

Formation of Aerenchyma in Seminal Root of Wheat under Nutrient Starvation and Transcriptome Analysis

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ABSTRACT

Excess moisture injury in wheat and barley is one of agricultural constraints. In Japan, over 60 % of wheat in area is grown in drained rice paddy fields. To overcome the wet injury in wheat, modification of the aerenchyma forming capacity in wheat root using genetic engineering is expected. However, the molecular mechanisms associated with aerenchyma formation are still unclear.

We observed the growth of primary seminal roots of wheat seedlings under two culture conditions, control and starvation. Root aerenchyma was found under starvation until 7 day after sowing. Transcriptome analysis showed the different gene expressions between the roots under two nutritional conditions.

Keywords: Excess-moisture injury, *Triticum* spp., aerenchyma, nutrient starvation, transcriptome

1. INTRODUCTION

Since we have much precipitation and large part of wheat growing area is drained paddy fields in Japan, the excess water in soil causes wet injury and considerable loss of grain yields in wheat production. Root aerenchyma, which is thought to function for gas exchange in root tissue, is not well developed in wheat comparing with rice plant. If wheat has more developed aerenchyma in root, the tolerance to wet injury might be increasing. A possible approach to improve the wet tolerance is modification of root formation through genetic engineering, however, well understanding of the mechanisms of root development and aerenchyma formation is necessary for that research. This paper presents the results from gene expression analyses of aerenchyma formation in wheat root under nutrient starvation. Specific gene expression during aerenchyma formation will be discussed.

2. METHODS

Seeds of wheat were surface sterilized and sown in the medium A (1/20 strength Murashige-Skoog inorganic salt - agar) or medium B (water - agar). The segments of primary seminal roots were removed from the junction level (proximal) and the tip (distal) of seedlings and their cross sections were observed under a light microscope. Total RNAs were prepared from proximal and distal of the roots with RNeasy Plant mini-kit (Qiagen) and were used for

transcriptome analysis with 38k wheat microarray slides.

3. ROOT CORTEX UNDER TWO NUTRITIONAL CONDITIONS

In the primary seminal root, aerenchyma was observed under starvation medium B in the root cortex at 1 cm below the root and shoot junction (Figure 1; right), while no aerenchyma was found in the root under medium A (Figure 1; left). No aerenchyma was found in the root tip under the two nutritional conditions (data not shown).

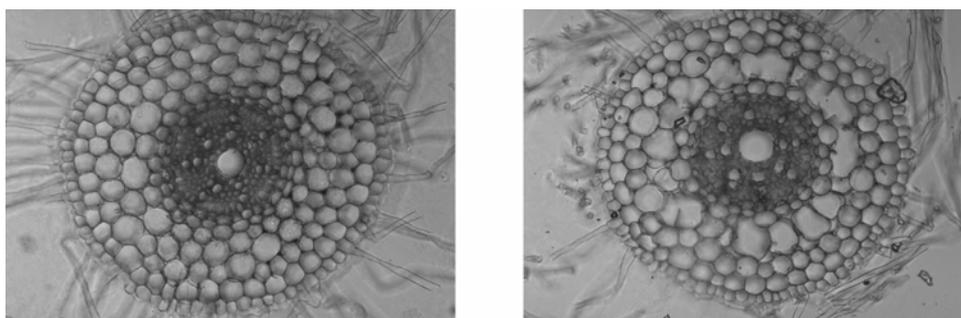


Figure 1. Cross sections of primary seminal roots of wheat under control (left; medium A) and under starvation (right; medium B).

4. GENE EXPRESSION IN SEMINAL ROOT OF WHEAT

Transcriptome analysis indicated that 27 genes expressed more than 5 fold change at the root tip under starvation. Functions of the genes are almost unknown, but 4 genes were N-metabolism related (Table 1).

Table 1. Genes expressed more than 5 fold change at the root tip under starvation.

No.	Gene Name	Annotation	Regulation in starvation
2	MUGEST2003_23lib_Contig3168	hemoglobin 2	down
4	MUGEST2003_23lib_Contig3205	ferredoxin-nitrite reductase	down
5	whr13o15	nitrite reductase apoprotein	down
6	wheat0130Contig6288	type 2 NADH dehydrogenase	down
14	MUGEST2003_23lib_Contig8102	GA10192-PA	up
16	wheat0130Contig5942	endochitinase	up
22	wheat0130Contig13722	plastid glutamine synthetase isoform GS2c	down
26	wheat0130Contig9162	putative Cen-like protein, FDR1	down

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