



# 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**

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**Proteomics & Genomics**

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## Plant-fungal symbiosis genes uncovered by researchers

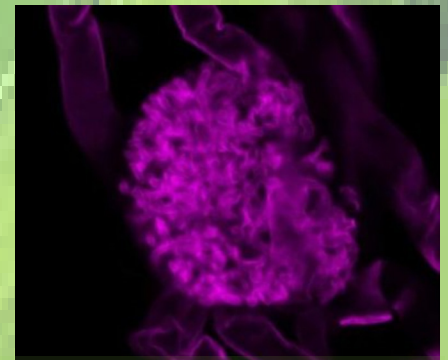
A new study by researchers at Boyce Thompson Institute (BTI) has uncovered a veritable trove of genes used by plants to form symbiotic relationships with nutrient-bearing soil fungi called arbuscular mycorrhizal (AM) symbiosis, vastly increasing the knowledge of the genetic basis for this agriculturally valuable interaction.

Despite decades of research, many of the genes involved in symbiotic relationship remain elusive. Now, with the advent of widely available genome sequences, BTI researchers were able to compare 50 plant genomes to identify 138 genes shared exclusively by plants capable of AM symbiosis. The findings, which appeared in the journal *Nature Plants*, 2016 may ultimately bring us closer to developing plants that thrive without added fertilizer. They compared the genomes of plants that form these symbiotic relationships to those that do not. A better understanding of the genetic basis of the symbiosis may one

day yield better crop plants that require less fertilizer input. According to Armando Bravo, a postdoctoral scientist and an author of the study said that the approach relies on the idea supported by fossil evidence, that AM symbiosis evolved just once, early on in the evolution of land plants, so all plants that host the symbiosis likely inherited a similar set of genes. Plant groups that lost the ability to form symbiosis are presumed to have lost the required genes.

A comparison study of the genome sequences of 34 plant species that can form the symbiosis with 16 that cannot was carried out by a bioinformatics analyst at BTI. Together, they picked out 138 genes that are found only in plants that form AM symbiosis from an initial list of 62,000 possibilities. Fifteen of these were already known to play a role in AM symbiosis and the accuracy of seven of the unknown genes in the group was tested by growing barrel medic with mutations in those genes and examining their ability to form a successful symbiosis. Mutations in six of these genes resulted in a faulty interaction. Analysis of the new genes that were found highlighted the importance of lipid biosynthesis during symbiosis. While the analysis cannot single out every gene that a plant needs for symbiosis, it did pick out the ones that serve no other function except in symbiosis.

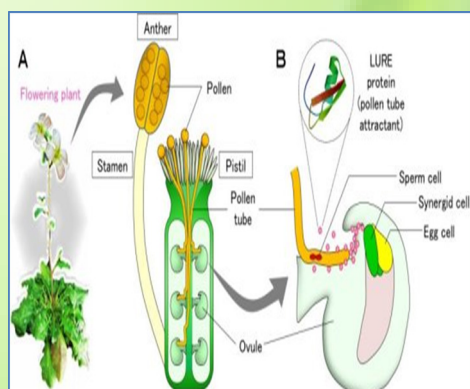
One of the authors of BTI said that it showed the power of bioinformatics to answer questions more powerfully if we have lots of genomes for analysis. In the future, the researchers plan to investigate the remaining 131 genes and to use them to learn more about the development and regulation of the symbiosis. Almost all staple food crops form AM symbioses, so optimizing this interaction through crop breeding could improve yield and reduce the need for fertilizers.



*A fungus forming a microscopic, tree-like arbuscule inside a plant root cell, which enables the fungus to transfer soil nutrients to the plant.*

## Where males sense females in plants ?

The researchers of the JST-ERATO Higashiyama Live-Holomics Project and the Institute of Transformative Bio-Molecules (ITbM) of Nagoya University have succeeded in discovering a key kinase receptor in the pollen tubes (male) of flowering plants responsible for allowing the pollen tubes to precisely reach the egg cell (female) to enable successful fertilization, without losing its way.



Pollen tube growth and guidance by the LURE peptide in *Arabidopsis*.

Pollen tubes grow inside the pistil and deliver their sperm cell to egg cells, which are located deep inside the pistil, to bring about fertilization. Higashiyama's group has previously discovered a pollen tube attractant peptide, called LURE, which is produced by the ovule to guide the pollen tube towards the egg cell. Studies have shown that the structure of LURE differs for each plant species and is specific for each plant's pollen tube, i.e. each LURE peptide preferentially attracts the pollen tube of the same plant species. However, the exact mechanism on how pollen tubes detect LURE has been unknown up to now.

In this study, published online on March, 2016 in the journal *Nature*, scientists have discovered a receptor that is required for detection of LURE at the tip of the pollen tube for the model plant, *Arabidopsis thaliana* (thale cress). By accepting the various signals sent from the pistil, the kinase receptors enable the pollen tubes to grow to a position inside the pistil where they can detect LURE. Subsequently, the pollen tubes are guided to reach the egg cell and pass on their sperm cells for fertilization.

In 2009, the research team discovered that a synergid cell, which is located next to the egg cell, produces molecules called LUREs that attract pollen tubes in *Torenia* plants. They also discovered similar LURE peptides in *Arabidopsis thaliana* in 2012. The generation of seeds through the fertilization of the pistil by the stamen has been known for over 2000 years ago and is an extremely important mechanism in agriculture. This study also reveals that the PRK6 receptor in pollen tubes is the main factor for detection of and growth towards LURE.

The researchers found that the insertion of a kinase receptor gene PRK6 allows attraction of the pollen tube of a different species. This may have potential in developing new methods to enable fertilization between different species. It would also lead to the development of techniques to increase the success rate in fertilization and improve the efficiency of seed production. Exploring molecules that target PRK receptors may lead to the production of agrochemicals that can improve seed production by increasing the fertilization rate. This study would trigger new research to enable fertilization between different species to create new and useful plant species that can contribute towards a sustainable food supply.



## An algorithm for faster and more accurate study of DNA

A team of scientists from Germany, USA, and Russia, including Dr. Mark Borodovsky, a Chair of the Department of Bioinformatics at MIPT, have proposed an efficient algorithm called BRAKER1 to automate the process of searching genes. The new development combines the advantages of the most advanced tools for working with genomic data which will enable scientists to analyse DNA sequences faster and more accurately and identify the full set of genes in a genome. The paper describing the algorithm appeared recently in the journal *Bioinformatics* (2016), which is published by Oxford Journals.

One of the most important areas of bioinformatics is annotating genomes -- determining which particular DNA molecules are used to synthesize RNA and proteins. These parts - genes are of great scientific interest. In many studies scientists do not need information about the entire DNA but only about its most informative part, the genes. Gene sections are identified by searching for similarities between sequence fragments and known genes, or by detecting consistent patterns of the nucleotide sequence. This process is carried out using predictive algorithms.

Locating gene sections in eukaryotes is a tedious task due to the fact that in these cells, the transfer of genetic information is complicated by "gaps" in the coding regions (introns) and because there are no definite indicators to determine whether a region is a coding region or not. The algorithm proposed by the scientists determines which regions in the DNA are genes and which are not.

BRAKER1 is a pipeline for unsupervised RNA-Seq-based genome annotation that combines the advantages of a gene prediction algorithm, GeneMark-ET and a gene finder algorithm, AUGUSTUS. It enables scientists to work effectively with the genomes of new organisms, speeding up the process of annotating genomes and acquiring essential knowledge about life sciences. The project was launched in 2008 involving researchers from 75 different laboratories and companies. As a result, sequences of rare gene variants and gene substitutions were discovered, some of which can cause disease. When diagnosing genetic diseases, it is very important to know which substitutions in gene sections cause the disease to develop. Under the project, genomes of different people were mapped, especially their coding sections, and rare nucleotide substitutions were identified. In the future, this will help doctors to diagnose complex diseases such as heart disease, diabetes, and cancer.

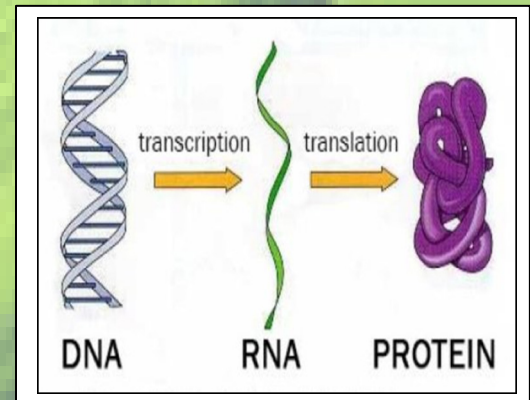
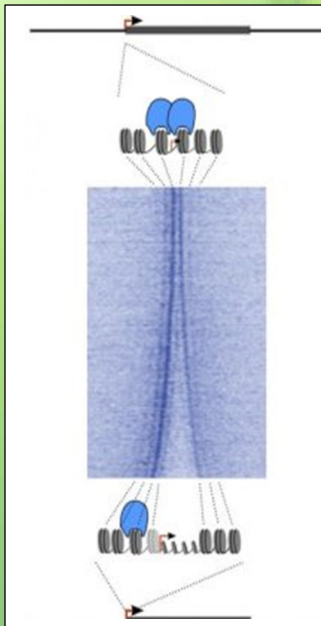


Diagram showing the transmission of hereditary information in a cell

## Discovered: How to unlock inaccessible genes

An international team of biologists from Penn State University and University of Paris-Sud in France has discovered how specialized enzymes remodel the extremely condensed genetic material in the nucleus of cells in order to control which genes can be used. The discovery was published in the print edition of the journal *Nature* on February, 2016. The research revealed that some remodeller enzymes promote gene expression, some repress gene expression, and some can do both.

It was known that the DNA in cells is wrapped around proteins in structures called nucleosomes that resemble beads on a string, which allow the genetic material to be folded and compacted in to a structure called chromatin. The compaction into chromatin makes genes inaccessible to the cellular machinery necessary for gene expression, and the enzymes opened up the chromatin to specify which genes were accessible and could be expressed in a cell, but until now, the mechanism by which these enzymes functioned was unknown.



*This image shows the binding profile of chromatin remodelers on 12,000 distinct genes. Visualized using bioinformatics*

The discovery was achieved by an international collaboration of scientists from the Alternative Energies and Atomic Energy, the National Center for Scientific Research in France, the University of Paris-Sud in France, Southern Medical University in Guangzhou in China, and Penn State University in the United States. The researchers first mapped the location of several "chromatin-remodeller enzymes" across the entire genome of the embryonic stem cells of the mouse. The mapping showed that remodeller enzymes bind to particular nucleosomes "beads" at the sites along the wrapped-up DNA that are located just before the gene sequence begins. These sites are important because they are the location where the process of expressing genes begins - where other proteins required for gene expression team up for the process of turning a gene on.

The researchers then tested how the chromatin-remodeller enzymes impact gene expression by reducing the amount of each of these enzymes in embryonic stem cells. The scientists found that some chromatin-remodeller enzymes promote gene expression, some repress gene expression, and some can do both. These enzymes help each cell type accurately express the proper set of genes by allowing or blocking access to the critical section of DNA at the beginning of genes.

**Source:** <https://www.sciencedaily.com/releases/2016/01/160129134413.htm>

## Gene trigger for asexual reproduction discovered

A German-Israeli team led by the biologists Professor Ralf Reski from Freiburg and Professor Nir Ohad from Tel-Aviv has discovered a gene trigger in the moss *Physcomitrella patens* which leads to offspring without fertilization. When a sperm and an egg cell merge a new life begins. Just like humans and animals, mosses possess egg cells and motile sperm. That is why they are particularly well-suited to answer fundamental questions in biology, Reski said. The researchers assume that this mechanism is conserved in evolution and holds the key to answer fundamental questions in biology. The study is published in the journal *Nature Plants*, 2016.

After fusion of sperm and egg cell, a network of genes is activated. That leads to the development of an embryo which grows into a new living being. Until now it was unclear whether a central genetic switch for this gene activation exists. In their latest publication the team described the gene BELL1 as a master regulator for the formation of embryos and their development in *Physcomitrella*. After the researchers activated this gene in the plants by genetic engineering, embryos developed spontaneously on a specific cell type. These embryos grew to fully functional moss sporophytes. These spore capsules could even form spores, which grew into new moss plants. Thus, the team identified BELL1 as a master regulator for embryo development in mosses. The protein encoded by this gene belongs to the class of so-called



*Physcomitrella patens* moss plantlet with a spore capsule

homeobox transcription factors. Similar homeotic genes are also present in humans and animals, where they also control pivotal developmental processes. Whether a congener of BELL1 is a master regulator of embryo development in humans is not yet known. The researchers explained how algae developed into land plants and thus shaped our current ecosystems and how they helped to revive the concept of genetic master regulators in the development of plants, animals and humans. The researchers also said that their results may help to modernize agriculture through the creation of genetically identical offspring from high-yielding crop plants. In seed plants such offsprings are formed by parthenogenesis or apomixis.

**Source:** <https://www.sciencedaily.com/releases/2016/01/160118134942.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 phyto compounds 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.



## **Antidiabetic and Anticancer Medicinal Plants Database (DIACAN)**

Medicinal plants and plant derived molecules are widely used in traditional cultures all over the world and they are becoming increasingly popular among biomedical researchers and pharmaceutical companies as a natural alternative to synthetic medicine. Information related to medicinal plants and herbal drugs accumulated over the ages are scattered and unstructured which make it prudent to develop a curated database for medicinal plants with taxonomical hierarchy, useful parts of the plants, name of phytochemical isolated from the plant and therapeutic uses. DIACAN- The antidiabetic and anticancer medicinal plants database aims at providing an integrated platform for plants and phytochemicals having antidiabetic or anticancer activity. Currently, DIACAN contains 437 antidiabetic plants, 239 anticancer plants, 242 anticancer phytochemicals and 340 antidiabetic phytochemicals with information on structure, therapeutic applications and manually curated published references for users. Availability: DIACAN is freely available for non-commercial use at <http://www.kaubic.in/diacan/>

### *Publications*

- James, P., Vipin, A.M., Silpa, S., Antony, P., Parvathi, S. and Keshavachandran, R. 2013. DIACAN: Integrated Database for Antidiabetic and Anticancer Medicinal Plants. *Bioinformation*. 9(18): 941–943
- Mala, S.K., Antony, P., Baby, B. and Nazeem, P.A. 2015. Bioactive compounds to target anti apoptotic proteins- Bcl 2 and Bcl XL - an in silico approach. *Int. J. of Phar. Sci. and Res.* 6 (7): 3034-3043
- Mohan, M., James, P., Ravisankar, V., and Nazeem P.A. 2015. Molecular docking studies of phytochemicals from *Phyllanthus niruri* against Hepatitis B DNA Polymerase. *Bioinformation*, 11(9): 426-431



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](mailto:bic@kau.in) or [kaubioinfo@gmail.com](mailto:kaubioinfo@gmail.com).

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### *How to Reach Us*

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