



BioBits

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*Quarterly E-Newsletter from Bioinformatics Centre (Dic)
Kerala Agricultural University, Thrissur*

About Us

The Bioinformatics Centre (DIC) at KAU runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was upgraded to Distributed Information Centre during 2004 to promote Bioinformatics research and education. The Centre enhances access to global information in life sciences especially plant sciences and plant biotechnology involving scientists and students of the University and other S&T institutions and acts as a support centre to the Centre for Plant Biotechnology & Molecular Biology. The Centre is involved in a wide range of research work on plant responses to biotic and abiotic stresses, plant metabolomics using systems biology approaches, plant-pathogen interaction studies and study of active compounds in anti cancer medicinal plants. In addition to this, the Centre offers a credit course in Bioinformatics to post graduate Plant Biotechnology students conducts routine training programmes in Bioinformatics and maintains various databases relevant to agriculture.

Cover Story

Bioinformatics is not only the hub of all life sciences but also the cutting edge knowledge for those who would like to make a breakthrough... Bioinformatics and computational biology involve the use of techniques including applied mathematics, informatics, statistics, computer science, chemistry and biochemistry to solve biological problems usually on the molecular level. Major research efforts in the field include sequence alignment, gene finding, genome assembly, protein structure alignment, protein structure prediction, prediction of gene expression and protein-ligand interactions etc.

Complex computational and biological problems are now being addressed and this has led to significant advances in our understanding of biology. No biological discipline will be unaffected by these technological breakthroughs. Bioinformatics can revolutionize not only the research sector but its judicious application can do wonders in transferring knowledge to millions of marginal farmers of the country. This issue of 'Biobits' present before you the recent, most relevant developments/Research outcomes in Plant Biotechnology/ Bioinformatics.

Cover Story

Plant Bioinformatics

Proteomics & Genomics

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Our Focus

Letters and Ideas

Simplifying SNP discovery in cotton genome

Researchers at Texas A&M and the Southern Plains Agricultural Research Center have developed a strategy that simplifies the discovery of useful SNPs within the complex genome of cotton. The protocol is freely available in a recent issue of *Applications in Plant Sciences* (2015).

The term "single-nucleotide polymorphism" (SNP) refers to a single base change in DNA sequence between two individuals. SNPs are the most common type of genetic variation in plant and animal genomes and are, thus, an important resource to biologists.

The growing popularity of next-generation sequencing has made SNPs a pervasive genetic marker in many areas of plant biology. This technique, however, becomes quite challenging when the species of interest has undergone whole genome duplication events (i.e., polyploidy), as is common in many plant lineages.

According to Dr. Alan Pepper, cotton presents a challenge for SNP marker discovery due to the polyploid origin of the two most widely grown species. So identification of potential SNPs without a reference genome may end up in aligning DNA regions that are duplicated within the genomes of the plants being studied, rather than mapping the orthologous regions between the plants. This problem is particularly acute in recent allopolyploids.



Allopolyploid species are the product of hybridization between two divergent taxa. The genomes of these plants, therefore, contain two very similar copies of their genes--one from each parent.

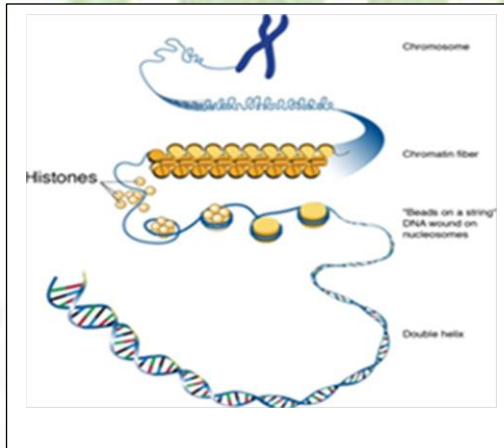
The strategy was presented using the Illumina next-generation sequencing platform, over 50 million DNA reads were collected from restriction enzyme-digested DNA from four *Gossypium* species and the team filtered these reads for pairs of alleles of a single orthologous DNA fragments rather than paralogs or homologs. It was carried out using bioinformatics software known as 'Stacks' (written by Julian Catchen at the University of Oregon).

Pepper concluded that the overall strategy for genotyping-by-sequencing, marker discovery and annotation that have been provided in this study will be useful for researchers working with the many economically important allotetraploid species (such as the crop brassicas), but can be extended to any species, including those that do not currently have a reference genome.

Source: http://www.biologynews.net/archives/2015/04/01/simplifying_snp_discovery_in_the_cotton_genome.html

Genetic inheritance: DNA obeys Histones

Professor Robin Allshire, of the University of Edinburgh's School of Biological Sciences, stated that characteristics passed between generations are not decided solely by DNA, but can be brought about by other material in cells called histones. Scientists studied proteins known as histones, which are not part of the genetic code, but act as spools around which DNA is wound. Histones are known to control whether or not genes are switched on.



Researchers found that naturally occurring changes to these proteins, which affect how they control genes, can be sustained from one generation to the next and so influence which traits are passed on. The finding demonstrates for the first time that DNA is not solely responsible for how characteristics are inherited. It paves the way for research into how and when this method of inheritance occurs in nature, and if it is linked to particular traits or health conditions. It may also inform research into whether changes to the histone proteins that are caused by environmental conditions such as stress or diet can influence the function of genes passed on to offspring.

The research confirms a long-held expectation among scientists that genes could be controlled across generations by such changes. Scientists tested the theory by carrying out experiments in yeast with similar gene control mechanisms to human cells. They introduced changes to a histone protein, mimicking those that occur naturally, causing it to switch off nearby genes. The effect was inherited by subsequent generations of yeast cells. The study, published in *Science* (2015), was supported by the Wellcome Trust and the EC EpiGeneSys Network.

The Scientists, who led the study, showed that changes in the histone spools that make up chromosomes can be copied and passed through generations. Their finding settles the idea that inherited traits can be epigenetic, meaning that they are not solely down to changes in a gene's DNA.

Source: <http://www.sciencedaily.com/releases/2015/04/150402161751.htm>

Diabetes Free Thar: What happens in genes?

Narinder Mehra, Dean of research at the All India Institute of Medical Sciences (AIIMS), New Delhi reported *Nature India* (2015) as given here. A study of the DNA of a nomadic tribe rearing camels called Raikas inhabiting the Thar desert of Rajasthan has overthrown a prevalent notion about the association of certain genes with diabetes. The prevalence of diabetes is almost zero prompting immunologists to discover the reasons.

The researchers found that their DNA contains a very high frequency (53%) of Human Leukocyte Antigen (HLA) gene called HLA-DRB1*03 which shows a remarkably high association with the development of Type 1 diabetes (T1D) in almost all populations around the world including the Indian population. Virtual absence of diabetes in the Raikas despite having a very high frequency of the susceptibility HLA gene is intriguing.

They have given an instance of the people of Sardinia in Italy, a diabetes hotspot, have the highest DRB1*03 allelic frequency of 55.7% and a correspondingly high prevalence of diabetes in the world. Similarly in the North Indian population, their earlier studies revealed that the frequency of this gene rises from a mere 16.4% in the healthy population to less than 90% in patients with T1D.

Sayed Hasnain, Head of Kusuma School of Biological Sciences at the Indian Institute of Technology, Delhi told *Nature India* that this is an outstanding observation directly linking our genes to diabetes.

The researchers explained the possible reasons for the absence of diabetes in the Raikas despite the presence of the susceptibility gene as the influence of protection conferring genes and environmental factors including dietary practices.

Raikas mainly survive on Bajra (*Pennisetum glaucum*) grown in their fields and camel milk. An insulin-like protein has been detected in camel milk, and clinical trials in 2005 by India's Bikaner Diabetes Care Research Centre have shown that the daily consumption of 0.5 litre camel milk reduces the need for insulin medication by an average of 30%. The other possibility is the consistent exposure of the community to sunlight as a part of their lifestyle. High levels of vitamin D might confer a preventive effect on the development of diabetes.

The research group says their study highlights the role of the environmental factors, food habits and level of physical activity in the manifestation of disease and calls for further research to define the gene-environment interaction in the context of a multifactorial disease like Type 1 diabetes.



The camel rearing Raika community with near-zero diabetes prevalence has been intriguing immunologists.

The color of lettuce determines the speed of its antioxidant effect

Antioxidants: Antioxidants provide long-term protection against the chain reactions of free radical processes. Free radicals harm our body by causing, in the best of cases, ageing and, in the worse, serious diseases. Lettuce is rich in antioxidants, as it contains compounds like phenolic acids, flavonoids, anthocyanins, and vitamins A and C, among other things.

Green, semi-red and red leaves: Since 2011, the researchers of the UPV/EHU, Faculty of Science and Technology and the University of Pisa (Italy) have been analyzing the compounds of three lettuce varieties: the green-leaf 'Batavia', the semi-red-leaf 'Marvel of Four Seasons', and the red-leaf 'Oak Leaf'. Using Electron Paramagnetic Resonance (EPR) techniques, they were able to observe the behavior of the kinetics of the compounds of each variety and the results show that the green-leaf lettuce contains water-soluble, antioxidant compounds that act at a slow and intermediate speed, the red-leaf one has compounds with intermediate and rapid kinetics, and the semi-red-leaf one has three kinds of compounds, with a



Dr Usue Perez stressed the fact that there are compounds that act at different speeds does not mean that some are better or worse than others. He also stated that, at the same time, it is also important that our bodies should acquire foods with antioxidants that have slower kinetics so that the latter will continue to act over a longer period of time.

Boosting the properties: Having determined the kinetics of the antioxidants, the research group is working towards achieving a nutraceutical improvement of these three varieties of lettuce. They are trying to boost the effect of the specific compounds in each variety by subjecting the plants to short stresses (such as watering them with salinated water, subjecting them to high lighting intensity or working with raised concentrations of CO₂). These compounds perform defense functions in plants and, as a result, the antioxidant qualities of the plants will be boosted.

The research confines to short-intensity stresses as excessive stress may reduce the plant growth. Their aim is to maintain production and achieve greater quality in this production.

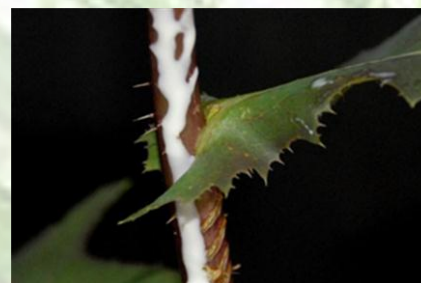
Source: <http://www.biocompare.com/Life-Science-News/172896-The-color-of-lettuce-determines-the-speed-of-its-antioxidant-effect/>

Rubber from lettuce using genetic marker

Ian Burke, a weed scientist at Washington State University and co-workers described the plant prickly lettuce's genetic code linked to rubber production in the *Journal of Agricultural and Food Chemistry* (2015). The findings open the way for breeding for desired traits and developing a new crop source for rubber in the Pacific Northwest *ie.* prickly lettuce could become a temperate-climate crop as a source of natural rubber.

Potential for sustainable source

In prickly lettuce, the wild relative and ancestor of cultivated lettuce, a milky white sap bleeds from the stem which could prove to be an economically viable source of natural rubber and help alleviate a worldwide threat to rubber production.



The milky sap, or latex, of prickly lettuce could be used to produce rubber.

Natural rubber is the main ingredient for many everyday products, from boots to condoms to surgical gloves. Roughly 70 percent of the global supply of rubber is used in tyres. But more than half of rubber products are made from synthetic rubber derived from petrochemical sources and the largest source of natural rubber, the Brazilian rubber tree, is threatened by disease.

After reviewing many studies of prickly lettuce and its cultivated cousins, the researchers highlighted a study published in 2006 stating that the latex in prickly lettuce was very similar to the polymers found in natural rubber.

Genetic markers for desired traits

Burke, doctoral student Jared Bell and molecular plant scientist Michael Neff began their studies with two distinct samples of prickly lettuce collected from eastern Washington. These differed in their rubber content, leaf shape and tendency to bolt. However, the rubber content in the two lettuce plants and their productivity are not mentioned here.

The scientists were able to identify genetic markers not only for rubber content but for the way the plants grow, including the number of stems produced and bolting. Sought-after traits in cultivated lettuce – like abundant leaves, a single stem and delayed bolting – are the exact opposite of traits desired for rubber production. Early bolting plants with multiple stems would allow for multiple harvests over the season and potentially maximize rubber yields and selection for other traits, like water use efficiency, could allow prickly lettuce to be grown with minimal rainfall by crop rotation.

Source: <http://www.sciencedaily.com/releases/2015/04/150406133615.htm>

The Centre is involved in a wide range of research work like plant-pathogen interaction studies, study of active compounds in medicinal plants, *in-silico* analysis of phytochemicals against various diseases and creation of databases and their maintenance. *In silico* docking studies on phytochemicals are carried out to predict the preferred orientation of one molecule to a second when bound to each other to form a stable complex. The binding efficiency, interaction and dock score would help a long way in identifying novel phytochemicals against serious diseases.

This particular column is especially for readers and those who are interested in the field of Bioinformatics. Here we are creating a new opportunity to share your valuable ideas with senior scientists. So post your comments and suggestions to mail bic@kau.in or kaubioinfo@gmail.com.

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