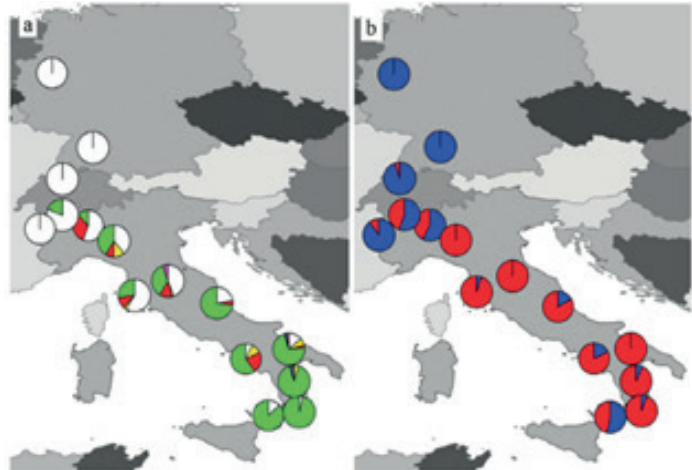


## Can geographic variation in intralocus sexual conflict maintain polymorphic sex determination mechanisms?

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Although sex determination is an essential process in the development of an individual, the mechanisms that determine sex are incredibly diverse. Even between closely-related species, different genes can determine sex, and different chromosomes may have become sex chromosomes. This suggests turnover in sex determination systems occur frequently. Various evolutionary phenomena may promote such turnovers, amongst which intralocus sexual conflict (IASC). IASC occurs when alleles with fitness benefits in one sex confer fitness costs in the other sex.



Kozielska et al. 2008. *Genet. Res. Cambridge* 90: 157–165.

Relative to normal autosomes, sex chromosomes may represent a refuge for IASC loci, because they are transmitted differently through males and females. Likewise, newly-mutated sex determination genes may spread when they are linked to an IASC locus. This new sex-determining gene may then outcompete the ancestral sex-determining gene, resulting in turnover of the sex determination mechanism. Different sex determination genes may also co-exist, though only under certain conditions. Houseflies have a polymorphic sex determination system in which populations in different geographic locations have different mechanisms that determine sex. It is currently unknown why this variation is maintained. Here, we will test whether geographic variation in the strength of IASC can result in stable polymorphism between populations in their sex determination mechanisms, similar to the housefly scenario. We will adapt previously-developed models to incorporate population structure, including factors such as spatial heterogeneity in selection and migration. Experience with C++ is preferred but not required, though some familiarity with programming (e.g. R) is recommended.

**Methods & keywords:** C++; computer simulations; individual-based modelling; R.

**Starting date:** open