



**IFAR 2008 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

Yes

Name of Applicant -----Changbin Yin-----

Sponsoring CGIAR Center

-----CIMMYT-----

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

Through the whole genome scanning, a high-density SSR marker map for the 65 CSS lines has been built. We selected 141 co-dominant SSR markers between the two parents Asominori and IR24. Among the 141 polymorphic markers, we found 137 SSR markers showing polymorphism among the 65 CSS lines. The high-density map showed that on average each IR24 marker allele exists in 4.1 CSS lines, while the original RFLP map showed that each IR24 marker allele exists in 3.7 lines. In the new map, on average each CSS line carries 8.6 segments from the donor parent IR24 which is nearly twice that of the original RFLP map (in the original RFLP map, each CSS line carries 4.6 IR24 segments).

Using the new SSR map, 13 CSS lines have been identified to be single IR24 substitution segment (SSS). To derive more SSS lines covering as much as the whole IR24 genome, we selected the other 22 CSS lines to make backcrosses. The new SSR map built and the SSS lines to be created are useful for fine mapping, genetic research and rice breeding. Most work was conducted in the CIMMYT China Office located in Beijing and Nanjing Agricultural University (NJAU).

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

In the next cropping season, we will use the 141 polymorphism SSR markers and an F2 population derived from Asominori and IR24 to build a linkage map for understanding the length of the donor segments in the 65 CSS lines and further QTL mapping studies. Genetic populations made in the previous season will be carried on for building SSS lines with better coverage of the IR24 genome. These SSS lines are valuable genetic stocks, which are extremely useful for genomic scanning for important breeding traits, QTL fine mapping, dissection of dominance and heterosis, and the design approach of breeding.

We will also use the SSR map and multiple environments phenotyping data to conduct QTL analysis. Based on the QTL information, we will do breeding for major quality traits through the design-led breeding approach. In addition, we plan to use SSS lines and their derived lines to study the high-level gene interaction which are extremely useful for increasing breeding gains in nearly future.

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

This project started in June 2008. The budget was spent as follows.

- Planting and growing materials (US\$1000)
- Laboratory cost for SSR marker screening (US\$2250)
- One laptop computer (US\$2928)
- Local travel to NJAU (US\$605)
- Books and journals (US\$1,000)
- Administrative and technical support (US\$1500)

A total of US\$9283 has been spent to date. The remaining funds (US\$1717) will be spent in the next two months for some lab work for marker screening in segregating populations.

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

The IFAR fellowship provides me a great opportunity to undertake this study with scientists at the CIMMYT China Office, CAAS and NJAU. Supported by the fellowship, I learned many practical experimental skills and gained a lot of valuable experience, and improved my experimental approaches. From the field work which I have never done before, I was profoundly aware of its complexity and importance, and I also now recognize that field-lab-consistency is very important. These experiences, skills and good habits will help me to further my research work in crop breeding and genetic research. As we have known, PCR-based SSR markers are more cost-effective, time-saving and operationally convenient than RFLP markers, and can be easily used in large-scale marker-assisted selection. Also, the 65 CSS lines population derived from Asominori and IR24 is a useful and typical CSS population. It is widely used in fine mapping, map-based clone, pyramiding breeding and genetic research. Many researchers who previously used the CSS population have asked me to build the linkage map and SSS population. I sincerely appreciate the IFAR fellowship for giving me this great opportunity and thank CIMMYT, CAAS, and NJAU for hosting me and their scientists for providing supervision.