# Trends in Bioinformatics

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## A Taxonomic Analysis of Albumin Seed Storage Proteins in Eight Tunisian Pomegranate (*Punica granatum* L.) Ecotypes

Walid Elfalleh, Narjes Sarrai, Ferdaous Gasmi, Nithal Marzougui and Ali Ferchichi

In order to improve the understanding of the taxonomy of some Tunisian pomegranate ecotypes, albumin fraction from pomegranate seed proteins has been analyzed by means of SDS-PAGE (Sodium dodecylsulphate polyacrylamide gel electrophoresis). The albumin (32% from total storage protein) represents three groups. The first group ran from 116 to 58 kDa, the second group ran from 46 to 33 kDa and the third groups of four subunits ran from 23 to 15 kDa. We conducted two methods to analyze Albumin gel; gel analysis (Gelpro software Ver. 3.1) and Image processing (Image J software Ver. 1.38). Tow dendrograms were obtained with rooted trees from drawgram drawing program. In most cases first and second clusters were in agreement. They practically lead to same cluster group, in exception of supplementary cluster obtained in image processing method with Jebali cultivar. *(Trends in Bioinformatics 1 (1): 1-6, 2008;* ***doi:*** *10.3923/tb.2008.1.6)*

## Study on the Conserved and the Polymorphic Sites of MTHFR Using Bioinformatics Approaches

Muhummadh Khan and Kaiser Jamil

This study determines conservation and functional divergence of Methylenetetrahydrofolate reductase (MTHFR) focusing on sites which bear single nucleotide polymorphisms (SNPs). We constructed its phylogeny and calculated type 1 divergence to identify regions of MTHFR under selection. We found that MTHFR is present throughout the three domains of life; Archaea, Bacteria and Eukarya. MTHFR well conserved preserving its function. It has been reported in earlier studies that polymorphisms in this gene are potential modulators of therapeutic response to anticancer drugs. Hence, SNPs in protein coding region were analyzed for the conservation and functional constraints. We report in this study that SNPs of MTHFR gene occur at sites under functional constraint i.e., these sites tend to be conserved. It is possible that SNPs at such sites could be fixed and propagated in a given population. *(Trends in Bioinformatics 1 (1): 7-17, 2008;* ***doi:*** *10.3923/tb.2008.7.17)*

## *In silico* Mutation Study of Haemagglutinin and Neuraminidase on Banten Province Strain Influenza A H5N1 Virus

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The aim of this study was to analyse the mutation possibility of influenza A (H5N1) virus of Banten Province strain. The H5N1 amino acid sequences of haemagglutinin (HA) and neuraminidase (NA) were analysed by multiple alignment method using BLAST tool, ClustalW and Bioedit 7.0.1. programs. The results of analysis were followed up by mutation analysis using Amino Track, secondary structure, post translation modification analysis, phylogenetic tree and homology modelling. From the analysis, five point mutations were revealed, namely change of haemagglutinin at position 185, 272 and 309 and neuraminidase at position 244 and 252. Conserved region prediction were determined to be at position 1-552 of HA and at position 1-39, 41-251 and 253-449 of NA. Secondary structure prediction showed a change in HA structure at position 309, namely coil into helix transformation and in NA structure at position 244, namely coil into extended strand transformation. Change of hydrophobicity happened only to HA at position 185 and 272. Mutation did not have any influence on post translation modification. Phylogenetic tree analysis and homology modelling also did not reveal the creation of a new strain. *(Trends in Bioinformatics 1 (1): 18-24, 2008;* ***doi:*** *10.3923/tb.2008.18.24)*

## The Phylogenetic Analysis of Animal and Plant D-Type Cyclins

D.R. Salomi Suneetha, P. Ajay Babu and P. Vijay Joshua

The phylogenetic relationships and divergence among different subgroups of plant and animal D-type cyclin sequences are studied. The orthologous plant and animal D-type cyclin translated sequences are extracted from NCBI GenBank database categorically identified as D, D1, D2, D3 and D5 types. Multiple sequence alignment was carried out using Clustal W tool of EBI and phylogram was constructed. Further, distinct nodes of phylogram were identified and their pattern was studied using cyclin signature from Prosite database. The results were discussed in terms of the relationships among different subgroups of D-type cyclins forming distinct nodes of phylogram and the conservation of their patterns at each node. *(Trends in Bioinformatics 1 (1): 25-32, 2008;* ***doi:*** *10.3923/tb.2008.25.32)*