A Big Earth Data Platform for Three Poles

**Drought-response transcriptome of ammopiptanthus mongolicus**

1、Description

The leaves and roots of ammopiptanthus mongolicus were sequenced by Hiseq2000 with high throughput transcriptome, and 44,959 unigene were found. Through database comparison, 43,192 unigene were annotated. It was found that under drought treatment, 1035 and 1210 genes were differentially expressed in leaves and roots (the expression level was up-regulated or down-regulated by more than 2 times respectively). These differentially expressed genes are mainly related to material transportation, stress response, metabolic process, and molecular structural activity. 40 differentially expressed (specific) response genes under drought stress were identified. By analyzing the transcription factors of Ammopiptanthus mongolicus, we also found that Ammopiptanthus mongolicus contains 50 transcription factor families and 1575 transcription factors. The expression of 7 transcription factors increased and 50 decreased in leaves. In the roots, 11 rose and 33 fell.

2、Keywords

Theme：Vegetation,Ammopiptanthus mongolicus,Physiological indexes
Discipline：Terrestrial Surface
Places：Heihe River Basin
Time：2012

3、Data details

1.Scale：None

2.Projection：4326

3.Filesize：1.02MB

4.Data format：PDF

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：38.62545 | - |
| west：103.10507 | - | east：103.10507 |
| - | south：38.62545 | - |

5、Time frame:2018-11-19 10:48:30+00:00--2018-11-19 10:48:30+00:00

6、Reference method

References to data:

SU Yanhua. Drought-response transcriptome of ammopiptanthus mongolicus. A Big Earth Data Platform for Three Poles, doi:10.3972/heihe.096.2013.db2016

References to articles:

7、Supporting project information

8、Data resource provider

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