

Graduate Schools
Infection Immunity and Cancer, UniGe & UniL: CUS
Biology & Medicine, CMU

Seminar in Microbiology

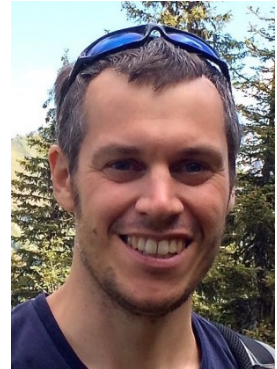
Monday, 1st December, 2014

Salle de séminaire 7172, CMU

11:30 – 12:30

Prof. Philipp Engel

Department of Fundamental Microbiology, UNIL



“Honey bee gut microbiota - a versatile model for microbial symbiosis”

The Engel lab uses different sequencing technologies and comparative analyses to mine the genomes of honey bee gut symbionts for genes involved in bacterial symbiosis. Furthermore, they use the genomic information to understand the evolution of gut communities. Like in mammals, bee gut bacteria have diversified by adapting to different host species, but also by colonizing different niches in the gut (Kwong et al. 2014, Engel et al. 2014, Engel et al. 2012). Using their genomic approaches they analyze the diversification of gut communities and aim to understand the evolutionary driving forces of their complexity and diversity. The honey bee is an ideal model to discover and study such determinants because the gut microbiota has a relatively simple composition compared to other animals and harbors bacteria specifically adapted to this environment. This allows Philipp Engel and his team to study a well-defined symbiotic system with a limited number of interactions and assess their underlying genetic determinants.

References:

Engel P, Stepanauskas R, Moran N1 (2014) Hidden diversity in honey bee gut symbionts detected by single-cell genomics. *PLoS Genet.* 10(9):e1004596.

Kwong WK, Engel P, Koch H, Moran NA. (2014) Genomics and host specialization of honey bee and bumble bee gut symbionts. *PNAS.* 111(31): 11509-11514.

Engel P, Martinson VG, Moran NA. (2012) Functional diversity within the simple gut microbiota of the honey bee. *PNAS*, 109(27):11002-11007.

Contact: P. Viollier

Sandwiches will be offered after the seminar