

Population genetics of *Glossina fuscipes fuscipes* from southern Chad

Review

The author has embarked on a very important topic regarding the establishment of data on trypanosomose, in areas that have previously been the subject of vector control intervention, but also the exploration of new foci.

This is an original work considering the fact that control programs were initiated in some tsetse infested areas and was interrupted. It is urgent to understand and predict the sustainability of such vector control programs by gathering population genetics indices, accessed here in order to curb further reinvasion risks.

L1 Avoid columns in the engaging sentence and I suggest to say "Tsetse flies (genus *Glossina*) are vectors of Human African Trypanosomosis (HAT) and Animal African Trypanosomosis (AAT) where they transmit the deadly trypanosomes to human populations and domestic animals in sub-Saharan Africa". I suggest to singularize the word "Trypanosomosis" and instead say Trypanosomiasis.

L78 Delete "e.g." and make just the reference

L479 Was the correlation between H_s and G_{ST} necessary when we already have F-statistics which is more accurate?

L586 A part from FCA), DAPC, why not try to use Migrate to Estimating migration rates between populations and also establish distance matrix between sites, using the geosphere package in R.

As junior reviewer, I have no expertise to evaluate dispersal data and analysis since I had not work intensively with these tools.

All populations' genetics indicators have been extensively tackled with mathematical models, which I am not familiar to some, and to my view, this paper stand a higher profile review and I suggest that senior reviewers(e.g Adalgisa Caccone or Richard Echodu) could give strong recommendations to this paper.

The paper is publishable as per this journal guidelines and will contribute strongly the further tsetse control operations in Chad.