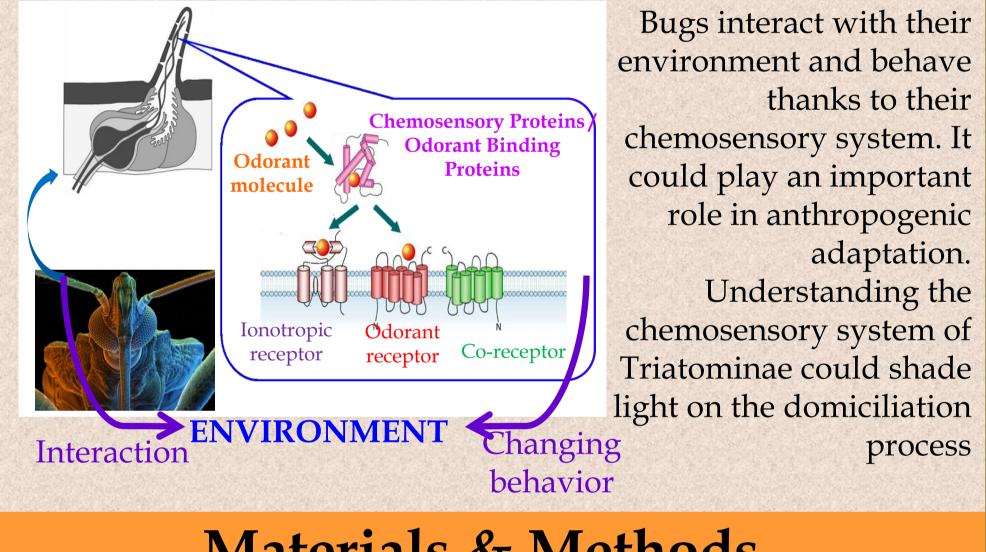


process



# **Materials & Methods**

**RNA extraction and sequencing** 

2 sylvatic populations (A and C)



domiciliary population (B)

Log2 fold change: Attributable to a variable over the mean of normalized counts Red points: genes differentially expressed (Padj < 0.05)

Among top 50 differentially expressed genes of environment comparisons, a majority of chemosensory genes:

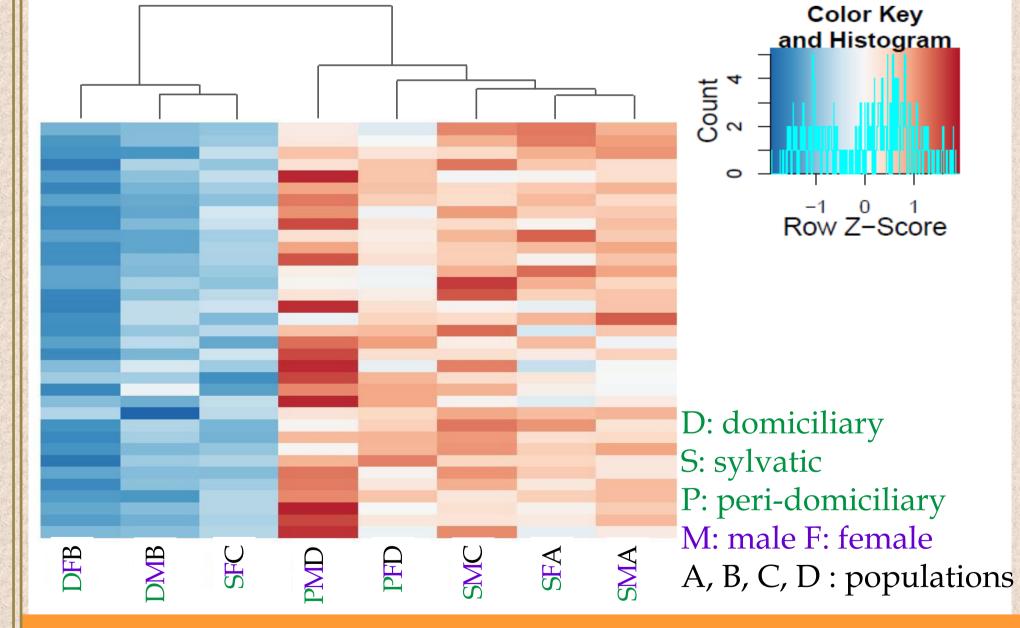
-Odorant-binding proteins: transport odorant molecules to olfactory receptors in sensilla

-Pheromone-binding proteins: transport pheromones to olfactory receptors

-Cytochrome P450: have been proposed to act as odorant-degrading enzymes in several insect species

-RNA-binding proteins: participate in forming ribonucleoprotein complexes

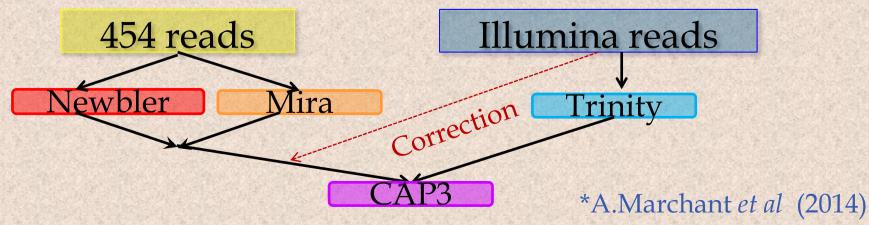
### Genes clustering based on differentially expressed OBP or P450 genes (under-expressed in domiciliary samples)





 $\rightarrow$  RNA extraction from antennae and rostrum of Triatoma peri-domiciliary brasiliensis populations population (D)  $\rightarrow$  454 and Illumina Sequencing

## De novo assembly of the T. brasiliensis reference transcriptome pooling all data



## **Differential expression analysis**

-Mapping each sample on *T.brasiliensis* reference transcriptome with **BWA** 

-Differential expression analysis with DESeq2  $\rightarrow$  comparison of environmental conditions

-Annotation of differentially expressed transcripts with blastx against swissprot database

# Conclusion

As expected, differences of expression are found in the chemosensory system between different environments. These results remain to be confirmed by qPCR.

Domiciliary samples present gene expression profiles which significantly differ from sylvatic and peridomiciliary populations, while sylvatic and peridomiciliary samples show few differences in expression profiles.

\*A.Marchant et al . De novo transcriptome assembly for a non model species, the blood-sucking bug Triatoma brasiliensis, a vector of Chagas disease. Genetica, submitted









