A new model for TB drug discovery proposed

By Sunderarajan Padmanabhan

New Delhi, April 20 (India Science Wire): A group of Indian scientists has developed a new model of drug discovery that promises to help in finding non-toxic drugs against tuberculosis in future.

The emergence of multidrug and extreme drug resistant TB is of great concern as these forms of the infection can lead to persistently progressive disease with a high morbidity and mortality rates. The treatments of resistant forms of TB are longer and may also require the use of second line drugs, that are also expensive, more difficult to procure and more toxic. To deal with the situation, over the years extensive efforts have been undertaken in different parts of the world to develop newer therapeutics and targets. However, the drug discovery pipeline has not been able to keep pace with the need.

The new model promises to solve the problem and help fuel the pipeline by providing a more effective starting point for medicinal chemists in generating new chemical leads. It is based on systems biology and provides for a deeper understanding of the complex biological responses of the bacteria with a view to help predict its non-toxic metabolic targets.

The team has proposed a new integrated methodology that employs systems level analysis followed by genome-scale variation analysis of the clinical isolates and then structure wise chemical tailoring of molecules.

The team of scientists is led by Dr. Samir Brahmachari, presently a J.C Bose National Fellow and former Director General of Council of Scientific and Industrial Research along with his post doctoral associate Dr Divneet Kaur.

Dr. Samir Brahmachari and his colleagues, who have developed a new model for TB drug discovery.

Speaking to India Science Wire, Dr Brahmachari, said the methodology was tested on a list of 890 metabolic genes which were identified with the help of a novel systems biology spindle map approach adopted in his previous study and the results were highly promising.

The study highlights the most critical targets in pathogenic organism like TB bacteria which should be evolutionarily conserved and functionally critical. In other words they should not have too many genetic variations.

“The new methodology raises hope that in-silico drug designing based on integrated experimental data will reduce the cost of drug designing by reducing the chance of failure at the clinical trial level”, he added.

The team has published its findings in journal *Scientific Reports*. The co-authors of the paper are: Divneet Kaur, Rintu Kutum and Debasis Dash. The team works at CSIR’s New Delhi based Institute of Genomics and Integrative Biology. (India Science Wire)