J Oral Res
oral and craniofacial sciences

Editorial

Challenges of genomics in public health.

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Public health systems have generally been based on an essentially biological model, with actions taking place in a fragmented way. These systems were founded on medical knowledge, which has focused on pathologies rather than on health status.

At present, public health urgently requires the inclusion of the social determinants of health and the deep conjunctural and structural transformations that extend across contemporary societies. Some of these transformations are associated with demographic changes such as a fall of the fertility rate and decreased infant mortality, coupled with an increase in life expectancy. These characteristics have substantially modified the structure of the population pyramid, incorporating demographic changes that have a direct impact on public health at a global scale, as a result of the increase in chronic noncommunicable diseases and the presence of chronic co-morbidities. The epidemiological profile is also affected; in the Americas an increasing prevalence of chronic-degenerative diseases has been observed, in addition to the infectious diseases already present in the region.[1]

Science and technological development have advanced rapidly, incorporating new discoveries and paradigm shifts into curative and preventive medical care. These advances include bio-drugs, robotics, nano-devices, therapeutic vaccines, individualized treatments, among others. Genomics is a relevant area of the present and future of medicine. It is responsible for many of the abovementioned advances. Genomics is aimed at a predictive, personalized and preventive medicine. However, as in many other medical fields, access to genomics is unequal and determined by the patients' socioeconomic background. This is a challenge for the current health systems, in terms of improving the availability of these advances to the entire population.

Over the past decades, there has been increasing interest in the study of genetic predispositions to complex diseases. This interest has materialized in a large amount of epidemiological publications on associations between gene and disease. However, the magnitude of the association between a given genotype and a given condition has not always been determined. Given the above, it is necessary to identify the true genetic associations between the presence of a complex disease and the underlying genotype. Authors such as Khoury *et al.*,[2] point out that the synthesis of knowledge

Conflict of interests: None.

Acknowledgements: None.

Cite as: Brunotto M. Challenges of genomics in public health. J Oral Res 2017; 6(10):258-259. doi:10.17126/joralres.2017.073

ISSN Online 0719-2479 - www.joralres.com © 2017

is crucial to the integration of evidence-based genomics and public health in the 21st century.

The use of informatics and databases contributes to improving the monitoring and follow-up of patients and their pathologies in the field of genetics. This monitoring corresponds to the systematic and continuous collection, analysis and interpretation of the data to guide actions in public health. At present, big data allows for the identification of patterns for early detection of infectious or chronic diseases. Big data also allows the monitoring of population movements and potentially infected individuals, as for example, in the case of Ebola in Africa. The latter was possible thanks to the use of mobile phones to track in real time the movement of people who may be infected and thus prevent future outbreaks.[3]

In this context, it is necessary to implement sufficiently strong computer networks to achieve good connectivity and interoperability of clinical, laboratory and public health systems. In addition, the storage and use of genetic and non-genetic information for research and development must consider bioethical aspects such as privacy, protection of genomic data and informed consent.

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