GENETIC VARIABILITY AND PHYLOGENETIC ANALYSIS OF INTESTINAL ZOONOTIC PROTOZOANS: THE "ONE HEALTH" APPROACH

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Intestinal zoonotic protozoans are causative agents of infectious diseases worldwide: they affect hundreds of millions of individuals in the developing such as in the developed countries. Despite this, surveillance and the development of new tools for their diagnosis have been neglected (Castellanos-Gonzalez *et al*., 2018). Zoonotic protozoans infections can be insidious and predicting their biogeographic patterns is still a remarkable challenge (Han *et al*., 2016). Therefore, in order to successfully face the emergence and re-emergence of these zoonotic infections, a multidisciplinary approach is necessary to understand the zoonotic interaction between different hosts, reservoirs and the environment. Indeed, the evolutionary and ecological dynamics are heavily involved in parasites transmission, and this becomes mostly evident in the food and water-borne parasitic diseases (Webster *et al*., 2016).

The One Health approach fulfills these requests, integrating human, animal and environmental health to improve diseases prediction and surveillance (Rabinowitz *et al*., 2013).

Giardia duodenalis is a flagellated protozoan which causes giardiasis, a globally re-emerging disease with veterinary and public health implications worldwide (Abdel-Moein & Saaed, 2016). The species presents at least a complex of eight morphologically identical but genetically different assemblages, variables even at the sub-assemblage level (Wang *et al*. 2019).

This project aims to apply molecular tools for the detection of zoonotic intestinal protozoans in Italy, with a focus on *Giardia duodenalis* human-pathogenic assemblages, in order to perform an analysis of their geographical distribution, transmission patterns and population dynamics using a One Health approach. The study will implement the fragmented giardiasis epidemiological data currently present in Italy, which result as "*no recorded*" in the last annual epidemiological report from the European Centre for Disease Prevention and Control (ECDC, 2017). The molecular characterization will be conducted at assemblages and sub-assemblages level, both using the standard *G. duodenalis* genotyping loci and the assemblage A- specific multilocus sequence typing method (MLST) for a higher resolution (Arkanklev *et al*., 2018). Through comparative genomics an improvement of the MLST strategy for assemblage B will be approached, in order to have a better understanding of the genetic, biological and epidemiological differences within the two zoonotic assemblages.

A phylogenetic analysis performed with DNA-based genotyping strategies will determine the genetic groups spatial distribution, the evolutionary patterns and the phylogenetic network analysis. The final purpose will be the clarification of local and global giardiasis patterns of transmission to improve the last updated (Giangaspero *et al*., 2007) Italian epidemiological scenario.

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