STUDY OF THE ROOT TRANSCRIPTOME OF BREAD WHEAT USING HIGH-THROUGHPUT RNA SEQUENCING (RNA-SEQ)

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MOTIVATION AND AIM

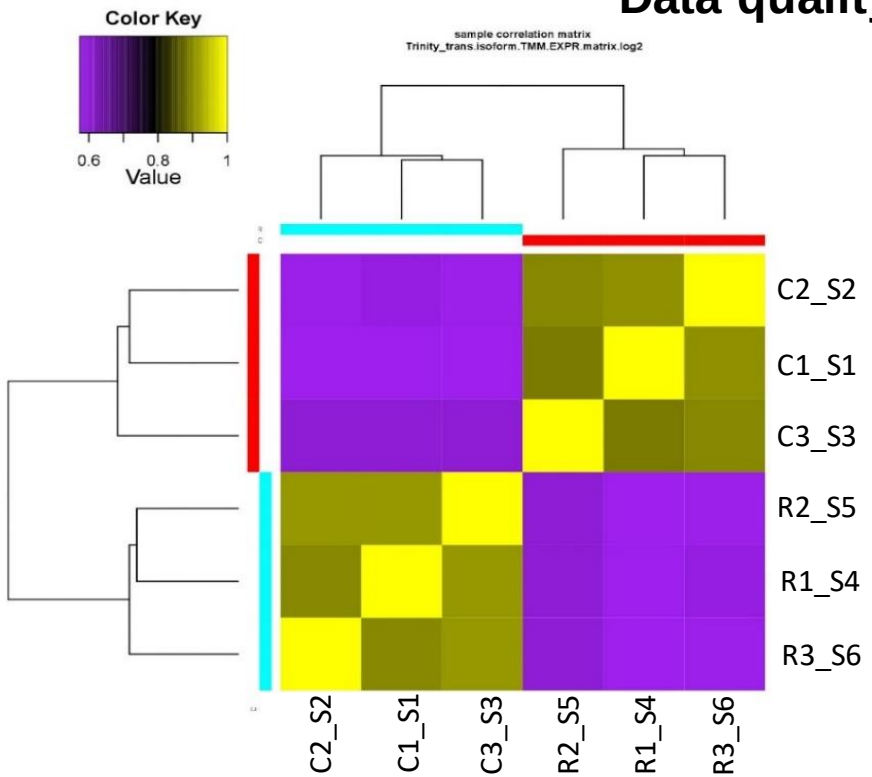
- Bread wheat (*Triticum aestivum* L.) is the most important crop in the world. It provides about 20% of the total calories consumed by humans. For a long time, wheat selection was mainly based on phenotypic traits of the shoot, while the roots were given little attention. As a result, the root system of modern wheat varieties has weakened. Therefore, the study of genetic control of wheat roots development is an urgent issue. A convenient method to study the genetics of roots development is transcriptome profiling using high- throughput RNA sequencing (RNA-seq). The method allows us to evaluate gene expression across the entire genome, as well as to find specific genes responsible for roots development that will be used in the future during marker-assisted selection of wheat varieties with resistant root system.
- The aim of the current study is revealing differentially expressed genes between the root and shoot transcriptomes of allohexaploid wheat using RNA-seq analysis and identifying root-specific genes involved in the wheat root system development.

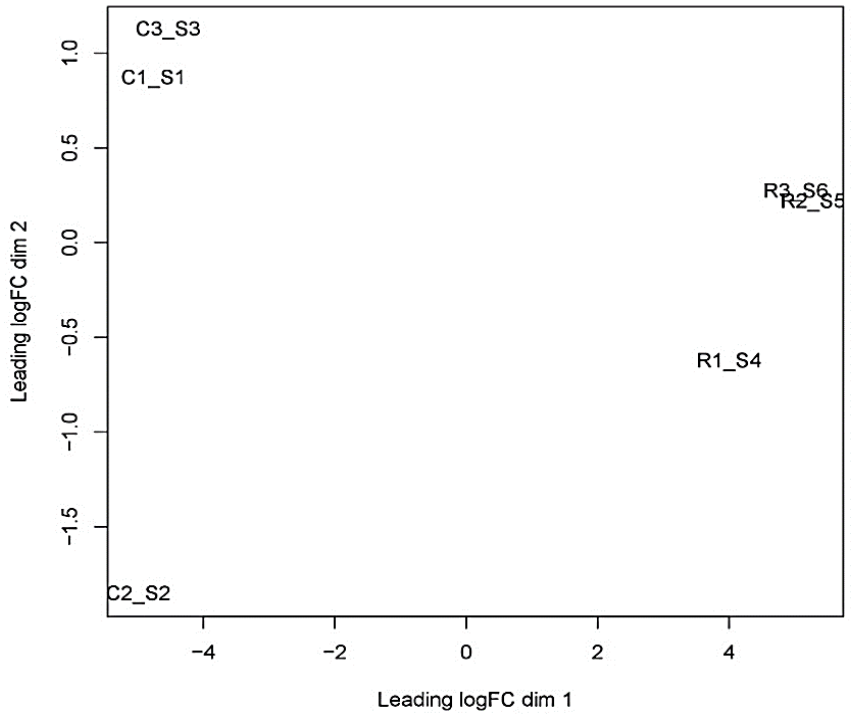
Plant material and RNA sequencing

RNA was extracted from 4-days roots and coleoptiles of seedlings of Russian spring wheat cultivar “Saratovskaya 29” in three biological replicas. One sample contained roots or coleoptile from six different plants. Sequencing was performed using Illumina NextSeq 550 platform in Institute of Cytology and Genetics SB RAS, 75-bp reads was obtained.

De novo assembly of transcriptome was performed using Trinity software. To evaluate quality of obtained transcriptome Transrate software was used. Quantification of reads was performed using Salmon software. To obtain different expressed transcripts edgeR package was used. For functional annotation Transrate, AgriGO and BlastKOALA services were used.

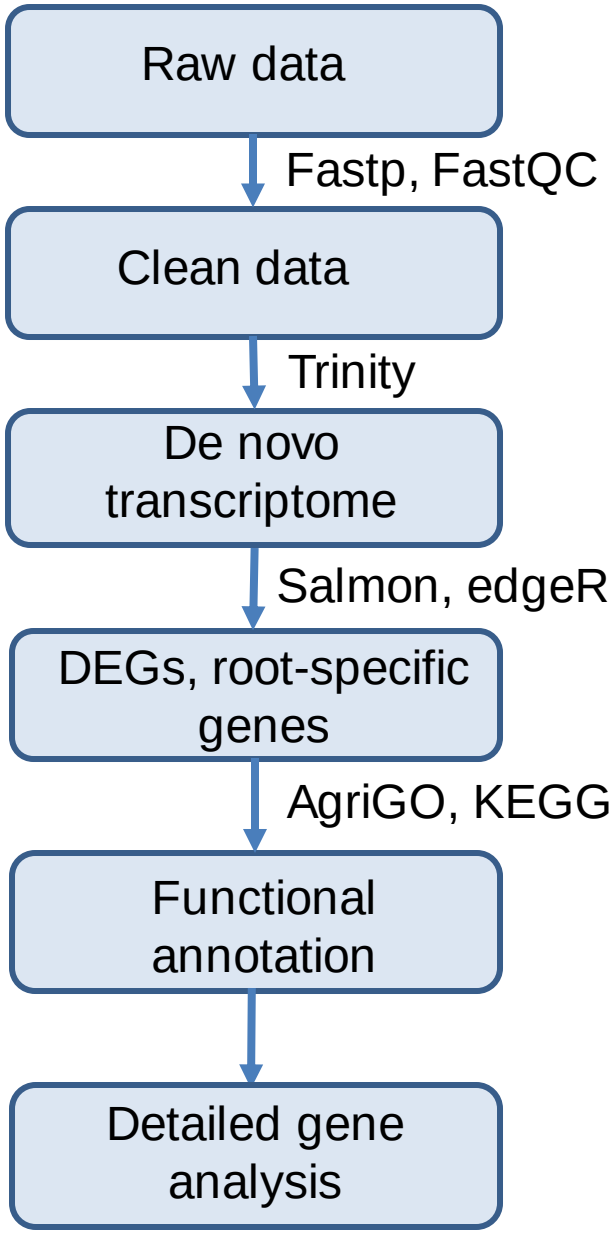
Data quality assessment





C1_S2, C2_S2, C3_S3 – coleoptile libraries, R1_S4, R2_S5, R3_S6 – root libraries

Pipeline



Transcriptome *de novo* assembly metrics

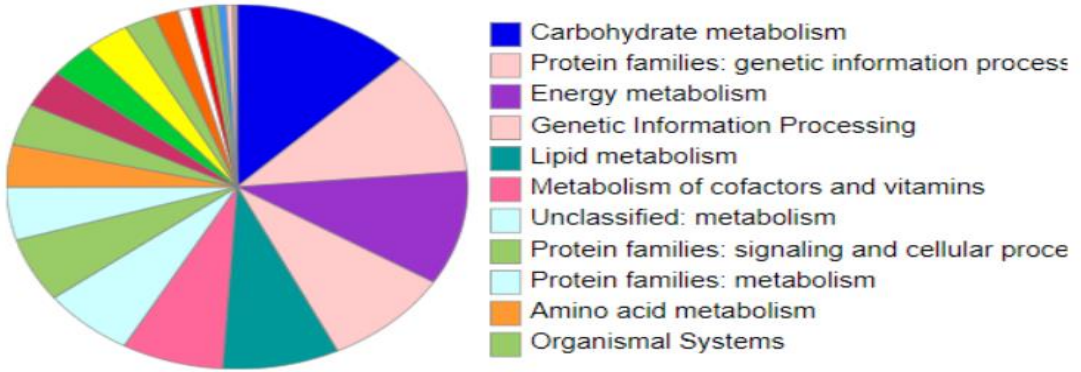
	Transcript number	Up-regulated in root	Down-regulated in root	Root-specific
Total	330,112	31,488	35,851	18,040
With ORF	112,934	20,793	21,094	7,216

DEG functional annotation (Agri GO)

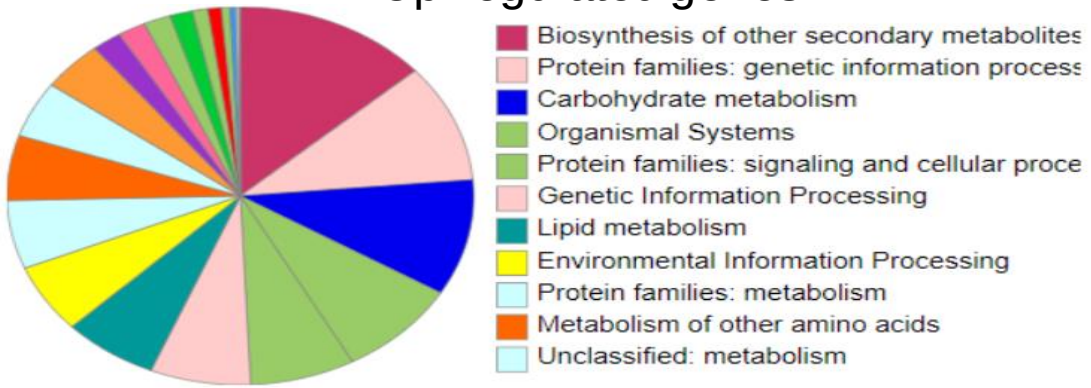
	GO term	DEGs amount	FDR
Up-regulated	response to oxidative stress	287	3.8e-50
	oxidation-reduction process	1137	4.7e-33
	single-organism metabolic process	1712	1.1e-28
	response to stress	465	1.7e-21
Down-regulated	single-organism metabolic process	1612	1.3e-51
	single-organism process	2040	8.6e-43
	oxidation-reduction process	974	3e-31
	metabolic process	3914	5.9e-27

DEG functional annotation (KEGG)

Down-regulated genes



Up-regulated genes



Root-specific genes