the transcriptome project have been deposited in NCBI's BioProject accession number PRJNA382490. The obtained transcriptomic data will be useful for further studies focusing on heavy metal tolerance and comparative transcriptome analysis in barley.

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