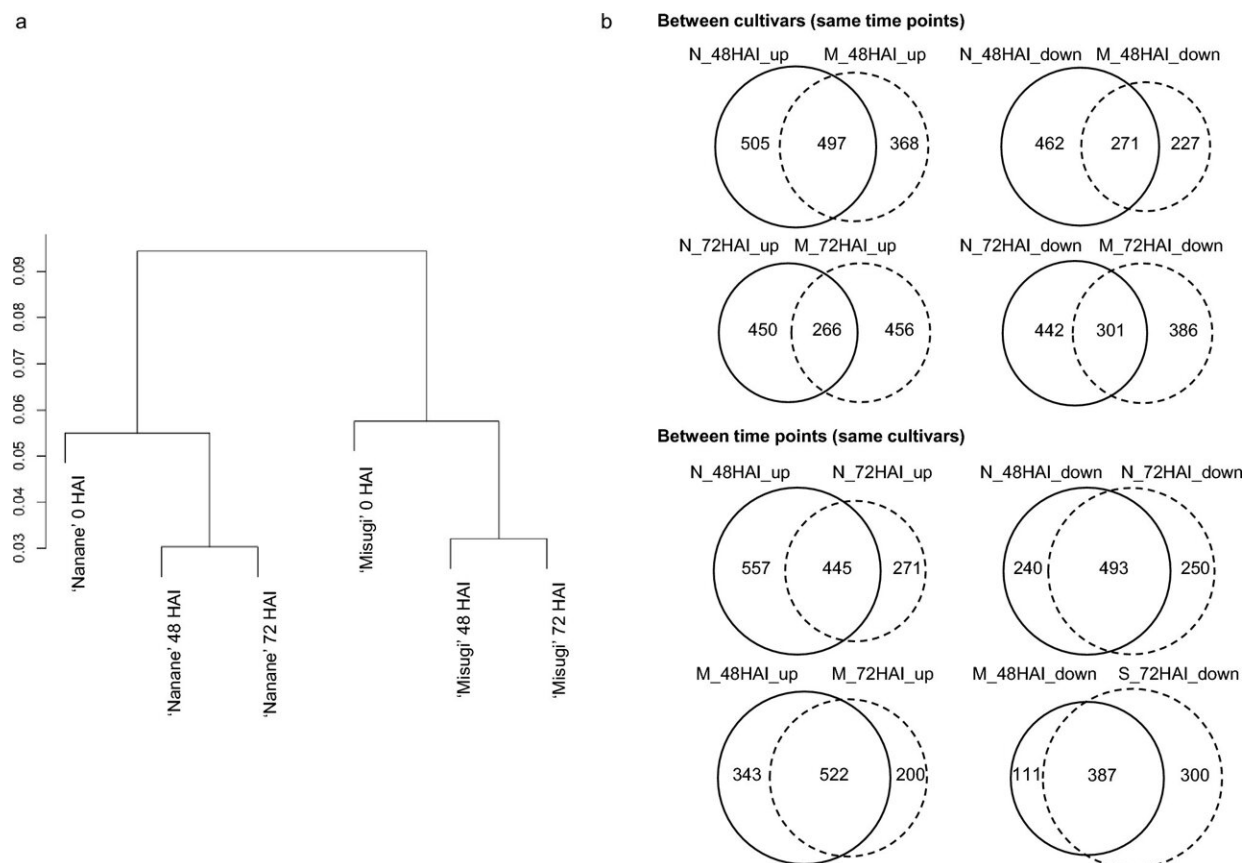


Discovery of differences in gene expression between white rust resistant and susceptible cultivars in *B. rappa*

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Comparison of differentially expressed genes at 48 and 72 h after *A. candida* (WMB01) inoculation (HAI) in resistant ('Nanane', N) and susceptible ('Misugi', M) cultivars. (a) Clustering analysis using fragments per kilobase per million (FPKM) values of all genes. (b) Venn diagram showing the number of up or downregulated genes between cultivars or between time points. Credit: *Scientific Reports* (2023). DOI: 10.1038/s41598-023-35205-5

Dr. Miyaji Naomi, who is currently a researcher at Iwate Biotechnology Research Center) and Arjina Akter, who is a Ph.D. student in the same doctorate program with their colleagues, elucidated that the alterations to gene expression induced after infection of Japanese mustard spinach by white rust disease were different in disease-resistant cultivar and disease-susceptible cultivar.

These research results lay the groundwork for clarifying the [disease](#) resistance mechanism in Japanese mustard spinach through future research.

This research was a cooperation between Associate Professor Fujimoto Ryo of Kobe University Graduate School of Agricultural Science, Associate Professor Chuma Izumi of Obihiro University of Agriculture and Veterinary Medicine, Department of Human Sciences, Iwate Biotechnology Research Center, Sylhet Agricultural University (Bangladesh) and the Commonwealth Scientific and Industrial Research Organisation (CSIRO) of Australia.

The research results were published in the online version of *Scientific Reports*.

White rust disease is one of the important diseases in cruciferous vegetables such as Japanese mustard spinach (*Brassica rapa* var. *perviridis*) and Chinese cabbage (*B. rapa* var. *pekinensis*). The disease caused by white rust fungus (*Albugo candida*) is characterized by the generation of lesions with a whitish suppuration appearing on the leaves, stems, stalks and flowers .

In the [cruciferous vegetables](#) such as Japanese mustard spinach and Chinese cabbage, the onset of the disease adversely affects quality such

as the appearance and leads to the problem of greatly reduced product value. There are disease preventative and curative measures against white rust disease such as spraying with agrochemicals, but the most effective measure is to use disease resistant cultivars. For that reason, the development of resistant cultivars is a much-demanded outcome in agriculture.

Plants grow, adapt and respond to the environment by controlling the expression of a variety of genes. To date, in a variety of plant species, it has become clear that resistance is induced in response to disease by the control of gene activity.

On the other hand, it has not been clear how genes are expressed during infection of Japanese mustard spinach by white rust disease fungus, and it was not known whether there were differences in [gene expression](#) between cultivars which are strongly resistant to white rust disease and cultivars susceptible to the disease (disease susceptible cultivars).

Content of the research

The white rust disease causing fungus was inoculated to white rust disease resistant [cultivar](#) and white rust disease susceptible cultivar, and the gene expression before and after infection was analyzed. Genes were identified which increased/decreased in the level of expression as a result of infection by white rust disease fungus, and the commonality of these genes across the cultivars was investigated.

As a result, while there are genes which are common to resistant and susceptible cultivars, there were many genes which were specific to each type of cultivar.

Next, by classification of known genes whose expression was altered by infection by the white rust disease fungus, the researchers were able to

predict what kind of expression response was occurring in each variety. Many of the genes whose expression was altered in the resistant cultivar were classified into categories related to protective responses (whole organism protective resistance, programmed [cell death](#)/apoptosis, etc.) or categories related to salicylic acid.

On the other hand, among the genes whose expression was altered in the disease susceptible cultivar, there were hardly any genes present which could be classified into these categories.

Based on this research, it became clear that when infected by the white rust disease fungus, the genetic expression was different between the white rust disease resistant cultivars and the disease susceptible cultivars. Moreover, the expression of the [salicylic acid](#) response genes was altered when infected by the white rust disease fungus.

In relation to important gene candidates in the exhibition of white rust disease resistance derived in the research performed here, the research group aims to clarify the molecular mechanism of white rust disease resistance, by investigating the functionality of particular [genes](#) in respect of the disease response. Furthermore, they plan to identify white rust disease resistance gene, and develop white [rust](#) resistant cultivars.

More information: Naomi Miyaji et al, Differences in the transcriptional immune response to *Albugo candida* between white rust resistant and susceptible cultivars in *Brassica rapa* L., *Scientific Reports* (2023). [DOI: 10.1038/s41598-023-35205-5](https://doi.org/10.1038/s41598-023-35205-5)

Provided by Kobe University

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