別紙２

Results report

１． Title of Research and Development： Integrated research program for the control of dengue fever mosquito in Burkina Faso, West Africa

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４． Results of Research and Development:

Dengue fever is a viral vector-borne disease caused by infection of four dengue virus serotypes (DENV1-4) via blood-sucking of *Aedes* mosquito. In Burkina Faso, dengue represents an added burden in an epidemiological landscape dominated by malaria. Although *Ae. aegypti* and *Ae. albopictus* are present in Burkina Faso, there has been no recent entomological study that would provide information about its distribution, especially in the country's large cities, where populations of this very urban mosquito have likely become widespread. Additional new strategy to control the vector should absolutely be developed and involved in integrated vector management (IVM), because it is one of the most effective means to deal with the problem while waiting for a vaccine or another effective dengue control strategy. In the proposed project of fiscal year 2015, based on collaboration between Japan and Burkina Faso, entomological studies promoting multilateral approaches were performed to gather fine knowledge of diagnosis, ethology, immunity, and epidemiology of vector species on effective vector control, as described below:

1) *In vitro* pathogen detection system for the dengue virus (at least 4 types) with LAMP was established. We verified a method of preserving mosquito specimens suitable for dengue virus RNA detection (silicone gel, flattened specimens, etc.) considering long-term and mass preservation.

2) We collected *Aedes* mosquitoes via insecticide spraying, manual catching, etc., in the fixed mosquito collection sites of Burkina Faso. To assess seasonal prevalence, we set up a collaborative framework to collect mosquito specimens throughout the year. *In vivo* imaging to create a mapping of the proliferation and environmental adaptation of the dengue virus in the life cycle of *Aedes* mosquitoes (*A. aegypti* and *A. albopictus*) was established.

3) We isolated and identified mosquito fungi and intestinal bacteria with 16S ribosomal DNA analysis. We performed screening of a genetic expression library that randomly forces the expression of genes in the genomic sequence in *Drosophila* (fruit flies) and identified genetic candidates for resistance/tolerance function control in arthropods for human non-pathogenic viruses such as FHV and VSV.

4) We created a *nanos-Cas9* mosquito that expresses Cas9 in fertilized eggs with the transgenic method to efficiently construct gene deletion in *Aedes* mosquitoes (particularly *A. aegypti*). We established a GAL4/UAS system for tissue-specific expression in *A. aegypti*. We also conducted genetic screening to control the recognition of a full stomach in fullness-perceiving neurons of *A. aegypti*.