genotypes besides S/S, S/N and N/N, indicating the gne flow from Site II. Based on the genotype frequencies of breeding trees in Sites I and II, and those of seeds in Site I, interpopulational pollen flow rate ($u=0.315$) was estimated together with outbreeding rate ($t=0.634$) and selection coefficient for N/N genotype ($s=0.486$).

Publications from Genetic Resources Section, Genetic Stocks Research Center

Shin-ya IYAMA

The following publications were released from Genetic Resources Section this year.

1. "Stocks of experimental organisms maintained in the universities in Japan". 42 pages. (in Japanese).

Names of experimental organisms, location (laboratory) where the stocks are maintained, person in charge, and number of stocks were listed according to the universities. In total, 1141 locations in 172 universities and research institutes were included: 336 locations for animal stocks, 125 for plant stocks, 318 for microorganism stocks and 362 for cultured cell stocks.

2. "Drosophila Stock List in Japan 1985." 61 pages.

This list contains 1360 drosophila stocks kept in various places in Japan. Each stock is indicated with the place of maintainance. Wild and mutant stocks of *D. melanogaster*, *D. simulans*, *D. ananassae*, *D. hydei*, *D. virilis* and other species are included.

3. "Rice Genetics Newsletter Vol. 2". 122 pages. (in English).

This volume contains lists of recommended gene symbols and gene marker stocks of rice, a list of about 240 recent publications on rice genetics and 46 research notes on rice genetics. Rice Genetics Newsletter will be published annually.

Data Base Design of DNA Base Sequences

Sanzo MIYAZAWA

Experimental analyses of DNA base sequences have been developed and known DNA base sequences are rapidly growing. To make DNA sequence data, published in scientific journals, readable by computer and accessible to public domain, DNA sequence data banks have been established in Europe

and USA. This recent trend prompts biologists to use computers to analyze DNA base sequences. Typical examples of common analyses are those such as homology search, restriction enzyme site map, and open reading frame search. Search and retrieval of specific base sequences from DNA sequence data are prerequisite to such analyses. Thus, a DNA data base is demanded to efficiently manipulate sequence data. UNIX operating system has been chosen as a target system to develope a data base, because of a portable operating system. By taking advantage of superior tools for interprocess communication in UNIX such as shared memory and pipeline, basic tools for data manupulation will be implemented as commands at the shell level. In addition, a wide variety of application programs for sequence analyses will be incorporated into the data base system.