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Analysis of viral quasispecies as quality control of live vaccines-e.g. Lassa vaccine candidate, ML29

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When referring to a virus strain we are describing the most abundant variant from a closely-related virus swarm containing individual particles with broadly-distributed mutations. A viral isolate containing many variants, called quasi-species, could act as a unit of selection through a continuous dynamic process of genetic variation, competition, and selection. However, it is important to emphasize that the whole "virus swarm" contributes to the characteristics of the virus strain and will be the target of selection instead of individual variants. For example, some variants carrying lethal mutations not only compete with the fittest replicating unit but also cooperate with other mutants complementing each other, thus assuring the survival of the units containing "lethal mutations". Several studies describe the effect of the mutant spectra in the virus population phenotype making it more virulent or more attenuated according to the predominant quasi-species. For example, defective interfering particles could play a role in attenuating the virulence of a viral swarm by interfering with virus replication. In the case of live vaccines, the final goal is to select one population with attenuated phenotype (low pathogenicity) and high genomic stability (increased fidelity of replication). Ensuring that the viral population, contained in the preparation, does not have the capacity to adapt to new conditions in the host due to low quasi-species diversity but replicating enough to induce protection.

Thus, changes in virus diversity, can affect virus fitness and viral tropism and produce a spectrum of unexpected outcomes after vaccination depending on particular conditions of the virus-host interaction.

With the new sequencing tools, it is easy to characterize viral populations, in this case in vaccine preparation, which allows controlling the proportion of each viral-quasispecies.

This talk will be focused on the use of the study of viral populations for vaccine characterization using as a model a Lassa vaccine candidate.

Biography:

Juan Carlos Zapata research interest is in virus-host interactions using animal models, genomic profiling, and basic molecular virology. It is focused not only on host responses but also on changes that occur in the viral population in order to describe virus-host coevolution. During the characterization of the Lassa vaccine candidate ML29, he identified mutations in the arena virus nucleo capsid protein (NP) that are likely to impact viral pathogenesis and the induction of protective immunity. Additionally, he is involved in a new line of work focusing on retroviral latency. Under Dr. F. Romerio leadership he is working in detecting and characterizing viral factors related with HIV latency in the reservoir cells and with Dr. Y. Tagaya he is implanting patient-derived ATL cells into NSG mice to study cancer pathogenesis, treatment options, and vaccine development against HTLV-1.