



Development of 12 Autosomal STR Markers Allowing Cimicidae Identification

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Abstract

Bedbugs are a very recurrent pest all over the world which is often difficult to eradicate. This is the case for *Cimex lectularius*, a species whose bites can be manifested in a wide variety of ways. Thus, it seems necessary to develop a mechanism that confirms the presence of this insect in order to eliminate the pest as soon as possible. For this reason, the Basque Institute of Forensic Sciences in Sanfran (BIFSS) has been working on this research field and has developed 12 new autosomal STR markers that allow the identification of the Cimicidae family of insects.

Keywords: Cimicidae Identification; STR Markers; Plague Eradication

Abbreviations: STR: Short Tandem Repeats; BIFSS: Basque Institute of Forensic Sciences in Sanfran; DNA: Deoxyribonucleic Acid.

Introduction

Bed bugs are animals belonging to the phylum Artropoda and, more specifically, to the order Hemiptera and the family Cimicidae. Hemipters have modified their mouthparts into a "stylet" which is adapted for pricking or sucking [1]. Bed bugs are widely distributed around the world and, even though they have not been reported as vectors of disease transmission so far, they cause serious pests. *Cimex lectularius* is a hematophagous species with humans as primary hosts that severely affects the population worldwide since individuals are able to fit in extremely small spaces [2]. Thus, this makes it very difficult to localize and reach all the

individuals and so, to exterminate the pest. *C. lectularius* bites may leave from no visible effects to prominent marks [1], further complicating pest detection and, therefore, eradication.

Materials and Methods

STR Markers

Autosomal STR markers are used in order to differentiate species from DNA molecules. STRs are elements consisting of single DNA sequences (from 1 to 6 base pairs) repeated in tandem. The polymorphism of STRs lies in the fact that the different alleles have different numbers of base sequence repeats, so they differ in the total length of their sequence. STR markers used for species identification display a certain interspecific variability but are very little variable between

individuals of the same species [3], thus providing each species with a characteristic combination of distinct alleles that allows it to be distinguished from the rest.

Given the fact that these genetic markers allow to identify mainly mammals so far [4], the BIFSSF has discovered a new set of 12 STR markers by conducting massive sequencing studies with Cimicidae family insects that makes their identification possible. In addition, the performance of *in situ* hybridization techniques revealed the location of these sequences on the chromosomes 3, 6 and 8 of cimicids.

DNA Extraction and Analysis

Bed bugs introduce genetic material into the blood of their human hosts through the bite [1]. Thus, by extracting a blood sample from an area which is adjacent to the bite of a human individual, genetic information from both the human and the insect can be obtained. The processing of this information through multiplex PCR amplification and subsequent sequencing allows us to see the specific allele combinations in the sample and so to make inferences about species.

Discussion

Given the importance of identifying species that cause serious pests for the resolution of legal cases, a great deal of research is actually focused on the development of markers that make this possible. For instance, the Shanghai Forensic Institute has been lately working on the development of STR markers in mitochondrial DNA aiming to identify mosquitoes, which are vectors of serious diseases [5]. Likewise, the German Forensic Research Council recently published on the use of the same type of markers to control infestations of

bark beetles which severely damage forests [6].

Conclusion

Molecular identification of cimicids represents a reliable and effective alternative to the limitations of their identification via bites or morphological characters. However, it would be necessary that these techniques gave us approximations on genera or even species, since not all of them produce equally serious damage [2]. Therefore, considerably more work will need to be done to obtain more precise results and thus take more economically adjusted measures in each case.

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