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Editorial
Molecular epidemiology of infectious diseases – expanding horizons for IJMEG

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With the publication in this issue of the first article on molecular epidemiology of hepatitis C virus in this issue [1], IJMEG has broadened its scope of coverage of molecular epidemiology from purely focusing on chronic diseases to include both chronic and infectious diseases. Accordingly, IJMEG has begun to make adjustments to its editorial board.

Molecular and genetic tools are widely used in studies in the epidemiology of both chronic and infectious diseases. This is reflected in the considerable number of recent publications in both areas. A search of "All databases" hosted by the ISI Web of Knowledge resource (http://apps.isiknowledge.com/) on July 6th, 2010 using the keyword "molecular epidemiology" in the search heading of "Topic" identified a total of 13,863 entries recorded for the last five years across the databases *Web of Science*® and *Medline*®. Of these, 10,083 of the entries were listed under the subject area of "Genetics and Heredity" while the number of articles also listed under the subject area of "Infectious Diseases" was a relatively comparable 9,086 entries. As many of the same molecular/genetic diagnostic approaches and analytic tools are used in molecular epidemiologic studies of both chronic and infectious diseases, it is logical to have some scientific journals that cover both areas and for articles to be listed under both subject areas.

While there are already some journals publishing articles on the molecular epidemiology of infectious disease a more detailed analysis of the 9,086 results generated showed that these were published across approximately 500 different journals. Moreover only a small number of these articles were published in journals with significant coverage of epidemiology of infectious diseases, such as *Emerging Infectious Diseases* (No. 3 in the ranking of all publications); *Infections, Genetics, and Evolution* (No. 5); *Journal of Infectious Diseases* (No. 16); *American Journal of Tropical Medicine and Hygiene* (No. 17); *Clinical Infectious Diseases* (No. 19); and *Epidemiology and Infection* (No. 20). These contributed to less than 10% of the total number of publications. The remaining top 20 journals were all specialty journals in microbiology, virology, and parasitology and hosted just over 32% of all publications. A drawback to the publication of molecular epidemiologic research in various journals focusing on any one discipline is the potential for variability and inconsistency in terminology, tools, and approaches. As an example for microbial typing, "researchers in various disciplines tend to use different vocabularies, a wide variety of different experimental methods to monitor genetic variation, and sometimes widely differing modes of data processing and interpretation" [2].

The increased scope that allows for the consolidation of published research papers on molecular epidemiology of both chronic and infectious diseases into the same journal will serve to ad-

dress current reporting inconsistencies and promotes the sharing of analytic techniques and expertise amongst researchers of the two fields. As an example, the linkage disequilibrium analysis-based association studies that are widely used in molecular epidemiologic investigations of chronic and genetic diseases have already begun to be effectively applied in molecular epidemiologic characterizations of microbial pathogens. The target of the widely used antimalarial drug chloroquine and the identification of drug resistance-associated nucleotide mutations were initially identified through association studies [3]. This approach is now used commonly in molecular epidemiologic comparison of drug resistance occurrence in different malaria-endemic areas [4]. This same approach can also be used in the identification of other targets under selection pressure, such as virulence elements [5-6]. Another example is the explosion of whole genome sequencing of many pathogenic microorganisms and its usage in molecular epidemiologic studies that may inform approaches that may be useful in genome-wide association studies of chronic diseases.

Microbial typing and molecular epidemiology of infectious diseases are entering a new era. Just like the advent of DNA recombinant technology, PCR and sequencing that revolutionized core molecular epidemiologic technical approaches in the late 1980s and 1990s, the recent development of high throughput DNA sequencing makes extensive genomic typing of microorganisms a reality. The utility of such typing of pathogenic microbes was best demonstrated in the investigation of the 2001 anthrax bioterrorist attack, which identified subtle differences among passages of the Ames strain of *Bacillus anthracis* kept in different laboratories [7]. Other notable successes of whole genome typing of infectious pathogens included the tracking of the source of 2002/2003 outbreaks of SARS coronovirus to civets and bats [8-9] and investigations of recent H5N1 avian influenza virus outbreaks in humans [10], the foot and mouth disease virus spread in farm animals [11], and food-borne outbreaks of several bacterial pathogens [12-13]. In addition, genome-wide typing of parasites is now used in malaria control and eradication efforts in Africa [14]. It is expected that genomic typing based on high throughput DNA sequencing and microarray analysis will be routinely used in molecular epidemiologic studies of infectious diseases in both endemic and epidemic settings.

It is in this context that IJMEG has expanded its scope to encompass the reporting of molecular epidemiologic studies of infectious diseases shortly after the founding of the journal. We believe that this will foster the sharing of analytic techniques between researchers across the two related molecular epidemiologic areas and with this the potential for new collaborative research. In return, we hope IJMEG will continue to go from strength to strength with the submissions of new high quality research and over time become flagship journal for the reporting and dissemination of all aspects of molecular epidemiologic research.

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