**Parallel evolution in mosquito vectors – a story of insecticide resistance**

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**Introduction**

* parallel evolution
* the evolution of insecticide resistance

**Results**

Selection Scans (G123, or H12, H123) and expression data - evidence

* + A plot which on top is a GWSS with multiple lines for different pops , below is a diagram of chromosome 2L arm, with 2La and labelled genes (vgsc, rdl, coe). Below that is zoomed in diagram of genome region. Below that is integrated expression data boxplot of log 2 fold changes per gene

Haplotype clustering of sweep region,

* + Plot of haplotype clustering and below amino acid variants in COEAE1F/COEAE2F
  + Plot of different haplotype cluster frequencies on map
  + Information on karyotype differences between sweeps
  + EHH

Perhaps a large plot with a panel per sweep, within, info on LD, CNV, amino acids, prevalence

CNVs information, EHH around the CNV non CNV

* + Plot of CNV frequency, and close look at the breakpoints
  + Moshi arabiensis (large CNV spanning 10 genes)

Protein modelling

* Regulatory mechanisms
  + maf-s/keap1 sweep
* Comparative evolution section - culex, coluzzii, arabiensis. Think about how to do efficiently.
* qPCR
* CRISPR validation
  + In Tiassale? Ideally would have west african gambiae colony.
  + Outsourcing? recombinant protein.