Volume 12, Issue 07, July, 2019



About us

Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division) North-East Institute of Science & Technology Jorhat -785006, Assam (http://www.rrljorhat.res.in/biotechnology.html)



Inside.....

About us	1
Cover story	1
softwares/tools	2
Bioserver/softwares/tools	2
Bioinfo. Animation	3
Upcoming Events	3
Molecule of the month	4

Contact Us

Advisor:

Dr Samit Chattopadhyay

Editors:

Dr Y S Devi

Dr R Saikia Dr SB Wann Dr H P Deka Baruah

Ms. Esther Jamir Ms. Kasmika Borah Ms. Ng Yaipharembi Ms. Priyakshi Nath Ms. Debjani Chanda



chemistry, computer aided drug design, genomics and proteomic data analysis etc.

CRISPR-Cas9 technology in translational research and its recent advancements.

The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was established on 2nd February, 2008 to promote innovation in Biological research and education through Bioinformatics accomplishment. The main goal is to facilitate and expose students and researchers from different academic institutions of North East India in Bioinformatics. The center conduct training and workshops for enlightening the use of bioinformatics applications in biological research and development. The Centre has access to global information through 24 hour high speed internet facility, and also e-journal facilities with DeLCON, Science Direct etc. To date the Centre has profoundly extended support in R & D work with a great intensity to different biological discipline including medicinal

CRISPR-cas9 technology is a unique technology that enables geneticists and medical researchers to edit parts of genome. Expanding CRISPR-Cas9 technology is an easily accessible, programmable and precise gene-



Figure 1. Genome Editing Technologies Exploit Endogenous DNA Repair Machinery

editing tool with numerous applications, such as in biomedical research. There are major advancements in the application of CRISPR-Cas9 in genetic diseases. Successful examples include gene rectification in Duchene muscular dystrophy, sickle cell disease (SCD), β-thalassemia and hereditary tyrosinemia type I (HT1) . Specifically for DMD, some data regarding the efficacy and safety of CRISPR-Cas9 gene editing are available from studies on large animals. Considerable ethical and regulatory issues remain to be addressed but major progress has been made with the use of CRISPR-Cas9 technology to rectify pathogenic gene mutations in human embryos. The CRISPR-Cas9 base editor (BE) has been reported to yield targeting efficiency of 89% in rectifying FBN1 mutations in Marfan syndrome but only 23% in rectifying HBB -28 (A > G) mutations in b-thalassemia. More encouragingly, CRISPR-Cas9 gene editing has successfully helped rectify MYBPC3 mutations associated with hypertrophic cardiomyopathy in human embryos, with a targeting efficiency of

72.2%, and embryos exhibited no mosaicism, no off-target gene editing, and no other abnormalities. CRISPR-Cas9 genome editing has been considered a powerful tool in cancer research. The technology can be used to investigate tumorigenesis and tumor invasion. Encouraging studies suggest that CRISPRCas9 is valuable for the rapid development of cancer immunotherapy.

Recent years have witnessed deepening functional dissection and the ever-expanding translation prospect of CRISPR-Cas9 tools, yet translating these into the clinic remains intractable. Safety is one of those factors that hold us back, including uncontrolled off-target effects, potential immunogenicity, and immunological adverse effects. Efficiency is another one, because advanced-tumor patients after multiline therapy have insufficient immunity and anergic even exhausted immune cells. Altogether, notwithstanding significant advancements and newly emerging challenges for CRISPR-Cas9 technology, major improvements and therapeutic applications can be envisioned.

Human papilloma virus its molecular characterization, phylogenetic analysis and its prevalence in married woman.

Human papillomavirus is the most common sexually transmitted infection. Human papilloma viruses (HPVs) are responsible for causing cervical cancers, which affect a large number of individuals of the younger generation, also cause cancers of the vagina, vulva, penis, and anus, as

well as infections of the head and neck region, conjunctiva, ear canals, nasal sinuses, and oral cavities .cervical cancer is the second most common cancer in the world among women, after breast cancer which has a higher frequency of incidence and rate of mortality in developing countries than in developed countries. Genotypes of HPV are divided into two categories—high-risk (HR -HPV) and low-risk (LR-HPV)-according to their ability to cause cancer.

The HPV-DNA test is recommended for the detection of patients with infection in the latent period and that of HPV types. HPV-DNA detection is also necessary to produce effective vaccines. Women positive for the presence of HPV-DNA are considered to be infected and follow-up of HPV infections is based on HPV-DNA measurements at four, six, and twelve-month intervals. Phylogenetic analyses and determination of the similarity of the HPV strains isolated from different regions help to clarify how viral genes and species de-Figure 1.Human Papilloma virus infection and its

velop, and which strains should be used for developing effect in causing cancer such as Cervical Intraepithevaccines. Steps for studying Human Papilloma Virus lial Neoplasia (CIN) are 1. collection of cervical samples 2. collection of



play a role in Healthcare.

specimen 3. isolation of DNA samples homogenized by vortexing. 4. Polymerase Chain reaction 5. Sequencing and phylogenetic analysis using the Sanger Sequencing method 6. statistical analysis using χ^2 method.

In order to contribute to vaccine studies and to enrich the global HPV data, it is necessary to perform a greater number of such studies with larger sample sizes. The reason for the low rate of HR-HPV in this study is probably the fact that the subjects include women without malignant conditions. It is possible to say that their traditional and conservative lifestyle also contributes to the low rate of HR-HPV. Nonetheless, 1.5% women representing the normal population are at a risk of encountering HR-HPV strains.

Source: Ayse Erdem Yayla et al, 2019 Korean Society of Obstetrics and Gynecology.



1.<u>https://in.explara.com/e/ngs-data-analysis-genome-editing-crispr-mumbai</u>

2. https://in.explara.com/e/ngs-data-analysis-genome-editing-crispr-mumbaihttps://biotexcel.com/event/genomic-medicine-2019-cambridge/

AMPA Receptor

A neurotransmitter is a small molecule released at the presynaptic axonal membrane of one neuron into the synaptic cleft to bind with the receptors present in the postsynaptic membrane of another neuron and result in either excitation or inhibition of the passage of signals across the synapse, such as acetylcholine, serotonin and endorphins, are present in the nerve cells of the



brain. Glutamate (Amino acd) ,one of the most common neurotransmitters when released by neurons into synaptic clefts carry excitatory signals and stimulate neighboring neurons by binding to glutamate-specific receptors.

AMPA receptors through they serve as receptors for excitatory synaptic transmission mediated fast by glutamate and allow calcium and other cations like sodium and potassium to flow through the membrane. They have modular structures, and each part has an activity of its own to perform. The top of the receptor recognizes and binds to glutamate and to much similar neurotransmitters and the the bottom portion forms an ion channel through the membrane. AMPA mechanism of action results when change in shape takes pace due to binding of glutamate to the receptor, causing channels to open and allow movement of ions through the membrane. The property of an additional tail at the bottom, of the receptor, flexible in nature interacts with scaffolding proteins and contribute in organizing the structure of the neuronal synapse.

AMPA receptor, with an inhibitor (red) bound to the glutamate-binding domains. The location of AMPA receptors each have four chains, each with a separate the cell membrane is shown schematically in gray binding site for glutamate . Simple action of AMPA recep-

tor shows closing of receptor immediately after receiving a message and becoming desensitized for a time against additional messages. Layers of complexity help to store memories, by adding more receptors to a synapse or taking them away, or by modifying amino acids in individual receptors to increase their level of action more complex. Several accessory proteins bind to AMPA receptors, such as the TARP protein. Receptors such as NMDA and kainite receptors which help to build up the rich envi-

thought., have proven to be much useful discovery.



ronment of signaling that controls our inner world of Three types of ionotropic glutamate receptors. An accessory protein is shown in green bound to the ion channel portion of the AMPA receptor

Source: http://pdb101.rcsb.org/motm/235

Kindly send us your feedback to

Dr Ratul Saikia BIF Center, Biotechnology Group, BSTD CSIR-North East Institute of Science and Technology, Jorhat, Assam E-mail: rsaikia19@gmail.com

Dr Yumnam Silla Devi BIF Center, Biotechnology Group, BSTD CSIR-North East Institute of Science and Technology, Jorhat, Assam **E-mail:** bio.sillayumnam@gmail.com