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The Two Phases of HIV-1 Group O Diversification

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BACKGROUND

HIV-1 is subdivided into 4 groups: M, O, N and P.
Each group represents an independent cross-species transmission of SIV (Simian Immunodeficiency Viruses) to humans.
Group M is pandemic: >34,000,000 infections worldwide;
Groups N and P very rare: <20 infections linked to Cameroon;
Group O is endemic in Cameroon: ~10,000 to 30,000 infections.
Group O MRCA (Most Recent Common Ancestor) has been estimated to be as ancient as group M based on few sequences available. But group O genetic diversity and evolution remains poorly characterized.

OBJECTIVE

To explore HIV-1 group O genetic diversity and evolution through the largest series of HIV-O sequences, from Cameroon (samples used for HIV-O diagnosis and follow-up in the Centre Pasteur du Cameroun), France (RES-O surveillance network of the HIV National Reference Center) and Gabon.

RESULTS

HIV-1 group O ML tree topology is atypical, with a predominant clade emerging from and broad and genetically diverse base population.
The natural presence of the Y181C mutation, conferring resistance to NNRTIs, is significantly associated to the emergent clade (p<0.01).

HIV-1 group O MRCA is estimated around 1930 (black curves). The predominant clade is more recent, with a MRCA estimate around 1960 (blue curves). Several subclusters emerged even more recently, in the 1980's (yellow, green and red curves).

HIV-1 group O diversification went through two exponential phases, in the 1950's and in the 1980's.
The now predominant population arose during the second phase, from an ancestral level of genetic diversity which had developed during the first diversification wave.
According to the historical context in Cameroon, the 1st wave might have been favored by iatrogenic routes of transmission in the 1950's, while the second would have benefited from the development of urbanization.

CONCLUSIONS

HIV-1 groups M and O share a similar age but group O has remained largely confined to Cameroon.
Group O local diversification resulted in a broad genetic diversity that cannot be compared to group M subtypes. However, two subgroups can be observed, corresponding to two successive phases of diversification.
The viral properties of the two subgroups need to be investigated, in order to better understand why the most recent population to emerge has now become predominant.

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