DISRUPTIVE TECHNOLOGIES FOR UNDERSTANDING AND IMPROVING DISEASE RESISTANCE IN CROP PLANTS

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Although more remains to be learnt, great strides have recently been made in the understanding of the molecular and genetic basis of disease resistance in plants. It is now time to deploy this knowledge to provide more durable disease resistance. Much of these advances have been enabled by improvements in analytical technologies and further advances are anticipated. In particular, high throughput DNA sequencing enables detailed analysis of crops and their pathogens. It is now possible to characterize variable pathogen populations and use this information for the rational deployment of resistance genes so as to maximize the evolutionary hurdle for the pathogen to become virulent.

Much of our work over the past thirty years has focused on resistance to downy mildew in lettuce. Lettuce (*Lactuca sativa*) is one of the most valuable vegetable crops and downy mildew, caused by *Bremia lactucae*, is the most important foliar disease of lettuce worldwide. The use of resistant varieties is the most effective method for controlling this disease; however, pathogen variability has led to the rapid defeat of individual resistance genes. Over 50 resistance genes have been identified and lettuce downy mildew is one of the best genetically characterized plant diseases. Whole genome sequencing of multiple genotypes has allowed the identification of candidate resistance genes in the host and virulence factors in the pathogen. Knowledge-driven deployment of effective resistance genes as gene pyramids provides the opportunity for more durable resistance to *B. lactucae*.Gene stacking using genome editing has the potential making this process more efficient. In addition, host-induced gene silencing of vital pathogen genes presents potentially insurmountable evolutionary hurdles for the pathogen to overcome in order to become virulent.