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Introduction
Head and neck cancers (HNC) are the fifth most common cancer worldwide (over 600 000 cases/year). Tobacco and alcohol are established risk factors, though other factors may affect HNC risk. Increasing evidence suggests that physical activity (PA) could prevent cancer by improving antioxidant properties, enhancing circulation of immune cells and modulating specific immune parameters (salivary IgA). The aim of our analysis is to clarify the effect of recreational PA (rPA) on HNC, as very little data are present in the literature.
Methods
We analysed data from three European, one Asian and one American case-control studies participating in the INHANCE consortium, including a total of 3481 HNC cases and 7262 controls. According to the International Physical Activity Questionnaire, rPA was classified in three levels: none/low (reference group), moderate and high. We estimated odds ratios (ORs) from each study using logistic regression models adjusted by age, gender, number of cigarettes per day, duration of cigarette smoking, alcohol consumption, years of drinking, education level, race, occupational PA and study center. Summary ORs and 95% confidence intervals (CIs) were estimated by pooling study-specific ORs using a random effects model.
Results
Moderate rPA significantly reduces the risk of HNC (OR = 0.77, 95% CI: 0.66–0.90), and the OR was (OR = 0.72, 95% CI: 0.45–1.15) for high rPA. By stratifying the results according to cancer sub-sites and selected covariates, the protective effect of moderate rPA was restricted to oral cavity (OR = 0.74, 95% CI: 0.56–0.97), pharynx (OR = 0.67, 95% CI: 0.53–0.85), males (OR = 0.77, 95% CI: 0.65–0.91), subjects age 45 years or more (OR = 0.75, 95% CI: 0.62–0.90), and ever smokers and ever drinkers (OR = 0.72, 95% CI: 0.59–0.88). High rPA significantly reduces the risk of oral cavity (OR = 0.53, 95% CI: 0.32–0.88), pharynx (OR = 0.58, 95% CI: 0.38–0.89) and in subject <45 years old (OR = 0.65, 95% CI: 0.47–0.89), while it increases the risk of laryngeal cancer (OR = 1.73, 95% CI: 1.04–2.88).
Conclusions
We observed that moderate and high rPA reduces the risk of oral cavity and pharyngeal cancer. Promoting PA might represent an important primary preventive factor for HNC.

6.13 Workshop: Public health genomics: Integration of genome-based knowledge and technologies to fight infectious diseases

Chairs: Elena Ambrosino, The Netherlands and Arja Aro, Denmark
Organizer: EUPHA section on Public Health Genomics

Classical and emerging infectious diseases, drug-resistant pathogens and viral pandemics, continue to be among the most significant threats to human health and international security. Moreover, vaccine-preventable, food-borne, zoonotic and chronic communicable illnesses contribute considerably to health care costs. While such diseases are not among the leading causes of mortality and morbidity in the European Region, preventing and controlling them remain one of the fundamental public health functions of health systems within Europe, as well as in the rest of the globe. Both aspects will be covered during the EUPHA conference.

In this context, the information constantly generated by the rapidly growing discipline of genomics can play a decisive role in policymaking. The use of genome-based knowledge and technologies and its integration into Public Health (Public Health Genomics) can indeed benefit global health by providing new approaches to understand and fight old and emerging infectious diseases.

PHG can improve global health by elucidating basic mechanisms of disease, susceptibility and resistance, thus guiding the development of future health care innovations and interventions. Such advances can influence the prevention, diagnosis and treatments of several major infectious diseases, including Chlamydia, HPV, tuberculosis, malaria and HIV.

The workshop aims to exchange expertise and stimulate the discussion on how the genomes, and interactions of both host and pathogens are being revealed using novel genome-based technologies, and how this information can and will be translated into disease management and therapies to benefit population health.

Overview on the genetics and genomics of infectious agents

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The impact of host genetics on the susceptibility to infectious disease has been demonstrated for all kinds of infectious agents both in experimental animal models as well as in human disease. In part, differences in genetic make-up are associated with differences in susceptibility towards infection, vaccination response and/or differences in clinical course after infection. A major part of this susceptibility seems to be influenced by multiple host genes, most of which are low penetrance QTLs that were difficult to map in humans with classical genetic approaches. With the rapid advances in genomics, including GWAS and next generation sequencing, progress also in humans is advancing. Illuminating examples for different infectious agents (Plasmodium, Mycobacterium, HIV, Bordetella, Leishmania, etc.) will be summarized and presented. The translation of this advanced in part immunological knowledge with respect to vaccination, antibiotic resistance and clinical as well as public health utility will be discussed. In addition, the crucial role of Institutes of Public Health in this translational process will be stressed.

Host genetics variation in Chlamydia trachomatis infection: translation and valorization by the EU FP6 EpiGenChlamydia Consortium

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Twin studies and case–control studies have shown a substantial genetic component for many infec-tious diseases (IDs) with high morbidity explaining the interindividual differences in response to IDs. Identification of people at risk using genetic markers will give a new insight in the immunopathogene-sis of disease, will highly benefit individualized treatments for those infected, reduce the morbidity associated with disease and the considerable costs for society associated with these IDs. The EU FP6 EpiGenChlamydia (EGC) Consortium focuses on Chlamydia trachomatis (CT) infections which are responsible for both the world leading cause of blindness (trachoma) and the most prevalent sexually transmitted disease which is strongly associated with pelvic inflammatory disease, ectopic pregnancy, and tubal infertility. Twin study-based findings of members of this consortium showed that there is a 40% genetic predisposition to CT infections. In order to fully exploit human genomics in the battle against CT infections, it is necessary to reliably determine aforementioned genetic predisposition at the gene level to CT infection and to define a genetic fingerprint that can be used as a marker for this predisposition. The EpiGenChlamydia I Consortium aimed to structure trans-national research to such degree that comparative genomics and genetic epidemiology on large numbers of unrelated individu-als can be performed. The EGC Consortium lobbies a FP7 call on the HEALTH 2010/2011 list to perform as EpiGenChlamydia II the studies on the generated biobanks and datawarehouses to select, validate and valorise genetic traits to be used in patient management.

ECDC role in fighting infectious diseases in the field of public health genomics

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The European Centre for Disease Prevention and Control (ECDC) in Stockholm was established in 2004 by the European Council and the European Parliament as their reaction to new emerging micro-bial threats such as SARS. The Regulation EC No. 851/2004 which establishes the ECDC, as well as the name of this agency allows a much broader scope than just communicable diseases. However, until now all activities of the ECDC have been focused on infectious diseases. A recent external evaluation of the ECDC and its present significance has shown that the ECDC has indeed managed to take a central and highly appreciated position as the scientific advice centre in the coordinated fight against infectious diseases in the EU and abroad.

In ECDC's work, genomics of microbes has been of great significance, mainly for the study and typing of the pathogenic microbes. But the awareness is growing, that the genetics of the microbe is only one 'side of the coin'. There is increasing knowledge that someone's susceptibility to infections, the course and severity of the infection as well as the possible adverse effects of treatments and vaccination, are also determined by his/her genetic background. The knowledge of these genetic 'host-determinants' in infectious diseases is, therefore, one of the most promising subjects of Public Health Genomics and it is expected to be applicable in the years to come.

Global aspects of Public Health Genomics: fighting infection diseases in Global Health

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Infectious diseases are one of the major killers worldwide, but their distribution is quite different across countries. Indeed, their prevalence in developing countries is dramatically higher than in developed ones, as nearly all of the 9.5 million people annually dying for infections live in the former. Moreover, the impact of such diseases is most severe in resource-limited settings, where poorer people have fewer resources and limited or no access to health care, prevention tools and medications. Thus, strategies to fight such diseases should specifically target and be adapted to the most affected areas of the world.

The advances in Genomics, the increasing knowledge generated by genome-based technologies and its translation into Public Health interventions (PHG) can have a significant impact on infectious diseases, and can play a major role in meeting the health needs of developing countries for the benefit of global health.

Yet, since the beginning of the Genomics era, it has been evident that many countries will not be able to take advantage of such progresses, because of their limited scientific resources and the urgency of other health priorities. Nevertheless, there are already several examples of successful application of Genomics to Public Health in resource-limited countries. Many genome-based technologies, especially molecular diagnostics, are indeed now cost-effective and affordable for the developing world and will contribute to the prevention of infectious diseases and the promotion of health.

Therefore, as the balance in infectious diseases burden continues to widen, making them more and more diseases of poverty, PHG could help reduce the gap. However, in order to harness the benefits of Genomics in the global fight against infections, a more concerted effort should be made to include in the genomic research countries with limited resources, and help them translate the genome-based knowledge into Public Health.

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