

# INE: The Rice Genome Sequence Database

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## 1 Introduction

One of the major aims of the second phase of the Rice Genome Research Program (RGP) which started in 1998 is the complete sequencing of the rice genome. This is also part of the International Rice Genome Sequencing Project (IRGSP), in which Japan is in charge of sequencing chromosomes 1 and 6. In order to cope with the huge volume of sequence information that will be accumulated from this project, we have developed a rice genome database called INE (INtegrated rice genome Explorer, <http://www.dna.affrc.go.jp:82/giot/INE.html>) to serve as the central data resource for the rice genome sequencing effort.

### 2 Features of INE Database

INE is primarily designed to integrate all the genome information in rice. Therefore all the genomics data that have been accumulated during the first phase of RGP are incorporated as well. These include the genetic [1] and physical mapping [2] data of rice with detailed entries on marker information and ordered YAC clones. An EST mapping data, which is also a major project of RGP, will be incorporated soon.

The genetic and physical maps are presented as graphical interface to facilitate an easily comprehensible integration of relevant data. Thus the DNA markers in the genetic map are integrated with the physical map and the EST marker information are also presented in relation to the YAC physical map. The PAC contigs, which are the main template for sequencing, are shown together with the STS and EST markers identified in the PAC insert.

INE utilizes a Java-based application GIOT (Genome Information displayed Orderly Tool) developed by Mitsubishi Space Software (Fig. 1). It has a Java-based viewer and all the operations are performed once the data have been downloaded to the client's computer as INE applets from the server. Then the data file written in a text format is read through the CGI (Common Gate Interface). This allows rapid display of the integrated maps.

## 2 Repository for Rice Genome Sequence

INE aimed at incorporating all rice genome sequences contributed by participating members of the international collaboration and to accelerate the release of sequence information to the public domain. So far sequenced PACs with the completed annotation are already incorporated in this database. As the different groups accumulate genome sequence, the data will be deposited in this database. In order to ensure high quality sequence data, we have incorporated a file on low quality information of the annotated sequence to provide a check on the accuracy of the submitted sequence.

In the future we hope to build enhanced applications for data browsing, data editing and direct data submission to meet the ever-growing demands of the international rice genome sequencing efforts.

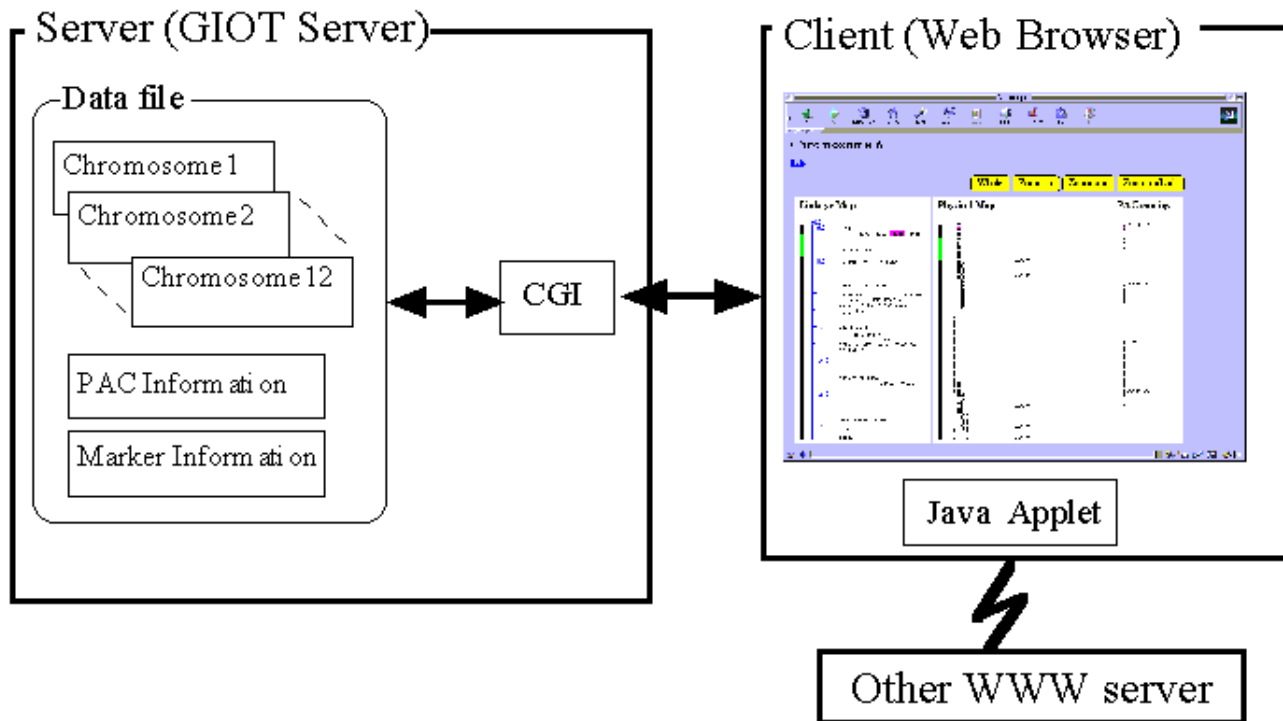


Figure 1: Data flow of INE (INtegrated rice genome Explorer).

## Acknowledgment

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## References

- [1] Harushima, Y., Yano, M., Shomura, A., Sato, M., Shimano, T., Kuboku, Y., Yamamoto, T., Lin, S.Y., Antonio, B.A., Parco, A., Kajiyama, H., Huang, N., Yamamoto, K., Nagamura, Y., Kurata, N., Khush, G.S., and Sasaki, T., A high-density rice genetic linkage map with 2275 markers using a single F2 population, *Genetics*, 148:479–494, 1998.
- [2] Tanoue, H., Baba, T., Saji, S., Itonuma, A., Hamada, M., Katagiri, S., Nakashima, M., Chiden, Y., Hayashi, M., Okamoto, M., Wu, J., Antonio, B.A., Koike, K., Umehara, Y., Matsumoto, T., Jong, P.J., and Sasaki, T., Construction of PAC ordered clones on rice chromosome 6, *Proceedings of Plant and Animal Genome VII*, p.207, 1999.