

Unexpected genomic change through 400 years of French-Canadian history

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Researchers at the Sainte-Justine University Hospital Center and University of Montreal have discovered that the genomic signature inherited by today's 6 million French Canadians from the first 8,500 French settlers who colonized New France some 400 years ago has gone through an unparalleled change in human history, in a remarkably short timescale. This unique signature could serve as an ideal model to study the effect of demographic processes on human genetic diversity, including the identification of possibly damaging mutations associated with population-specific diseases.

Until now, changes in the relative proportion of [rare mutations](#), that could be both detrimental and adaptive, had only been shown over relatively long timescales, by comparing African and European populations. According to Dr. Alan Hodgkinson, the co-first author of an article published online in *PLOS Genetics* recently and a postdoctoral fellow, "through this first in-depth genomic analysis of more than a hundred French Canadians, we have been surprised to find that in less than 20 generations, the distribution and relative proportion of rare, potentially damaging variants have changed more than we anticipated."

Such an increase in rare variation is presumably due to a high birth rate of the settlers and the genetic isolation from France, with limited exchange with other non-French communities in the same geographical area, since emigration virtually stopped after 1759, just before the English conquest. Indeed, the founding population is estimated to have contributed 90% of the current French Canadian genetic pool.

According to Dr. Philip Awadalla, senior author and principal investigator, "the fact that two very close populations (French versus French Canadians) accumulate such an excess of differences in rare variants has important consequences in the design of genetic studies, including the identification of possibly damaging mutations associated with diseases specific to this population." The model unveiled by the researchers could also serve conservation genetics, namely in determining the impact of [genetic diversity](#) on the minimal number of individuals required for the survival of specific species or captive populations.

Provided by University of Montreal

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