Proteome analysis on non-host resistance to plant viruses

Plant viruses cause serious damages on various kinds of crop production, but there are no chemicals yet that can inhibit virus infection and virus diseases are difficult to control. The strong option is breeding cultivars with resistance (R) genes to virus infection, which can drastically reduce the damages by plant viruses. Therefore, it is important to analyze R-mediated resistance to plant viruses. This project is aimed to employ cutting-edge differential proteome analysis between tobacco mosaic virus (TMV)-inoculated resistant and susceptible tomatoes. There are difficulties in plant proteome. One major difficulty is that plant proteins are difficult to extract compared to other organisms due to a lot of reasons. Low concentration and low solubility of plant proteins as well as proteases, polysaccharides, polyphenols, secondary metabolites and chlorophyll rich in plant tissues interfere with protein extraction. Another major difficulty is that large abundant proteins hinder low abundant proteins. Most abundant protein is Rubisco that accounts for more than 40% of total plan leaf protein amount. To cope with these difficulties, I optimized methods for protein extraction from plants and methods for exclusion of high abundant proteins that intervene proteome analysis. Taken these into consideration, I performed differential proteome analysis between resistant and susceptible plants during virus attack and found that 88 proteins were upregulated and 5 proteins were downregulated at 1 hour post induction of N-mediated resistance to TMV. These results are expected to provide novel insights in anti-viral plant immunity and future industrial application for crop production through the decrease of plant virus losses.