BELPHG-21

Belgium Public Health Genomics: Methodology development linking 'Health Survey'

DURATION BUD	OGET .
1/10/2013 - 31/12/2015	000€

PROJECT DESCRIPTION

Context

The aim of this pioneer study is to define a technically feasible but affordable approach of assessing/estimating genetic variability at the level of the Belgian population and exploit this information for public health. For this, advantage will be taken of the experience and information gathered within the frame of the Belgian Health Interview Survey (HIS), a federal government project coordinated by the Scientific Institute of Public Health.

To estimate the genetic variability at the Belgian population level samples (buccal, saliva, urine or blood) will be taken from individuals who participated in the HIS. A genetic profile will be obtained from a sample of them e.g. by genome wide DNA microarray analysis. Genetic variability maps for various valuable pathways reported to be linked to diseases or other health factors will be assembled. The information obtained from the genetic pathways analyses will then be integrated into the information gathered from the HIS and compared to outcomes from other sources.

In this way, for the first time, through this so-called 'HIS-genomics' map insight will gained on the complexity and feasibility of obtaining and combining/integrating genomics data with results previously obtained from the Belgian HIS

General objectives and underlying research questions

In this pioneer study we aim:

- to explore how 'population genomics' information could be incorporated into knowledge of internal, host-specific factors and their interactions with environmental exposures to strengthen effectiveness of public health interventions
- 2. to bring together the necessary expertise and create a multidisciplinary forum supporting the translation of health survey information and genomic data into a format usefull for Public health.

For this, information on the Belgian population obtained in the 'Health Interview Survey' will be complemented with genomic date.

This pioneer project aims alligning 'genomics' as a novel technology with future societal needs at many different levels (individual, population, etc) in many aspects (public health, health care, prenatal screening, insurance, labour, ...).

This project resides on systemic, multi/interdisciplinary and integrative approaches; allowing to maximize the output either at the interpretative level or at precisely identifying the future needs and caveats to come to a robust 'HIS-genomics' population evaluation at larger scale.



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Methodology

The project contains six major steps:

- 1. Collecting of the samples from candidate participants to the HIS-2008
- 2. DNA extraction, annotation and storage
- 3. Genomic study by micro-array analysis
- 4. Determination of the set of candidate targets for comparison between the HIS and the genomic analysis
- 5. Descriptive analysis of the 'Belgium HIS-genome' map
- 6. Comparative analysis of HIS genomic outcomes with current state of the art information on health parameters of the Belgian population

Milestones

- 1. Development of a 'Belgian HIS-Genomics' map
- 2. Belgian HIS-Genomics map' mergeon
- 3. Samples from individuals who participated in the HIS 2008 study.
- 4. Genome-wide DNA microarray analyses from individuals who participated in the HIS 2008 study
- 5. A descriptive map of the 'Belgium HIS genome'

Nature of the Interdisciplinarity

This project brings together researchers in the field of public health with colleagues in the area of molecular biology, human genetics and computational mathematics in different research institutes.

Moreover, through the HIS a connection with the federal government is possible to allow gaining knowledge and understanding of the role of genomic information in public health

Potential impact of the research on science, society and on decision-making

This study will for the first time in Belgium perform a combined analysis of general health information and genomic information of a subsample of a representative sample of the population with the aim of providing a baseline methodology for future molecular epidemiology studies. Genomic information linked to general health information of a particular population has to our knowledge not been performed to date.

The study will allow to i) demonstrate the feasibility of a pathway-based approach to link survey and genomics data, ii) identify possible bottle necks and gaps in such kind of analyses and iii) will help addressing the need and interest of future support by the government on developing genomics approaches in personal and public health.

In this study, we will bring together the necessary expertise and create a multidisciplinary forum at the Belgian level to explore the translation of health survey information and genomic data into a format useful for Public health.

Descriptive of the finished products of research

A methodology and first experimental try out for the development of descriptive statistics of the 'Belgian HIS-Genomics' map

CONTACT INFORMATION

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