A New Robust Diagnostic Polymerase Chain Reaction for Determining the Mating Status of Female Anopheles gambiae Mosquitoes

Kija R. Ng’habi, Ashley Horton, Bart G. J. Knols, and Gregory C. Lanzaro

Ifakara Health Research and Development Centre, Tanzania; Center for Vectorborne Diseases, University of California, Davis, California; Wageningen University and Research Centre, Wageningen, The Netherlands

Abstract. The principal malaria vector in Africa, Anopheles gambiae, contains two pairs of autosomes and one pair of sex chromosomes. The Y chromosome is only associated with males and other Y chromosome–specific DNA sequences, which are transferred to women during mating. A reliable tool to determine the mating status of dried wild An. gambiae females is currently lacking. DNA was extracted from dried virgin and mated females and used to test whether Y chromosome–specific polymerase chain reaction (PCR) markers can be successfully amplified and used as a predictor of mating. Here we report a new PCR-based method to determine the mating status among successfully inseminated and virgin wild An. gambiae females, using three male-specific primers. This dissection-free method has the potential to facilitate studies of both population demographics and gene flow from dried mosquito samples routinely collected in epidemiologic monitoring and aid existing and new malaria-vector control approaches.

INTRODUCTION

Current knowledge suggests that sex chromosomes of many groups of animals and plants evolved from a pair of ordinary autosomes that acquired a major sex-determining locus. The Y chromosome, frequently associated with sex determination, and its associated genes have been well explored in a range of vertebrate organisms. Natural selection is believed to have suppressed the ability of the Y chromosome to recombine with its counterpart. Recombination suppression is considered to be responsible for a gradual Y chromosome genetic degradation. The silencing of most of the genes present on the Y chromosome as a result of degradation explains why only a few male fertility–determining genes remain functional on this chromosome. Among invertebrates, Y-linked gene studies have been limited to Drosophila and were recently extended to An. gambiae.

The An. gambiae mosquito has a karyotype consisting of two pairs of autosomes chromosomes 2 and 3 and one pair of sex chromosomes chromosomes X and Y. The Y chromosome constitutes ~10% of the whole genome and is normally associated only with males, and when present in a XX/XY system, induces male development. Y chromosome–linked DNA fragments have been characterized and Y chromosome–specific polymerase chain reaction (PCR) markers have been developed. This finding has been viewed as a milestone toward the application of novel vector control strategies for which a thorough understanding of population structure and gene flow among An. gambiae populations is necessary.

Traditionally, detection of mating success among females relied on microscopic dissection of females to determine the presence or absence of a mating plug in the bursa copulatrix or examination of sperm in the female spermatheca. This method is reliable and robust but is time consuming, labor intensive, and requires fresh specimens. A simple and rapid method to determine the mating status of dried female An. gambiae is therefore required to analyze large sample sizes within a short period of time.

In this study, we tested the hypothesis that Y chromosome–specific PCR markers can be successfully amplified from male sperm DNA present in recently inseminated females of An. gambiae sensu stricto and An. arabiensis. We present this technique as a new dissection-free (PCR based) method to determine the mating status of samples collected during routine entomologic surveys.

MATERIALS AND METHODS

Experimental design. Mosquitoes used in this study were from laboratory colonies obtained from the Malaria Research and Reference Reagent Resource Center (MR4) and maintained at the University of California, Davis, CA. These included a colony of Anopheles gambiae s.s. (Kisumu, East Africa) and a colony of An. arabiensis (Dongola strain) originating from northern Sudan. Pupae of both An. gambiae s.s. and An. arabiensis were isolated in cages allowing males and females to emerge separately. In this experiment, 100 female pupae and 50 male pupae were isolated to provide an appreciable number of virgin females and males, respectively. After adult emergence, 25 virgin females were mixed with 25 males for 3 days and exposed to natural sunlight (dusk) to stimulate mating. Another 25 virgin females were kept in a separate cage for 3 days as a control.

On Day 3, 15 virgin females, 15 potentially mated females, and 10 males were killed and stored at 4°C. After 5 days, when the samples had dried, DNA was extracted from the whole body of males and virgin and potentially mated females, following the DNAzol extraction protocol. A subsample of 10 potentially mated females were dissected under the microscope to confirm insemination by examination of the spermatheca. The experiment was done in triplicate.

The PCR reactions consisted of the following concentrations: 5 μL of 10× reaction buffer containing 1.5 mmol/L of MgCl₂, 0.2 μL of each DNPT at a concentration of 2.5 mmol/L, 25 pmol of each primer, and 0.5 μL of Taq polymerase in a total of 50 μL. Primer sequences to amplify DNA have been published for An. gambiae. Primer pairs were S23 (635 bp; F: 5'-TAAACCAAGTCGCGTCTCC-3'; R: 5'-TAAACCAAGTCGCGTCTCC-3') as described.
Thermal cycling for all reactions were performed using an MJ Research PTC-225 tetrad thermocycler. Conditions were the same for all primers (S23, 128125B, and 128125I): 94°C for 3 minutes, 35 cycles of 94°C for 20 seconds, 55–64°C for 30 seconds, and 72°C for 1 minute, followed by 72°C for 10 minutes. Loading buffer (6×) and 3% agarose gel was used. The agarose gel was submerged in the electrophoresis chambers, two thirds filled with 10× TBE running buffer. The gel was run for 1.5 hours at 85 mA.

RESULTS

We performed experiments to determine whether a multi-copy locus (ribosomal DNA) can be amplified in inseminated females. The experiment determined whether the DNA from the male partner of mated An. gambiae s.s. and An. arabiensis females could be amplified by PCR. A total of 50 virgin females, 57 potentially mated females, and 28 males of both An. gambiae and An. arabiensis were used in the study. Primers S23 and 128125B gave strong amplification in An. gambiae s.s. females, whereas primer 128125I gave the strongest amplification in An. arabiensis females. DNA from dried specimens amplified in a similar way as those from fresh specimens. All dissected females were found to have sperm in their spermathecae. Figure 1, A and B, shows that male DNA from inseminated females of both species can be amplified using Y chromosome–specific PCR markers with similar efficiency as the males themselves. As expected, no amplification was obtained from virgin females.

DISCUSSION

We showed that this method is suitable for distinguishing mated females from virgin females for both An. gambiae s.s. and An. arabiensis specimens and that this approach lends itself to screening large numbers of recently mated and dried specimens. This finding has useful implications for novel vector control strategies based on the release of large numbers of factory-reared male mosquitoes with the expectation that they will successfully mate with wild females to confer sterility or drive parasite-refractory genes into wild populations. In these cases, the transfer of sterile or transgenic sperm from released mosquitoes to wild conspecifics will depend on the frequency of mating between males carrying the trait (to be introduced) and the females that do not—even if target genes are linked to transposable elements.15 Because mating is ultimately the most appropriate mechanism to deliver the desired traits or genes into a target population,16 an effective method for evaluating mating success is of critical importance. Thus, this new dissection-free technique has potential useful application to novel vector control approaches.

Additionally, this technique will help improve our understanding of gene flow within An. gambiae populations. As opposed to methods based on microscopic dissection and direct observation that are conventionally used to assess male An. gambiae mating success, this method will make it possible to screen a substantially greater number of wild-collected females either in fresh or dried state. Contained semi-field systems are now becoming a central focus for release trials in many studies.17–19 The method developed here can thus make large-scale evaluation of mating success of released males by repetitive female sampling and screening possible.

In conclusion, we showed that mating can be determined by PCR amplification of inseminated female DNA. The speed and ease of this technique, and the fact that dried specimens can easily be evaluated, indicate that this process should allow robust and extensive analysis of large field-collected samples.

Received January 31, 2007. Accepted for publication April 30, 2007.

Acknowledgments: We thank the Vector Genetic Laboratory (University of California) for cooperation during the entire period of this study; Claudio Meneses for invaluable technical assistance during mosquito rearing and PCR optimization; Dr. Mark Benedict for suggestions and literature that made this study possible; and Dr. Heather Ferguson for reviewing the manuscript before submission.

Financial support: We acknowledge the International Atomic Energy Agency (IAEA) for financial support through a fellowship awarded to KRN to work at UC Davis. This research forms part of a VIDI Grant 864.03.004 from the Dutch Scientific Organization (NWO) awarded to BGJK. In addition, we acknowledge support to GCL through Grant AI040308 from the National Institutes of Health.

Authors’ addresses: Kija R Ng’habi, Ifakara Health Research and Development Centre, PO Box 53, Ifakara, United Republic of Tanzania, E-mail: kija@ihrcd.or.tz. Ashley Horton and Gregory Lanzaro, Department of Entomology, University of California, Davis, 396C Briggs, One Shield Avenue, Davis, CA 95616-8584. E-mails: gclanzaro@ucdavis.edu and ahorton@ucdavis.edu. Bart G. J. Knols, Laboratory of Entomology, PO Box 8031, 6700 EH, Wageningen University and Research Centre, Wageningen, The Netherlands, E-mail: Bart.Knols@wur.nl.

REFERENCES