

## Abstract of Thesis/Dissertation

## Applicant

Doctoral Program in Animal and Food Hygiene

Graduate School of Animal Husbandry

Obihiro University of Agriculture and Veterinary Medicine

Student ID: 25610Signature of Applicant: Khavleezelle Jardin Moendeg

Title : Diagnostic and Microsatellite Studies of *Schistosoma japonicum* in Humans and Animal Reservoir Hosts

(患者及び保虫宿主を対象とした日本住血吸虫症診断法の開発と寄生虫マイクロサテライト解析に関する研究)

## Abstract

Schistosomiasis is a neglected tropical disease affecting almost 240 million people with more than 700 million are considered to be at risk of infection. Endemic in 78 countries throughout the world, this parasitic disease is caused by the blood fluke under the genera *Schistosoma*. *Schistosoma japonicum* is considered to be the most virulent species among the five human schistosomes because of the larger number of eggs it can produce. In addition, *S. japonicum* is zoonotic with a wide variety of animals which can serve as reservoir hosts making the schistosomiasis control difficult. Thus, this study aims to develop and perform tools that will lead to a better understanding of the transmission epidemiology of *S. japonicum*. These includes the development of a uniform diagnostic test that can be used for a variety of mammalian hosts and microsatellite markers that will provide a better understanding on the genetic diversity of the parasite. These are considered to be important in the assessment and monitoring of the success of control programs done against

schistosomiasis.

The first chapter of this study focused on the development of a cocktail-ELISA for the diagnosis of *S. japonicum* infection in different mammalian hosts including humans, dogs and water buffaloes. Animal reservoirs serve as sources of the parasite that contributes to the transmission of the disease to humans. Such role of these animals has been neglected as proven by the absence of a suitable diagnostic test. Therefore, a uniform diagnostic test for the detection of zoonotic schistosomiasis in humans and important reservoir hosts will be useful in formulating a unified disease surveillance. In this study, combinations of recombinant proteins that had already been evaluated as potential antigen for each host species were examined for its common use in humans and other animal species. Results showed that the combination of three recombinant antigens, SjTPx-1/Sj7TR/Sj1TR presented the highest sensitivity in humans (84.1%), water buffaloes (80%) and dogs (80%) and specificity (100%) in all host species. Cocktail antigens are therefore very useful in possibly improving the surveillance of zoonotic schistosomiasis and also emphasizing the neglected importance of animal reservoirs.

The second chapter of this study aimed to determine the presence of genetic diversity in the parasite in different endemic areas through microsatellite analysis. *S. japonicum* populations collected in different endemic sites in the Philippines were characterized using 10 microsatellite markers. Results showed that a high genetic diversity was observed among all the samples examined, especially in those from the highly endemic municipalities of Irosin, Catarman and Socorro. A positive correlation between the genetic diversity in the parasite population and the prevalence of the disease confirmed the results shown in previous studies done in other schistosomiasis-endemic countries. This

information on the genetic diversity of the parasite can be utilized for monitoring and modifying the disease control program.

Using the microsatellite information obtained in the previous chapter, the population structure of *S. japonicum* was determined in the third chapter of this study. Analysis showed that the parasite samples collected from different endemic areas in the Philippines did not form a particular spatial structuring. The lack of geographical structuring suggested that an ongoing gene flow is occurring among the *S. japonicum* populations amidst extensive control measures. These findings imply that there is a continuing transmission of *S. japonicum* across geographic areas, possibly attributing to the migration and movement of infected hosts. A safeguarding precaution should therefore be implemented in areas with high genetic diversity in the parasite population to ensure localized elimination of schistosomiasis.

In conclusion, two important tools necessary for a more effective disease surveillance for schistosomiasis have been presented in this study. A more wholistic approach in eliminating schistosomiasis can be obtained by developing a unified disease surveillance among various mammalian hosts utilizing diagnostic tests like cocktail-ELISA. On the other hand, genetic surveillance using microsatellites has proven to be important in predicting disease outcomes and the success of control programs in schistosomiasis-endemic areas.