

Abstract: Population genetics of transposable elements

Andrea BETANCOURT, Population Genetics

For this project, the postdoctoral applicant would work broadly in the area of population genetics, with particular focus on transposable elements. Specifically, transposable elements are a source of mutation, via insertion of new transposable element copies, most of which will be deleterious to the host. Animal hosts counter this attack with, among other means, a small RNA system specifically targeted toward silencing germline TEs, preventing these new mutations from being passed on to offspring. The existence of a specialized system for suppressing TEs suggests that the burden on the host of due to transposition is considerable, but otherwise, little is known about the magnitude of this selective burden: it will depend on the rate of transposition, which has never been measured under natural conditions. The proposed project will use next generation sequencing of large natural samples of the genetic model organism, Drosophila melanogaster, whose transposable elements are well-characterized, to quantify transposition rates. To this end, we will efficiently survey rare variants in a natural population. Very rare variants- e.g, occurring twice in a sample of 1000- primarily reflect the mutation rate unfiltered by selection (Messer 2009). Compared to mutation accumulation lines, this approach allows us to survey transpositions that have occurred in a range of natural conditions, important as transposition rate can be affected by environmental stresses (reviewed in Capy et al. 2000).

This project would be an excellent training opportunity: in the course of the project, the postdoctoral researcher would gain expertise in sequence analysis, a sought after skill set both within academic research labs and elsewhere. Further, within the general topic area of population genetics, there will be opportunity to develop other projects or specific aspects of this project, depending on the skills and interest of the postdoctoral applicant, fostering independent career development for the researcher. Finally, the project allows the researcher to investigate questions of general interest. While the main focus of the PI's research is on Drosophila, the basic principles apply as well to vertebrates of veterinary relevance, for example. In fact, in mammals, an even larger fraction of the genome is derived from transposable element DNA than in Drosophila—usually close to 50% instead of 10% (Wicker et al. 2007). Though most of these elements are dormant, they can be reanimated via retroviral infection or stress; in humans, these newly activated elements are suspected proximate causes of cancer and schizophrenia.

References

Capy P, Gasperi G, Biemont C, Bazin C. 2000. Stress and transposable elements: co-evolution or useful parasites? Heredity (Edinb). 85:101-106.

Messer PW. 2009. Measuring the rates of spontaneous mutation from deep and large-scale polymorphism data. Genetics. 182:1219-1232.



Wicker T, Sabot F, Hua-Van A et al. 2007. A unified classification system for eukaryotic transposable elements. Nat Rev Genet. 8:973-982.

Biémont, C, C Vieira. 2006. Genetics: Junk DNA as an evolutionary force. Nature 443: 521-524.

Hancks, DC,HH Kazazian. 2012. Active human retrotransposons: Variation and disease. Curr Op Genet Devel 22: 191-203.

Bundo, M, M Toyoshima, Y Okada, W Akamatsu, J Ueda, T Nemoto-Miyauchi, F Sunaga, M Toritsuka, D Ikawa, A Kakita, M Kato, K Kasai, T Kishimoto, H Nawa, H Okano, T Yoshikawa, T Kato,K Iwamoto. Increased L1 retrotransposition in the neuronal genome in schizophrenia. Neuron http://dx.doi.org/10.1016/j.neuron.2013.10.053.