

S.5-4

Compared population genetics of pathogenic microorganisms (parasites, fungi, bacteria, viruses); epidemiological consequences

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In this talk, I will insist one more time on the urgency to disrupt the distressing separation between molecular epidemiology and evolutionary biology. I will show how much population genetics and phylogenetic analysis can confer a considerable added value to all attempts to characterize strains and species of pathogens. A population genetics approach gives a convenient framework to all studies dealing with the genetic diversity of pathogens, including molecular epidemiology, clinical studies, design of drug/vaccine/molecular diagnosis, and experimental evolution.

The problems dealing with the mere definition of basic concepts such as species, subspecies or strains will be briefly summarized. Lastly I will show the important contribution of molecular epidemiology to our knowledge on the basic biology of pathogens and will insist on the necessity not to separate the studies dealing with pathogens from those that concern the hosts, and the vectors in the case of vector-borne diseases.

The clonal model of evolution, which gives a convenient framework for this approach, will be exposed. Some telling examples will be taken in parasitic protozoa, viruses, bacteria and fungi, in order to underline the fact that these approaches are valuable, whatever be the pathogen considered.



EPIDEMIOLOGÍA MOLECULAR Y

EVOLUCIÓN DE ENFERMEDADES INFECCIOSAS EN AMÉRICA LATINA



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MOLECULAR EPIDEMIOLOGY AND EVOLUTION OF INFECTIOUS DISEASES IN LATIN AMERICA

LIBRO DE RESÚMENES ABSTRACTS

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