



## **IIIT Delhi's Department of Computational Biology offers life-changing solutions against the threats posed by Covid-19 vaccine**

New Delhi, 08<sup>th</sup> October 2020: Given the sheer magnitude of devastation caused by the Covid-19 pandemic, various companies all over the world have entered a race to become the first company to produce the vaccine for the dreaded Covid-19 strain. Several vaccines are under clinical trials but they're still not showing positive results as they still seem to be struggling with several limitations, including side-effects.

However, the ever-innovative Computational Biology Department at IIIT Delhi, India's leading technology-driven institute has reviewed these different vaccines and has come up with several probable solutions to overcome the challenges faced by the doctors, genetic engineers, and epidemiologists in developing a viable vaccine for the virus.

In most cases, vaccine targets are all viral proteins or a specific protein, mainly spike protein. According to research studies that have been previously conducted on Coronavirus strains these vaccine targets may cause a wide range of side effects, including induction of cytokine storms (i.e., IL6), lung immunopathology, hepatitis, hemotoxicity, cytotoxicity, cross-reactive antibodies, allergenicity. The Computational Department at IIIT Delhi has discovered that switching from proteins to epitopes/peptides as viable vaccine candidates will help overcome the side effects. The department has also suggested that there is a need to utilize computer-aided techniques for the identification of potential vaccine candidates to fight against COVID-19.

It has also been noted that many patients who are infected with Covid-19 remain asymptomatic but prone to transmitting the disease. This means that both innate and adaptive immunity play a role in the transmission of Covid-19 but how their interaction mediates viral control as well as host toxicity, and it is, therefore important to keep these things in mind while designing the vaccine for the disease.

Addressing the importance of utilizing bioinformatics in finding the right vaccine, Gajendra P. S. Raghava from Department of Computational Biology, IIIT Delhi, said, *"There are many in silico tools that can predict interleukin-inducing properties, pro/anti-inflammatory properties as well as the toxicity of the peptides. Besides this, many in silico tools are available for designing subunit vaccines and immunotherapeutics. There are 244,682 proteins and 22,892 nucleotide sequence information about SARS-CoV-2 available in the NCBI virus datahub, as of September 8, 2020. It is quite obvious that all 244,682 proteins cannot be a vaccine candidate; this means that we can use various in silico tools to identify potential vaccine candidates to speed up the process."*

*"As we move to dedicate our precious time and resources towards developing much-needed vaccine against Covid-19, we should rely on bioinformatics resources as they will help us significantly cut down the chances of failure. Given the urgency of the matter, the vaccines are being pushed through the trials at a frenetic pace, which has significantly increased the chances of severe side effects. Given the scale to which the crisis has evolved, we need to*

*speed up the trial and this can be done by reducing the number of vaccine candidates instead of dropping the subset of populations and reducing the numbers. Bioinformatics resources may aid to a greater extent while eliminating those most likely to cause side effects. The pandemic has taken a serious toll on the physical and mental well-being of the entire global population and it's about time we leverage the power of bioinformatics to combat the issue,"* added Salman Sadullah Usmani, Research Associate from Department of Computational Biology, IIIT Delhi.

For more details, please contact:

Mr. Sumit Kumar: +91- 9999560239

Ms. Simran Jain: +91-8368504309