Abstract of Presentation

Presentation Title:

It takes two to tango: gene conversion in the *Rhizobium* genome.

Abstract:

Gene conversion (GC) is defined as a non-reciprocal transfer of information between homologs during recombination. Given the wealth of repeated sequences in the genome of *Rhizobium etli*, a nitrogen-fixing a-proteobacterium, we undertook the detection, analysis and impact of GC in this organism, using the nitrogenase (*nifH*) multigene family as a model. Our work, combining molecular strategies and population genetics approaches, has illuminated important aspects of GC. Among the main conclusions of this work are:

i) GC occurs at a frequency higher than spontaneous mutation.
ii) Frequencies of GC are not affected by the disposition of the interacting repeats (either in *cis* or in *trans*).
iii) GC is frequently associated with crossover events occurring nearby.
iv) GC tracts in the wild-type strain have a mean length of 400 bp.
v) The mismatch repair system (*mutS*) participates in elongation of the GC tracts.
vi) The extent of migration of Holliday Junctions plays a crucial role in determining the length of gene conversion tracts.
vii) GC generates a pattern of concerted evolution between members of the *nif* multigene family.