Global Science Research Journals

Available online at
www.globalscienceresearchjournals.org/

Global Journal of Public Health and Epidemiology

ISSN: 2465-7557 Vol. 10 (1). pp. 003 February, 2022

Perspective Open Access

Inferences in psychiatric genetic epidemiology

J Muin*

Department of Health Research and Policy, University of Stanford, Stanford USA
*Corresponding author. E-mail: John.Muin@gmail.com

Received: 02-Feb-2022, Manuscript No. GJPHE-22-59498; **Editor assigned:** 04-Feb-2022, PreQC No. GJPHE-22-59498 (PQ); **Reviewed:** 18-Feb-2022, QC No GJPHE-22-59498; **Revised:** 21-Feb-2022, Manuscript No. GJPHE-22-59498 (R); **Published:** 28-Feb-2022, DOI: 10.15657/2465-7557.22.10.217.

DESCRIPTION

Genetic epidemiology is the study of the function of genetic elements in determining health disease in families and in populations of such genetic elements with environmental factors. Genetic epidemiology seeks to derive a statistical and quantitative analysis of how genetics work in large groups. It is a relatively new medical discipline that seeks to understand how genetic factors interact with the environment in the context of disease in populations and areas of study include the causes of inherited disease and its distribution and control.

It is the study of how genes and environmental elements influence human traits and human health and disease. It is developed initially from population genetics, specifically human quantitative genetics, with methodological contributions from epidemiology. It has made important contributions to medicine and public health. One example is using newborn screening to detect inherited disorders in offspring. The application is designed to be completed in educational years and the degree requirements include classes in biostatistics, public health and human genetics, and statistical genetics plus the completion of a research-based Master's thesis.

Molecular epidemiology and genetic epidemiology seeks to combine traditional epidemiological concepts on study design and risk measurement with principles from molecular and cellular biology, making it uniquely able to establish disease etiology. Characterize the disease risk factors and Identify susceptible populations. Genetic screening is a term that is used to help us identify a smaller organization of humans from a large population and this smaller organization of humans actually might have a higher risk of either having a developing that disease having children who may have that disease as well.

One of the early proponents of genetic epidemiology, American geneticist Newton Morton, described the field as one that addresses the distribution, and control of disorder in groups of related individuals and the inherited reasons of diseases in populations and later was broadened to include the role of the environment, owing to the realization that genetic factors frequently interact with environmental factors to influence disease in human populations.

It has the ability to significantly affect human health. We observe the important developments in the field's history and the modern state of the field, which includes both promising avenues of studies and potential challenges genetic epidemiologists face. Advances in molecular genetic generation have led to the Human Genome Project, a long-term initiative to map and sequence the human genome. In the next decade, most if not all of the estimated 50,000-100,000 human genes can be sequenced. So far, only a small fraction of these genes has been identified. The number of detected human genes has more than quadrupled over the last 25 years. Although most identified human genes are associated with uncommon disorders, genes play important roles in the etiology and pathogenesis of most human diseases.

Genetic risk elements interact with the environment broadly defined to consist of physical, chemical, biologic, and infectious agents in causing various human diseases. Molecular technology is being used in family studies to identify disease genes. These studies are usually based on high-risk families with multiply affected individuals. They rely on using genetic analysis techniques including linkage and segregation analyses.