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Epidemiology in Genetic Studies from the Public Health Perspective

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Epidemiology is the most important and frequently used scientific basic tool for public health researchers. There are different definitions given for epidemiology, but it can be briefly defined as the process of detection, investigation, and analysis of the causes of diseases in the human populations [1]. It is a methodology, which preventive medicine use to control and prevent the diseases also to improve the health status of the public in general. It is known that there is a heredity role in the majority of common human diseases because of that a multidisciplinary approach is required for a full understanding of the etiology of diseases [2]. Many non-infectious chronic diseases (cancer, allergy, asthma, diabetes mellitus, obesity, occupational diseases, neurological diseases, mental diseases, cardiovascular diseases etc.) which are estimated that associated with genetic structure of the human are still being investigated in the worldwide [3,4]. Genetic epidemiology is fairly a new discipline that has to research very large different fields. Genetic epidemiology is the methodology that is used to investigate the frequency, distribution, and cause of disease, and to examine to what extent factors that play a role in diseases are genetic or environmental, and to reveal the genetic structure-environment interaction dimension. The research methods used in genetic epidemiologic studies can be similar with the designs that are used in general epidemiology (clinical trials, case controls, cohort studies etc.) [5]. Day by day, the attention on genetic epidemiology has increased as the mechanisms of genetic risk factors on health are diagnosed and understood. In particular, well-organized population-based molecular epidemiology studies and prospective cohort studies have an important role in understanding the interaction between genetics and the environment in multi-factorial human diseases.

While genetic epidemiology is dealing with genes as a whole, molecular epidemiology is concerned with the genes, infectious agents, and environmental risk factors, which are associated with diseases and are sensitive. Molecular epidemiology is in need of researchers that have special training in this field with advanced information and experience in epidemiology and public health issues [6]. The molecular tests to be used in molecular epidemiological studies need to be evaluated in terms of the criteria for epidemiological screening tests. Molecular epidemiology reduces prepossession in environmental influence, and provides early diagnosis through biological indicators, and enables a more accurate identification of the diseases in descriptive studies. Molecular epidemiology provides new standards and convenience for descriptive epidemiology, and helps analytical epidemiology to reach more precise and accurate results by revealing environmental and genetic factors and their interactions between themselves [7]. Molecular epidemiological studies provide a convenient guidance and reliable facility for health risk assessment of the public much more than classic epidemiological studies if used appropriate research strategy [8,9].

It is obvious that the tolerance of people to environmental factors (pollution, nutrition, occupation, smoking etc.) differs from person to person, and the sensitivities of people can be accurately demonstrated with the genetic screening tests [10,11]. People who have been found to be genetically sensitive to some environmental factors can keep a healthier lifestyle by avoiding from these risks with qualified medical guidance. When the relative risk values obtained from the classic epidemiological studies and data obtained from the molecular epidemiological studies are evaluated together, peoples' relative and absolute risk for a suspected disease may be detected with a high probability. Determining the absolute risk of the diseases is extremely important for the buildup of essential public health strategies for the prevention of diseases. The convincing information obtained by determination of the relative, absolute and imputed risks of diseases as a result of the presence of specific biological indicators should be made known to researchers, healthcare professionals and the public. Unless this potent information is provided, the progression of molecular diagnostic methods and disease prevention program cannot be expected to success. More comprehensive epidemiological research should be carried out in the genetic and chronic diseases of developing countries, which are considered priorities in industrialized countries. In the event that effective participation is provided to public health research units for genetic studies, more desirable results will be obtained for the diagnosis of diseases and protection of public health in developed and developing countries. In today, hereafter epidemiologists must use more new sophisticated combined methods that incorporate personal exposures and genetic structure for improving of new public health approach.

References

1. CDC (2012) Principles of Epidemiology in Public Health Practice: An Introduction to Applied Epidemiology and Biostatistics. (3rdedn), Self-Study course SS1978, Atlanta, GA.
2. Kuller LH, Bracken MB, Ogino S, Prentice RL, Tracy RP (2013) The role of epidemiology in the era of molecular epidemiology and genomics: Summary of the 2013 AJE-sponsored Society of Epidemiologic Research Symposium. Am J Epidemiol 178: 1350-1354.
3. Bakulski KM, Fallin MD (2014) Epigenetic epidemiology: Promises for public health research. Environ Mol Mutagen.
4. Ege MJ, Strachan DP (2013) Comparisons of power of statistical methods for gene-environment interaction analyses. Eur J Epidemiol 28: 785-797.
5. Hopper JL, Bishop DT, Easton DF (2005) Population- based family studies in genetic epidemiology. Lancet 366: 1397-1406.
6. Maojo V, Martin-Sanchez F (2004) Bioinformatics: towards new directions for public health. Methods Inf Med 43: 208-214.
7. Wagner B, Li J, Liu H, Guo G (2013) Gene-environment correlation: difficulties and a natural experiment-based strategy. Am J Public Health 103: S167-S173.
8. Zhang J, Zhang X (2013) Environment, heredity, and epidemiology. Asia Pac J Public Health 25: 4S-5S.

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9. Seyerle AA, Avery CL (2013) Genetic epidemiology: the potential benefits and challenges of using genetic information to improve human health. N C Med J 74: 505-508.

10. Taylor AE, Davies NM, Ware JJ, VanderWeele T, Smith GD, et al. (2013) Mendelian randomization in health research: Using appropriate genetic variants and avoiding biased estimates. Econ Hum Biol.

11. Bonassi S, Taioli E, Vermeulen R (2013) Omics in population studies: a molecular epidemiology perspective. Environ Mol Mutagen 54: 455-460.