POSTDOCTORAL POSITION IN COMPARATIVE ONCOLOGY

CANCER RESISTANCE AND SOMATIC MUTATION RATE

The research teams led by Mathieu Giraudeau (LIENSs, University of La Rochelle, France) working on cancer resistance in wild organisms and by Alex Cagan (University of Cambridge, UK) working on the accumulation of somatic mutations are recruiting a new postdoctoral researcher. The position is fully funded for 2 years by a Chaire d'Excellence Nouvelle Aquitaine to Mathieu Giraudeau. The postdoc hired will spend time in France and the UK (the time spent at each university can be discussed). We are looking for candidates who could ideally start between September and December 2024, though this is open to discussion.

Project information

All organisms accumulate mutations in the cells in their DNA as they age. While most of these mutations are thought to have no impact on organismal function, mutations in certain genomic regions can transform healthy cells into cancer cells. It has only recently become possible to directly study this transformation from healthy cells into malignant ones through advances in the accuracy of genome sequencing technologies. This work is revealing how different cell types accumulate mutations at different rates (https://www.nature.com/articles/s41586-021-03822-7) and how cells carrying cancer causing mutations can spread to colonize apparently healthy tissues as we age (https://pubmed.ncbi.nlm.nih.gov/30337457/). While we are learning much about how these processes operate in humans we know virtually nothing about other species. We recently found that somatic mutation rates vary greatly across mammalian species (https://www.nature.com/articles/s41586-022-04618-z), which may partially explain differences in cancer risk that have been observed between species (https://www.nature.com/articles/s41586-021-04224-5). While this work has advanced our understanding of how mutation rates vary across species it was limited to one cell type in 16 mammalian species. A more comprehensive survey of mutational processes in a wider range of species with varying cancer susceptibilities would greatly advance our knowledge of carcinogenesis across species.

By collecting blood tissue samples from frozen collections and prospectively during necropsies we can extract DNA and perform next-generation DNA sequencing using an ultra-accurate sequencing method (https://www.nature.com/articles/s41586-021-03477-4). Using this data, we will compare mutational processes across species and relate this to cancer risk, longevity and other life-history traits. In addition, mutational signature analysis will be performed on these data to infer the different mutational processes that contributed to the mutations detected in each sample. Studying how different species accumulate these 'somatic' mutations as they age promises to advance our understanding of why cancer risk varies across species and may ultimately lead to the identification of mechanisms by which some species are able to reduce their cancer risk. It will also contribute to our understanding of how mutations accumulate, a fundamental biological process.

In summary this work will help to contextualize emerging data on mutational processes in humans, with relevance to our understanding of human cancers, as well as revealing the relationship between cancer rate, lifespan and mutation across the tree of life.

Job requirements

We are seeking for a highly motivated postdoc with a strong background in bioinformatics, computational biology, genomics, population genetics and/or cancer biology. Any experience with statistics or cancer genomics would also be highly relevant.

Proficiency in English, communication skills and team-work attitude are important requirements.

Salary of approximately 2500 to 2700 euros net/months

Applications should be submitted to Alex Cagan (atjc2@cam.ac.uk), Mathieu Giraudeau (giraudeau.mathieu@gmail.com) and Steve Desaivre (steve.desaivre@univ-lr.fr); and should include a CV including a publication list, a research statement, a cover letter and contact information for at least two references (name, address, email and phone number).