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NEW OPEN ACCESS DATABASE TO SPUR DEVELOPMENT OF MEDICINES FOR INFECTIOUS DISEASES OF THE DEVELOPING WORLD

GENEVA - An international network of researchers announced today the release of a new web-based resource designed to facilitate the development of medicines to fight infectious diseases afflicting the developing world. The Drug Target Prioritization Database may be accessed at http://TDRtargets.org.

"This is the first time that any group has assembled such a comprehensive set of information pertinent to drug target discovery, for such a diverse array of parasitic and bacterial diseases," says Dr. Wesley Van Voorhis from the University of Washington in Seattle, who coordinates the Drug Target Prioritization Network, which was established by the World Health Organization (WHO) based Special Programme for Research and Training in Tropical diseases (TDR) in 2005. The consortium includes a global team of academic laboratories, research centres and industry scientists, focusing on the pathogens responsible for malaria, tuberculosis, African sleeping sickness, leishmaniasis, Chagas disease and worm infections such as schistosomiasis and filariasis -- all of which are in desperate need of new treatments.

Together, these diseases are responsible for billions of infections in the developing world, and more than six million deaths per year. Since poor countries often don't have the funding or infrastructure to support health research and drug development, new collaborations like this one are working to improve the situation, providing a resource that brings together scientists from all over the world.

The network's goal is to identify and prioritize drug targets against diseases that predominantly affect developing countries. The database is unique in that it allows any researcher -- in both developed and developing countries -- to have access to this kind of information. Dr. Fernan Aguero, a member of the network from Argentina, who has been responsible for engineering much of the database architecture says, "I am very excited about the impact that this resource will have on the opening of new avenues for drug discovery. Through this collaborative effort we have an opportunity to develop new treatments for our citizens and others around the world."

The network "provides an outstanding example of how WHO can bring together multiple groups to develop joint solutions," says Dr Robert Ridley, Director of TDR. "We help to convene appropriate individuals and develop expertise within the countries that need it, leveraging global research resources to develop new treatments."

The database is building on a decade of intensive international investment that has already resulted in the complete genome sequences for organisms responsible for five tropical diseases, with more anticipated for the parasitic worms known as helminths. Pharmaceutical firms have

extensive libraries of chemicals that might act against the disease pathogens. The missing step, which this initiative takes, is to make available a list of proposed and validated drug targets, in addition to allowing users to define their own search criteria. Dr. David Roos of the University of Pennsylvania Genomics Institute, who has been primarily responsible for the database design, says, "This website allows researchers to prioritize drug targets by defining criteria tailored to the capabilities of their particular program. For example, a university laboratory that excels in studies on one class of drug targets can identify those enzymes that look most promising as drug targets, while a pharmaceutical company may select candidates tailored to their particular drug compound collections or expertise in assay development."

Dr. Solomon Nwaka, who leads drug discovery activities at WHO/TDR, says that this resource should expedite the time-consuming and high-risk early stages of drug development. "There is a growing awareness of the need for new therapeutic targets for these diseases. Pharmaceutical firms are increasingly interested in screening their chemical libraries against parasite targets, but a comprehensive list of validated drug targets for these organisms has not been readily available. The original intent of this project was to develop a 'top 10 list' of validated targets for each pathogen, but it quickly became apparent that enabling researchers to customize criteria for target selection in the database will provide added benefits, including the flexibility to continuously update the database."

The TDRtargets.org website combines available genomic and bioinformatic data for each priority organism with automatically extracted and manually curated information from the research literature and other databases relevant to each putative drug target. The network has invested substantial effort in annotation to assist scientists in the identification of high-value drug targets. The database also permits comments from experts in the field. User-defined weightings permit potential drug targets to be ranked according to their desirability, providing prioritized, customized lists. While this network was developed to facilitate drug target identification, it is highly likely to be useful for the identification of vaccine and diagnostic targets as well, and could spur fundamental research into areas such as target validation, assay development, biomarkers and drug resistance.

The network includes investigators from the Universidad Nacional de General San Martín (Argentina), the Sanger Institute (UK), the University of Melbourne (Australia), the University of Pennsylvania Genomics Institute (USA), and the University of Washington Seattle (USA). In kind support and information relevant to target structure, essentiality, and druggability has been provided by Pfizer, Inpharmatica, the University of California, San Francisco and New England Biolabs. The database also takes advantage of genomic-scale datasets made publicly available by genome sequencing centers and other researchers around the world.

The database is accessible at http://TDRtargets.org, and the network encourages the international community to take advantage of this resource, contribute additional data, and make suggestions for further improvement.

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