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Letter to the Editor

Schistosome Immunomics: High-Throughput Vaccine and Diagnostic Antigen Discovery

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Letter to the Editor

Schistosomiasis remains one of the highly prevalent and serious helminthiases in the countries of Asia, Africa and Latin America. Despite the accessibility of an effective drug against the fatal parasites, drug-based treatment projects still have certain limitations and it is likely that vaccine and effective diagnostic tools are essential for schistosomiasis control. Despite the several decade vaccine development has witnessed the finding and testing of couple of candidate targets, none have shown satisfactory protection. Upon the coming of genome era, it has revolutionized the study of the drug, vaccine, and immunodiagnosis, and also catalyzed a switch from traditional manual testing to automation operation.

The genomes of *Schistosoma mansoni* and *Schistosoma japonicum* have been deciphered simultaneously in 2009 [1,2]. It creates a significant milestone in genomic study [3]. The available resources of whole-genome has directed to the development and application of large-scale manner that promote rapid, targeted discovery of novel candidates for structure and function study [4]. Subsequently, the SchistoDB (http://www.schistodb.net) provides a global and valuable platform for the research community to facilitate the development of new interventions for schistosomiasis [1].

In The Lancet Infectious Diseases, Weiqing Pan and colleagues [5] carried out a genome-wide identification of diagnostic antigens for *S. japonicum* infection and evaluated diagnostic validity of these protein markers in a field study in China. They predicted putative secreted proteins of *S. japonicum* and expressed as Glutathione S-Transferase (GST) -fusion proteins. And then, the fusion proteins were arrayed on 96-well microplates and screened with sera from schistosomiasis patients. Their large-scale pioneering work is excellent and provides an effective clue for surveillance and early warning of schistosomiasis. But the following problem is that, as the protein fusion tag, the 26 kDa GST with strong immunoreactivity also derives from *S. japonicum* [6]. Thus, it difficult to confirm the value of serological diagnosis for these protein markers was derived from their own or contributed by GST. Furthermore, despite the conventional methods they used could effectively discovered fascinating targets for diagnosis of the life-threatening trematode, the huge project need to consume large amounts of resources, a lot in time and manpower. Thus, it urgently needs a novel, rapid, economical and microscale model to explore targets for vaccine and diagnosis development.

Immunomics, a comparatively novel omics member developed to deal with the recent huge invasion of biological dataset [7], integrates achievement of genomics, transcriptomics, proteomics and molecular immunology, and holds promise for a cogent approach to target antigen discovery for preventive and therapeutic measures on the genome level [8]. To accelerate exploring new potential targets, it is very necessary to macroscale, thoroughly and comprehensive excavate immunogenic candidates via a high-throughput immunoscreening platform constituted by techniques of seamless cloning, in vitro cell-free protein synthesis system and protein microarray [9].

For high-throughput platform, seamless cloning changes traditional restriction digestion and ligation model for a novel homologous recombination manner with high efficiency and easy processing. The cell-free system can be applied successfully in producing high quality protein without codon optimization, it provides a crucial tool for immunomics research [10]. The system supplemented with minor t-RNAs to help translate A+T rich genes, and there is highly tolerable to potentially deadly encoded proteins. Antibodies are typically measured using an Enzyme-Linked Immuno Sorbent Assay (ELISA), a technique that requires high amounts of coating-antigens and sera. To overcome these limitations, antibody-based microarray is developed [11]. In addition, it offers significant advantages in convenience, costing, and throughput.

In our previous study, the created platform has been applied to establish erythrocytic stage-specific immunoproteomic profile from *Plasmodium vivax* [12]. It provides a fundamental data for

prospective serological antigens. Furthermore, the platform could be used to assess immunodominant biomarkers. Recently, a combined immunoproteomics and bioinformatics approach was used to profile the *S. japonicum* teguments [9]. It provides clues of potential target molecules for vaccine development and immunodiagnosis of schistosomiasis [9].

We propose that by virtue of the omics approaches, particularly immunomics, it is very convenient, effective and rapid to explore and characterize target antigens. If it can with the help of a laboratory automation system such as an Automated Sample Storage System, Liquid Handling System, and so on, the platform can be applied in many more fields. It hopes these approaches will accelerate drug discovery, vaccine and immunodiagnosis development against the schistosomes, as well as other human parasites [7].

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