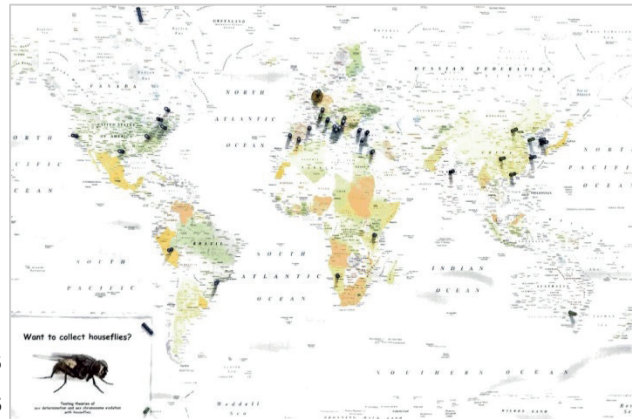


Why are sex determiners in the housefly (*Musca domestica*) duplicated?

Supervision by: Xuan Li, Ljubinka Francuski

Contact: x.li@rug.nl, room 5172.0666 or l.francuski@rug.nl, room 5172.0668;
language: English

As annoying as they are, houseflies are perfect organisms to study sex determination evolution, for housefly uniquely possesses multiple sex-determining systems. In some populations, a dominant male determining locus (*M*) decides male sexual fate, where in some other populations a dominant female determiner (*tra^D*) nullifies *M* function and makes individuals female. We have found that the *M* locus contains a male-determining gene named



Sample collecting points of houseflies

Mdmd (Sharma et al, Science 2017). Multiple copies of (pieces of) this gene appear to be present in the *M*-locus for unknown reasons. *M* usually locates on the Y chromosome it can jump within the housefly genome and be found on any of the autosomes. *M* loci in different populations vary at genome sequence level. *Tra^D* is a mutant of *tra*, which is a vital gene in the housefly sex-determining pathway. Recently, we discovered that *tra* is also duplicated within the housefly genome. We believe this duplication happened very recently and may vary in different geographical populations.

We have collected housefly samples worldwide. With this project, we propose to use these samples to investigate in detail: 1) *M*-locus variation in different housefly populations; 2) *tra* duplication frequency in different populations. By doing that, we want to answer: 1) whether the structure and genomic location of *M*-loci follow certain geographical patterns; 2) whether *tra* duplication has occurred worldwide in populations; 3) as *M* has to closely interact with *tra* in housefly sex-determining pathway, is there a relationship between *M*-locus variation and *tra* duplication? These results will give us a better understanding of housefly sex determination and increase our knowledge of sex determination mechanisms and sex chromosome evolution.

Methods: DNA extraction, primer design, PCR, Sanger sequencing.

Starting date: open