

Classification of nitrilases using support vector machine

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Classification of enzymes based on their stability and specificity is one of the most important tasks for their application. Various classifiers such as HMM (Hidden Markov Model) and Neural Network Classifiers previously used are found to be less sensitive and accurate as compared to Support Vector Machines (SVM's). Continuous increase in genomic/proteomic data new nitrilases are being discovered whose annotation and functional assignment of classes to these through various wet lab techniques involve lots of time consuming and laborious experiments. Machine learning techniques such as SVM's can be effectively used to complement them saving time, money and also applicable to various other proteins. In view of this the present investigations aims to describe a novel approach for predicting the two sub classes of the nitrilase on basis of their amino acid composition, a powerful method developed from statistical learning with wide applicability in the field of proteomics. The application of SVM tool have clearly differentiated two of nitrilases with accuracy of 88.46%, specificity 80.77%, accuracy 84.62% and MCC (Mathews Correlation Coefficient) of about 0.69 for the amino acid composition, whereas dipeptide and split amino acid composition showed accuracy of 88.46 % & 84.62% and MCC of 0.73 & 0.69 respectively for aliphatic and aromatic nitrilases.

Biography

Nikhil Sharma is presently working as a research scholar in the Department of Biotechnology and is working in the area of microbial enzyme technology both in vitro and in silico. He has contributed research article & chapter to renowned journals with other many in pipeline.

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Introgression of the low phytate (lpa2) traits into elite maize inbred through marker assisted backcross breeding

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Maize is one of the major food crops used for food and feed industries in World wide. In order to enhance the nutritional quality of maize grains the present study is formulated to develop maize lines with low level of phytic acid. The lpa2 mutant blocks the function of the inositol phosphate kinase gene in the biosynthetic pathway of phytic acid (Victor Robay 2009) and hence resulted in the low phytate maize grains (50 % reduction in phytate Phosphorus). The recurrent inbred lines selected for the crossing programme were environmentally stable with high phytic acid content and agronomically more advanced and adapted to Tamil Nadu agro-climatic condition. The donar lpa2 mutant line is associated with, nearly 50 % reduction in the Inositol (6) phosphate level and was used for introgression programme. Marker assisted back cross breeding method was attempted for the introgression of the alien low phytate (lpa2) mutant locus from the mutant line EC659418 (lpa2) obtained from Victor Raboy, USDA in to the popular inbred lines with high agronomic traits. The hybridization was done between the inbred lines viz., UMI285, UMI395, UMI936 and UMI1008 and the lpa2 line (EC 659418) in Rabi 2009. There was a considerable variation in the level of phytic acid content among the four F₁ s' evaluated during Rabi 2010. Among the four different crosses, the UMI395 x EC659418 (lpa2) was found to have low level of the phytic acid (1.96 mg/100g) with desirable agronomics traits. Genotyping of the F₁ s' was attempted for the identification of the true hybrid. Forty SSR markers of the lpa2 region (1.05 bin) were obtained from the maize gdb database (www.maizegdb.org). Those markers are distributed in the 1.05 bin location in the short arm of the maize chromosome. Out of forty SSR markers screened in the lpa2 region four markers were found to be polymorphic for UMI395 and EC659418. Hence, the marker umc2230 which closely linked (0.4cM) to the lpa2 locus was used as a foreground marker for screening the F₁s. The selected F₁ hybrid was backcrossed further to develop BC₁F₁ generation. The resultant single cross hybrids were again backcrossed to the recurrent parent UMI395 during Kharief 2011. The genotyping of the segregating BC₁F₁ backcross progenies was done with foreground SSR marker umc2230. Among the 75 BC₁F₁ progenies the number of heterozygous progenies was found to be 30. Resultant introgressed lines are advanced to further generations for the development of low phytic single cross maize hybrid.

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