

significantly different from each other, they were regarded as not-contributed.

Using these standards, the efficiencies of individual fungicides were assessed. The results varied considerably according to the year, reflecting the yearly differences in the intensity and time of infection. However, the number of positively contributed fungicides was usually less than that of the negative or not-contributed group. This fact strongly suggests that fungicides can be reduced through extension of the spray interval in the program.

Another fact suggesting the reduction of fungicide was obtained in an experiment to detect the maximum duration of the protective activity of the fungicides constituting the spray program against white rot. The fungicides were sprayed in late June when active infections occur, and the fruits were periodically bagged with two-layered fruit bags for 45 days from the spraying. The duration of protective activity was assessed by the disease incidence shown by the fruit bagged on different days. High protective activity of several fungicides including azoxystrobin and dithianon, was maintained for 45 days, and 30 days in iminocadine-triacetate. This also suggested that the spray interval could be extended more than 15-days.

Given the two facts above, spray programs of different spray intervals, 15, 20, 25 day, were made with same fungicides. However, as the spray intervals were extended the spray times decreased, and one and two fungicides in the 15-day spray program were excluded in the 20- and 25-day program, respectively. They were subjected to a pilot test on Fuji cultivar,

and the control efficiencies against various diseases were examined. The tests were conducted for two years with slightly different programs. Even though the results were slightly varied according to the year and the program, the control efficiencies of 20- and 25-day programs were superior to those of 15-day program, or not differ with them. Upon those experimental results, several 25-day programs varied in the kind of fungicides and spray sequences were subjected to a pilot test. Control efficiencies were quite different among the programs, but some of them turned out to be highly promising. One program that showed good control efficiencies on white rot, bitter rot, and Marssonina blotch was subjected to an actual orchard test at 16 and 54 orchards in 2002 and 2003, respectively. The results were quite satisfactory. The diseases were effectively managed in most of orchards but slight damage by white rot or Marssonina blotch was recognized in a small number of orchards. Especially in 2003, in spite of the adverse climatic condition in which 58 days of rain during the vulnerable season to various diseases from May to August, good control was obtained in most of the orchards. By 2004, several hundred of farmers have already adopted the 25-day program for Fuji cultivar, but most of farmers still hesitate because of possible failure.

At present, the 25-day program can be used without any concerns with Fuji, Tsugaru and a few mid-season varieties that are moderately resistant to bitter rot. Efforts to develop the programs for cultivars susceptible to bitter rot are on going and will be the subject of our future research.

AL-3

Young Plant Pathologist Award

A Platform for Functional Genomics of Chili Pepper Defense against Pathogen

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Large-scale single-pass sequencing of cDNA libraries and microarray analysis have proven to be useful tools for discovering new genes and studying gene expression. As a first step in elucidating the defense mechanisms in hot pepper plants, a total of 30,000 expressed sequence tags (ESTs) were generated and constructed as a public database. The cDNA microarray which contain 4,815 independent pepper clones is developed and gene expression analysis identified 613 hot pepper genes that were transcriptionally responsive to the non-host soybean pustule pathogen *Xanthomonas axonopodis* pv. *glycines* (*Xag*). Several functional types of genes, including those involved in cell wall modification/biosynthesis, transport, signaling pathways and divergent defense reactions, were induced at the early stage of *Xag* infiltration. In contrast, genes encoding proteins that are involved

in photosynthesis, carbohydrate metabolism and the synthesis of chloroplast biogenetic proteins were down-regulated at the late stage of *Xag* infiltration. These expression profiles share common features with the expression profiles elicited by other stresses, such as fungal challenge, wounding, cold, drought and high salinity. We also identified several novel transcription factors that may be specifically involved in the defense reaction of the hot pepper. All the gene expression data were constructed as a public database and opened to research community. Functional analyses of selected novel genes are underway and part of it will be presented in the symposium. This study is the first report of large-scale sequencing and transcriptome analysis of the hot pepper plant species.