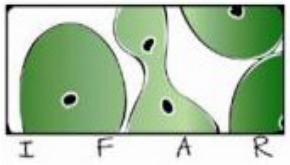

IFAR 2007 Professional Development Program
Completion Report
[800 words]

Instructions:
Please submit the completion report by email, using this form, through the sponsoring CGIAR Center to ifar@ifar4dev.org within three months after the completion of the fellowship.

Please check if Thalwitz Scholarship _NO

Name of Applicant ------Huihui Li----------

Sponsoring CGIAR Center ----------CIMMYT----------

I. Work Program goals achieved (maximum length: 200 words)

This project provides us an opportunity to conduct an in-depth study of QTL mapping for epistatic networks based on our proposed inclusive composite interval mapping (ICIM) for additive QTL, as well as a 3 month's staying (September to December, 2007) with Dr. Ed Buckler's Lab in Cornell University.

Two likelihood statistics were proposed in the two dimensional scanning in experimental populations derived from two inbred parental lines, one is used to test both additive and epistasis simultaneously, and the other is used to test epistasis. We also derived the theoretical formulas for calculating various components of genetic variation under linkage and epistasis, to determine whether the two-dimensional scanning is necessary. Extensive simulations were completed using three hypothetic genomes to confirm the efficiency of ICIM in mapping epistasis, and to demonstrate its ability to identify novel QTL networks which cannot be detected by using multiple interval mapping (MIM; Kao et al. 1999). The gains of ICIM compared with MIM and an empirical Bayesian model (Xu and Jia 2007) were obviously observed from the simulation study.

We have applied our novel method to two actual mapping populations. In a barley population consisting of 145 doubled haploids, we identified nine additive QTL affecting kernel weight and found that non-additive variation was less important for that trait in this population. In a maize population consisting of 224 recombination inbred lines evaluated under water-limited conditions, we detected seven additive QTL expressing about 37% of the phenotypic variance and seven digenic interactions expressing about 30% of the phenotypic variance for male flowering time. For the seven identified interactions, most QTL did not have significant additive effect. Permutation test was used to determine the appropriate threshold LOD score declaring significant epistatic QTL networks in this study. Part of the results has been published in the international journal Theoretical and Applied Genetics (Li, H., J.-M. Ribaut, Z. Li and J. Wang., 2008 Inclusive composite interval mapping (ICIM) for digenic epistasis of quantitative traits in biparental populations. Theor. Appl. Genet. 116: 243-260.)

We have integrated ICIM for epistasis into the software QTL IciMapping, which make IciMapping more powerful (available from http://www.isbreeding.net). The interface of QTL Icimapping will be continuously improved. The QTL method and mapping software supported by the IFAR fellowship have provided the CGIAR and NARS scientist the most suitable QTL mapping method, such that they can make a better use of the genetic data they have collected and gene information in improving their breeding efficiencies.

II. Plans for follow-up (maximum length: 200 words)

From a practical point of view, through our developed methods for additive and epistatic mapping, we can roughly know the number of genes for quantitative

traits, their locations in the genome and their effect on phenotype. Then we can use the genetics and breeding simulation tool of QuLine (Jointly developed and owned by CIMMTY and the University of Queensland, Australia) to combine different types of biological information and turn complex and voluminous data into knowledge that can be applied in breeding. This work will be collaboration with Crop Research Informatics Lab (CRIL), an alliance of IRRI and CIMMYT.

Theoretically, we want to extend ICIM to do multiple populations and environments joint analysis to catch more kinds of variance that can be utilized in molecular design breeding. This work will be collaboration with Dr. Ed Buckler, Cornell University.

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III. Report budget utilization including whether budget was spent as planned (maximum length: 100 words)

The budget was spent according the proposal budget item, as follows:

Upgrading of one laptop: US$1000;

Air tickets to Mexico (CIMMYT) and US (Cornell): US$2500;

US and Mexican visas: US$500;

Living and accommodation expenses in US and Mexico: US$4500

Books: US$1000;

Administrative and technical support
(en route costs, health insurance, consumables): US$1500

IV. Assessment of the fellowship experience and general comments. (maximum length: 300 words)

This fellowship provided a great opportunity for me to cooperate with the scientists in CAAS, CIMMTY and Cornell University. From the field work which I have not done before, I have learned the real problems in breeding, heard breeders' comments and suggestions, and developed more efficient algorithms to achieve excellent results. From a series of seminars either in CIMMTY or in Cornell University, I broadened my perception of the field of QTL mapping, not only on linkage analysis but also on association study, not only in plants but also in animals, and not only from a statistical point of view but also from a molecular point of view. It is also allowed me to identify further research needs that will help me to further my research work in QTL mapping.

I appreciate IFAR for financing the project, and I thank CAAS, CIMMYT, and Cornell University for hosting me.