

Data mining for simple sequence repeats in expressed sequence tags of cluster bean (*Cyamopsis tetragonoloba* (L.) taub)

Nagesh Kuravadi Aswathnarayana, Pranita Bhatele, Sangharsh Kumar Tripathi, Kanwarpal Singh Dhugga*, Kulvinder Singh Gill# and Gursharn Singh Randhawa

Indian Institute of Technology Roorkee, India

*Pioneer Hi-Bred International, Inc., USA

#Washington State University, USA

Cluster bean (*Cyamopsis tetragonoloba* (L.) Taub), which is also known as guar, is an annual, drought resistant plant, grown mainly in the semiarid regions of Rajasthan, Haryana, Gujarat, Punjab, Madhya Pradesh and some parts of Uttar Pradesh. Cluster bean is a well known industrial crop due to the galactomannan contained in its endosperm. Expressed Sequence Tags (EST) are considered as a quick and inexpensive source for obtaining Simple Sequence Repeat (SSR) markers. Available *C. tetragonoloba* EST (16108) sequences were mined from dbEST of NCBI. EST sequences were trimmed using EST trimmer and assembled into contigs

using CAP3. The candidate SSR containing sequences in the assembled contigs (1755) and singlet sequences (4320) were detected using the PERL script MISA. We found 327 and 580 EST containing sequences in contigs and singlet sequences, respectively. Mononucleotide 'A/T' repeats were the most abundant among the SSR types in *C. tetragonoloba* ESTs. Primers flanking the SSR regions were designed using primer3. Polymorphism is being tested in the primers obtained. The results of this study can be used for genetic studies and crop improvement in cluster bean.