A Big Earth Data Platform for Three Poles

**Karyotype analysis, genomic DNA purification and genome size prediction of Ammopiptanthus mongolica, a typical desert plant in Heihe River basin (2013)**

1、Description

Background: this data interchange is the first data interchange of the key project of "integrated study of eco-hydrological processes in heihe basin", "genomics research on drought tolerance mechanism of typical desert plants in heihe basin".The main research targets of the key projects is a typical sand desert plants are Holly, using the current international advanced a new generation of gene sequencing technology to the whole genome sequence and gene transcription of Holly group sequence decoding, so as to explore related to drought resistance gene and gene groups, and transgenic technology in model to verify their drought resistance in plants.  
Process and content: as genome sequencing requires special sequencing equipment, the project is huge and the process is complex (mainly including genome library construction, sequencing, data analysis and genome assembly), so it needs to be completed by a professional sequencing company.After contacting with sequencing companies, we learned that before sequencing an unknown genome, the size and complexity of the genome should be predicted, which is a necessary prerequisite for designing sequencing schemes and strategies.Therefore, in 2013, we mainly predicted the chromosome composition, genome size and complexity of sand Holly, and successfully established the extraction and purification method of its genomic DNA.The results showed that the plant was diploid, the genome was composed of 9 staining lines (18 lines of diploid), and the genome size was 1.07G.The quality test results of the genomic DNA indicated that the requirements of the obtained DNA complex sequencing have been sent to the sequencing company for library construction and sequencing, which is now in progress.In addition, in order to obtain a large number of uniform plant materials, we have discussed the induction of callus, which has been successful.Due to these reasons, we were unable to complete the genome sequencing and submit the relevant data of sand Holly in accordance with the original plan of the project this year, mainly because we did not count the predicted contents of the genome before.  
Data usage: the data obtained in this year on ploidy, karyotype composition and genome size of lycopodium SPP.The success of the callus induction provides a high-quality material guarantee for the subsequent transcriptome sequencing and drought-resistance mechanism research experiments, and it is also a new contribution to the cytological and physiological research of the plant.

2、Keywords

Theme：Desert,Vegetation,Genomics,Desert ecosystem  
Discipline：Terrestrial Surface  
Places：Heihe River Basin  
Time：2013

3、Data details

1.Scale：None

2.Projection：None

3.Filesize：5.4MB

4.Data format：word

4、Space scope

|  |  |  |
| --- | --- | --- |
| - | north：43.3 | - |
| west：96.1 | - | east：104.2 |
| - | south：37.7 | - |

5、Time frame:2012-01-09 05:55:00+00:00--2014-01-08 05:55:00+00:00

6、Reference method

References to data:

HE Junxian. Karyotype analysis, genomic DNA purification and genome size prediction of Ammopiptanthus mongolica, a typical desert plant in Heihe River basin (2013). A Big Earth Data Platform for Three Poles, doi:10.3972/heihe.005.2014.db2014

References to articles:

7、Supporting project information

8、Data resource provider

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