J Biotechnol Biomater 2015, 5:6
http://dx.doi.org/10.4172/2155-952X.C1.044

OMICS International
conferenceseries.com

6th World Congress on
Biotechnology
October 05-07, 2015 New Delhi, India

Molecular diversity analysis in cluster bean genotypes using EST-SSRs for disease resistance

Aditi Taneja, Neelam R Yadav and **R C Yadav**
CCS Haryana Agricultural University, India

Cluster bean or Guar (*Cyamopsis tetragonoloba* L Taub) is kharif crop is well adapted to arid and semi-arid regions of the world. It has been used as forage crop for green manuring and as a human food but it has gained the status of an industrial crop due to the presence of gum (galactomannan) in its endosperm which constitutes up to 42% of the whole seed which is used in wide range of industries from paper to cosmetics to mining and explosives. The cultivated guar suffers from bacterial blight disease and causes significant yield losses. Guar breeders are therefore interested in improving commercial genotypes for disease resistance and gum content Genetic diversity based on molecular markers is an important aspect of molecular breeding program. So far, there are limited reports using RAPD, ISSR and SCAR markers which are dominant in inheritance to analyze the genetic diversity in cluster bean or guar. However, genomic, EST-SSRs and RGAs are robust markers for molecular breeding in crops. RGAs are developed from R-genes conferring resistance to diverse pathogens in different plant species, share a number of common functional motifs. The guar germplasm lines along were raised in naturally lit net house and also in dry land research farm. EST-SSRs related to disease resistance were used for DNA amplification in cluster bean genotypes. EST-SSRs used in the study were developed in our laboratory using available EST database. These molecular markers showed polymorphism among all the genotypes. Allele scoring was done for the obtained EST-SSR primers in the form of 0/1 matrix which was used to calculate the similarity genetic distance using 'SIMQUAL' sub-program of NTSYS-PC (version 2.02) software. At a similarity coefficient value of 0.44 two major clusters were obtained. The major cluster II further divided into sub clusters at similarity coefficient value of 0.48. On the basis of genetic distance calculated all the genotypes distributed into 9 clusters.

aditi.nsv@gmail.com

Synthesis of catalase encapsulated silica nanoparticles

Girish C Mohanta[1], **Swati Verma**[2], **A K Paul**[1] and **Akash Deep**[1]
[1]CSIR-Central Scientific Instruments Organization, India
[2]Kurukshetra University, India

Catalase is a ubiquitous enzyme present in almost all life forms that are exposed to oxygen. It belongs to oxido-reductase class of enzymes (E.C No: 1.11.1.6.) and catalyses decomposition of hydrogen peroxide into water and oxygen. Due to its high rate of turnover, abundance, high thermal stability and catalytic activity in large range of pH, catalases have been employed in various applications in food, textile and biomedical industries. However, instability of enzymes in '*in vitro*' conditions poses a big obstacle for their industrial applications. Immobilization of enzymes particularly their encapsulation into an inorganic/organic matrix offers significant advantages such as increasing the stability of enzymes, protection against protease digestion, ease of separation from reaction-product mixture and reusability in industrial applications. Encapsulation of enzymes in porous silica matrices have been one of the most widely used method for immobilization. Early attempts of encapsulation in pre-formed silica matrix resulted into very little encapsulation/loading of enzymes because once an enzyme molecule is encapsulated it blocks the penetration of further enzyme molecules. In the present work, catalase molecules are encapsulated in silica nanoparticles (~100-200 nm) in two steps; Functionalization of catalase surface with (3-aminopropyl) triethoxysilane (APTES) through EDC/NHS cross-linking chemistry, *In situ* silica shell synthesis by TEOS hydrolysis in reverse micro-emulsion system. The APTES group of APTES-catalase will get integrated into silica shell through -O-Si-O- bonds. The catalase at silica nanoparticles (Cat-SiNPs) were characterized through different structural and optical techniques. The enzyme activity of catalase was monitored by modified Goth Method.

girish.csio@gmail.com