



20
MAR.
2024

🕒 de 13h à 14h

SÉMINAIRE

Deleterious mutations in archaic hominins and other species

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Deleterious mutations decrease the fitness of individuals, and can enter and accumulate in populations because of random drift, admixture and changes in selective pressures. One of the most striking examples of the effect of demography in leading to the accumulation of such deleterious mutations is Neanderthals. Neanderthals and Denisovans lived in Eurasia before ~45.000 years ago, where they lived in small populations for hundreds of thousands of years and accumulated deleterious variation. When modern humans migrated out of Africa, part of the genome of these archaic hominins entered in our gene pool via interbreeding, and now constitutes about ~2% of the genome of humans living today out of Africa. These admixture events shaped our genomes and introduced deleterious variation that impact human health. I will describe how ancient genomes from archaic hominins and modern humans inform us on these phenomena, and on the nature of our encounters with other human populations. I will finally discuss the relevance of deleterious variation for human health and for biodiversity, through examples from plants to primates.