

Cologne Evolution Colloquium

Molecular Basis of
Evolutionary Innovations

SFB 680

Ed Louis
University of Leicester

The complexities of genotype to phenotype mapping: lessons from yeast

Recent advances in quantitative trait analysis in yeast have revealed that most polygenic traits have a complex genetic architecture. Individual QTLs many times have opposite effects than expressed in their original parental genetic background. Many QTLs are linked and these linked groups are composed of QTLs of mixed effects. We are just coming to terms with the non-additive interactions between QTLs. All of these together can explain some interesting observations: the expansion of phenotypic variation in almost any cross, multiple genetic solutions to the same selective problem, the robustness of phenotypes in clean lineages of yeast that have not been outbred by human activity. There is good news for breeders and those trying to improve strains but bad news for those trying to understand the underlying genetic causes of certain traits.

Wednesday, April 9, 2014, 17:00
University of Cologne, Institute for Genetics
Seminar Room 0.46

Hosted by Michael Lässig