

## Detection of *Drosophila melanogaster* line admixture through targeted barcoding sequencing

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*Drosophila melanogaster* is a widely used model organism in many biological studies. Usually *D. melanogaster* inbreeding lines maintained in lab are with a high density, therefore one line might be invaded by other lines. Up till now, there is no effective way to check the line admixture in a large scale. In this study, we serve a new method, Line-seq, to solve this problem by taking advantage of both targeted sequencing and barcoding sequencing techniques. Using Line-seq, we successfully detected line admixture in 23 inbreeding lines and compared the performance of Line-seq and traditional Sanger sequencing in eight artificially admixed samples. Line-seq can detect exogenous DNA admixtures as low as 6%, while Sanger sequencing can do so when the proportion of exogenous DNA rises up to around 20%. Our results highlight Line-seq is an sensitive, accurate, as well as cost-effective method to detect *D. melanogaster* line admixture.

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## Blood ties: Metabolic convergence among gammaproteobacterial endosymbionts from blood-feeding arthropods and the Mexican leech *Haementeria officinalis*

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Endosymbiosis between eukaryotic hosts and microorganisms is a common phenomenon in insects, whose typically unbalanced diets are usually complemented by their obligate endosymbionts. While much interest and focus has been directed towards phloem-feeders like aphids and mealybugs, blood-feeders such as the Lone star tick (*Amblyomma americanum*), Glossina flies, and the human body louse (*Pediculus humanus corporis*) also depend on obligate endosymbionts to complement their B-vitamin-deficient diets, and thus are required for growth and survival. Strict blood-feeding glossiphoniid leeches, contrary to the predatory species, have also been found to harbour distinct endosymbionts belonging to the Gamma and Alphaproteobacteria housed in specialised morphologically-diverse organs. The Mexican leech, *Haementeria officinalis* is associated to the obligate endosymbiont *Candidatus Providencia siddallii* (Gammaproteobacteria). This symbiont resides intracellularly in spherical bacteriomes attached to the oesophagus, and possesses a highly-reduced genome with high A+T content and a reduced set of metabolic capabilities, all of which are common characteristics of ancient obligate endosymbionts of arthropods. Its genome has retained many pathways related to the biosynthesis of B-vitamins, pointing towards a role in supplementing the blood-restricted diet of its host. Through genomic comparison against the endosymbionts of the different blood-feeding arthropods, we were able to detect a high degree of metabolic convergence among these very distantly related endosymbiotic bacteria. These findings strongly support the widespread and conserved metabolic dependence of the strict blood-feeders in their bacterial endosymbionts and the similar constraints these have undergone in their evolution as obligate nutritional partners.

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## Using molecular clocks to investigate beneficial (and deleterious) microbe-host interactions in the agroecosystem

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The molecular clock is a powerful technique used to estimate divergence time among organisms using molecules. Although widely used in animal and plant studies, the molecular clock is rarely applied to microbes and microbiomes: while in few cases co-radiation with host can be exploited, calibration of molecules is generally impaired by a lack of fossils and a poor knowledge of generation times outside model organisms. Here we outline, however, how molecular clocks can provide interesting insight into the biology of complex microbe-host interaction within various types of agro-ecosystems. Our case studies include: 1) the concomitant radiation of a phytoplasma with its apple host and its insect vector: a complex partnership further characterized by endosymbionts with putatively protective role against the pathogenic phytoplasma; 2) the origin of a likely beneficial new grapevine endosymbiont whose divergence matches human domestication; 3) the co-radiation of garden strawberry with its main anthracnose fungal endophytic agent. Although methodologically challenging, these examples illustrate that molecular clock is a promising and powerful tool to study the evolution of microbes and microbiomes in the agroecosystems.

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## Exploring the role of segmental duplications in the phenotypic differences between humans and other great apes

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