



Understanding local population genetics of tsetse: The case of an isolated population of *Glossina palpalis gambiensis* in Burkina Faso

Thierry De Meeûs^{a,b,*}, Sophie Ravel^b, Jean-Baptiste Rayaisse^c, Fabrice Courtin^a, Philippe Solano^a

^a Institut de Recherche pour le Développement (IRD), Centre International de Recherche pour l'Élevage en zones Subhumides (CIRDES), IRD UMR INTERTRYP IRD-CIRAD, CIRDES 01 BP 454 Bobo-Dioulasso 01, Burkina Faso

^b Institut de Recherche pour le Développement (IRD), UMR INTERTRYP IRD-CIRAD, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France

^c Centre International de Recherche Développement sur l'Élevage en zone Subhumide (CIRDES), 01 BP 454 Bobo-Dioulasso 01, Burkina Faso

ARTICLE INFO

Article history:

Received 27 January 2012

Received in revised form 30 March 2012

Accepted 5 April 2012

Available online 22 April 2012

Keywords:

Tsetse flies

Population genetics

Isolation

Effective population size

Wahlund effect

ABSTRACT

Tsetse flies are the vectors of human and animal trypanosomiasis. For tsetse eradication programs, it is crucial to be able to identify and target isolated populations, because they can be targeted for eradication without risk of reinvasion. However, most data that are available on non-isolated populations fail to find how these populations are locally structured, because Wahlund effect (admixture of individuals from genetically different units) always interfere with interpretations. In this paper, we investigated the genetic population structure of a possibly isolated population of *Glossina palpalis gambiensis* in a sacred wood in South Burkina Faso, using microsatellite DNA markers. We found that genotypic proportions in this population were in agreement with random mating model and that these tsetse were genetically highly differentiated from other populations of the same Mouhoun river basin only a few kilometers away, confirming its genetic isolation. The population also displayed substantial temporal differentiation in a two years period that lead to an estimate of effective population size of ~100 individuals. The fact that no Wahlund effect was identified allowed us to accurately measure the basic genetic parameters of this isolated population. Identifying such isolated and small populations is crucial for eradication programs and should be implemented more often.

© 2012 Elsevier B.V. All rights reserved.

1. Introduction

For accurate demographic inferences to be made out of population genetics data, in particular dispersal, it is crucial to target as precisely as possible the true demographic units (subpopulations) of the organism under investigation. It is indeed preferable avoiding Wahlund effects that results from the pooling into the same subsample of individuals belonging to genetically differentiated subpopulations, because such Wahlund effects will tend to bias dispersal estimates. The population genetics of *Glossina palpalis gambiensis*, vector of African trypanosomiasis, is recurrently faced with Wahlund effect (heterozygote deficits due to the presence, in the same subsample, of individuals belonging to genetically different units) along riverine environments (Solano et al., 2000; Bouyer et al., 2009, 2010; Kone et al., 2011). On the opposite, “true” subpopulations (i.e. not displaying such heterozygote deficits) seem to be appropriately targeted in coastal areas of West Africa (Solano

et al., 2009, 2010a). This structuring of tsetse population at microgeographical scale in riverine habitats is believed to come from the fact that, along rivers, the trapping devices trap individuals belonging to different demographic units. It is indeed believed that riverine *G. palpalis gambiensis* look for hosts in a much wider zone than the site in which mating and larviposition occur, and where male and female tend to come back for reproduction as suggested by the ambit theory of Jackson (1941) and confirmed by Wahlund effects found within each trap even when traps are separated by no more than 200 m (Bouyer et al., 2009) while mark-release-recapture studies suggest a potential (feeding) dispersal that can reach 3 km (Bouyer et al., 2009). Wahlund effect thus constitutes a problem for estimating accurately effective population sizes and dispersal, which is a trouble as regard to decision making for control strategies. A way to prevent Wahlund effect would be to target sites known to be totally isolated at a scale defined by the dispersal capabilities of this tsetse species. Identifying isolated populations where they exist is crucial, because such isolated populations can be targeted for eradication and there will be less possibility of reinvasion. This is typically what the pan African tsetse and trypanosomiasis eradication campaign (PATTEC) wants to achieve (Schofield and Kabayo, 2008). To test this hypothesis, we investigated the case of the remote *G. palpalis gambiensis*

* Corresponding author at: Institut de Recherche pour le Développement (IRD)/ Centre International de Recherche pour l'Élevage en zones Subhumides (CIRDES), IRD UMR INTERTRYP IRD-CIRAD, CIRDES 01 BP 454 Bobo-Dioulasso 01, Burkina Faso.

E-mail address: thierry.demeeus@ird.fr (T. De Meeûs).

population that survives in the sacred wood of Bama in South West Burkina Faso near Bobo-Dioulasso, isolated among rice crop fields that, as opened habitats, are inappropriate for the dispersal of *G. palpalis gambiensis*. To test if this site was occupied by a single and isolated *G. palpalis gambiensis* population, we captured and genotyped tsetse flies from Bama sacred wood during two years, tested the existence of a Wahlund effect, measured their genetic differentiation compared to other flies sampled along the Mouhoun River basin, and estimated effective population size of this potentially isolated spot. We show that this site is indeed occupied by a relatively small and isolated population of *G. palpalis gambiensis*, and thus that when subpopulations are appropriately isolated and targeted in this geographic area, no Wahlund effect affects the genetic data and thus no migration (reinvansion in case of previous eradication) occurs from nearby sites.

2. Material and methods

2.1. Study area

Burkina Faso is a sudano-sahelian country of West Africa. The study area is located in the South West of Burkina Faso, where the landscape was originally savannahs that have now been replaced by crops (mainly cotton, but also millet and maize). Some forest galleries remain along the Mouhoun river (formerly called Black Volta), and constitute the main habitat of the riverine tsetse species *G. palpalis gambiensis*. The rainfall is around 1000 mm/year. Bama is a town of ~10,000 inhabitants located 25 km North from Bobo-Dioulasso. This area was originally a swamp located close to the Kou River (a tributary of the Mouhoun) and has been transformed into an important rice production perimeter in 1967. Nowadays, it has the particularity of constituting the greatest rice production area of this part of the country. The fact that rice cultivation is the main activity implies that the original vegetation does not exist anymore; hence this habitat is not suitable for *G. palpalis gambiensis* because fully opened, at the exception of the small isolated forested relict still preserved because it constitutes a sacred wood (see Fig. 1). This wood (11.38454 N, -4.409087 W) is very small (500 m long * 130 m large), but has permanent water and protected vegetation, as well as some monitor lizards (*Varanus niloticus*), crocodiles (*Crocodylus niloticus*) and humans that probably constitute the main feeding source of this *G. palpalis gambiensis* population.

2.2. Sampling

Tsetse flies were sampled using six biconical traps in 2007 and seven traps in 2009. Additionally, to measure the degree of isolation of this population, we used tsetse sampled along the Mouhoun River basin in Darsalamy, Samandeni and Banzon, sampled in 2007 that were already genotyped and analyzed elsewhere (Kone et al., 2011) and are respectively 36 km, 9.6 km and 55.2 km away from Bama (see Fig. 1). Raw data, with GPS coordinates and all information are also provided as tabulated text file as Supplementary Table S1.

2.3. Genotyping

All tsetse flies were genotyped at eight polymorphic microsatellite loci: X55_3, XpGp13, pGp24, A10, XB104, XB110, C102 and GPCAG with X signifying that the locus is heterosomal and thus haploid in males. Detailed procedures of genotyping have been described elsewhere (e.g. (Solano et al., 2009)). Genotypes obtained for each locus are presented in supplementary files S1 (data coded homozygous for X-linked loci in males) and S2 (data coded as missing for X-linked loci in males).

2.4. Data analyses

All data sets were handled with Create V 1.1 (Coombes et al., 2008) and converted into the appropriate format as needed.

Population structure was assessed through Wright's F -statistics (Wright, 1965). F_{IS} is a measure of local inbreeding of individuals relative to inbreeding of subsamples. It is thus also a measure of reproductive strategy and varies from -1 (all individuals heterozygous for the same two alleles within each subsample) to $+1$ (all individuals are homozygous with at least two alleles in subsamples) and equals 0 when all subsamples conform to genotypic proportions expected under random union of gametes (panmixia). It is thus also a measure of deviation from the random mating model. F_{ST} measures inbreeding resulting from subdivision of subsamples relative to the total inbreeding. It is thus also a measure of differentiation between subsamples. It varies between 0 (no differentiation) and 1 (all subsamples fixed for one or the other allele). These statistics were estimated with Weir and Cockerham's unbiased estimators (Weir and Cockerham, 1984) under Fstat V 2.9.4 (Goudet, 2003), updated from Goudet (1995).

The significant departure from 0 of these parameter estimates was tested by randomisation procedures under Fstat. For F_{IS} , alleles are randomly exchanged between individuals in each subsamples and the proportion of times a F_{IS} estimate is equal or higher than the observed one provides the exact P -value of the test. A significant positive value across loci can come from the reproductive strategy (sib mating) or the admixture of individuals belonging to different subpopulations. Locus specific excess of homozygotes can come from technical problems (null allele, dropout or stuttering) or selection (very unlikely for microsatellites that are non-coding sequences). For differentiation between populations, individual are randomised across subsamples and the statistic used here is the log-likelihood ratio G as recommended (Goudet et al., 1996).

Linkage disequilibrium (LD) between loci was also tested through randomisations of association between genotypes at each locus pair. For each pair of locus the tests were combined across subsamples with the G -based procedure as recommended (De Meeûs et al., 2009). There are as many tests as locus pairs (here 28). Consequently, some tests can be significant by chance. The significance over the 28 test series was assessed through an exact binomial test with k' success (the number of tests significant at level α), $k = 28$ attempts and mean $\alpha (= 0.05)$ and an alternative hypothesis $H_1 =$ "there are more than 5% significant tests" (unilateral test). This was undertaken with R 2.12.0 (R-Development-core-team, 2011).

Sex-biased dispersal between traps within Bama was assessed in each year separately. It was implemented with the biased dispersal option of Fstat using three statistics: Weir and Cockerham's estimate of F_{ST} , calculated separately in each sex; mean (mAI_c) and variance (vAI_c) of Favre et al.'s corrected assignment index AI_c (Favre et al., 1997) (see (Prugnolle and De Meeûs, 2002) for more details on these statistics). All three tests are based on a permutation procedure; the sex of each individual is randomly re-assigned in each population. The observed difference between male and female F_{ST} , the ratio of the largest to the smallest vAI_c and the AI_c -based t -statistics defined by Goudet et al., (2002) were then compared to the resulting chance distributions. For the most dispersive sex, F_{ST} and mAI_c are expected smaller and vAI_c is expected higher than for the less dispersive sex. This choice of statistics is motivated by the work of Goudet et al. (2002) where vAI_c was shown to be the most powerful statistic when migration is low (less than 10%), while F_{ST} behaves best in other circumstances. We also chose to keep mAI_c because it may be more powerful in case of complex pattern of sex specific genetic structure (De Meeûs et al., 2002; Kempf et al., 2010). Tests were bilateral (no sex is expected to disperse more than the other).

Download English Version:

<https://daneshyari.com/en/article/5911387>

Download Persian Version:

<https://daneshyari.com/article/5911387>

[Daneshyari.com](https://daneshyari.com)