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## Generation and analysis of expressed sequence tags (ESTs) from the drought-tolerant species *Cleistogenes songorica*

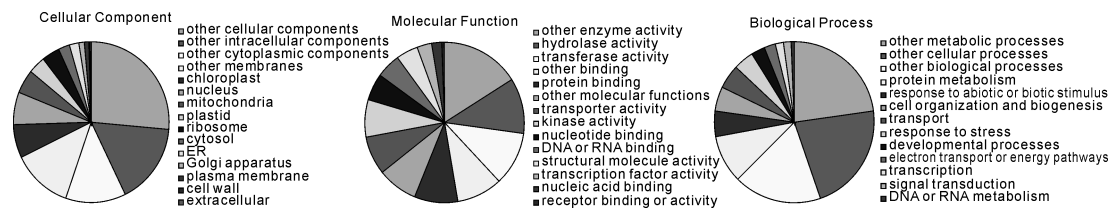
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**Key words:** *C. songorica*, expressed sequence tags (ESTs), comparative genomics

**Introduction** *C. songorica* is a dominant species of desert grassland with an annual rainfall of 120mm in Inner Mongolia. It has good adaptation in poor and sandy soil, and is truly drought tolerant (Xun 1989). A gene discovery and functional genomics project has been undertaken in *C. songorica* in order to isolate and characterize the genetic determinants to drought stress.

**Methods and results** Single pass sequencing of *C. songorica* cDNA libraries generated from leaves and roots of seedling plants under different water withholding stress treatment generated a pool of expressed sequence tags (EST) of 3,579 sequences. Sequence analysis resulted in the identification of a unigene set corresponding to 1499 contigs, including 805 singletons and 694 consensus (Figure 1). Several genes from *C. songorica* cDNA libraries were presented as ratios of the expression level under 8d of water withholding over the control from the quantitative RT-PCR experiment (Table 1).



**Figure 1** Gene Ontology annotation for *C. songorica* ESTs.

**Table 1** Differentially expressed genes from *C. songorica* under 8 d of water withholding versus control tissues detected by quantitative RT-PCR analysis.

Code	Annotation	Leaf	Root
Cs02	SAMDC : S-adenosylmethionine decarboxylase proenzyme	0.62±0.13	5.93±0.71
Cs03	S-adenosylmethionine decarboxylase 2	0.44±0.06	7.39±0.80
Cs04	putative aldehyde dehydrogenase MIS1	0.89±0.20	16.90±1.46
Cs07	betaine aldehyde	6.07±2.00	3.78±0.38
Cs10	PEAMT : Phosphoethanolamine N-methyltransferase	43.35±7.71	13.25±0.45
Cs12	Hydrophobic protein LTI6B (Low temperature-induced protein 6B) or drought-induced hydrophobic protein	3.87±0.80	11.40±0.68
Cs17	Na <sup>+</sup> /H <sup>+</sup> antiporter	0.45±0.04	2.95±0.14
Cs20	dehydrin-/LEA group 2-like	3.3E+07±9.2E+06	1.5E+07±1.9E+06

**Conclusions** In this study we identified and isolated several differentially expressed genes linked to water deficit stress from *C. songorica*. We are expecting to enhance our understanding how plants may regulate the expression of these candidate genes in response to a water deficit stress.

### Reference

Xun, G. N. 1989 The major wild turf grass species in Zhanye Corridor of Gansu province. *Pratacultural Science* 6(5) : 60-64.