Identification of genes in a partially resistant genotype of *Avena sativa* expressed in response to *Puccinia coronata* infection

Yolanda Loarce, Elisa Navas, Carlos Paniagua, Araceli Fominaya, José Luis Manjón, Esther Ferrer (2016) Frontiers in Plant Science 7:731.

doi: 10.3389/fpls.2016.00731

Contact: Esther Ferrer, Department of Biomedicine and Biotechnology, University of Alcalá, Campus Científico-Tecnológico, 28871 Alcalá de Henares, Madrid, Spain.

Summary:

Obtaining cultivars partially resistant (PR) to *Puccinia coronata* is an important goal of oat breeding programs for two main reasons. First, as it occurs in other cereals, it is believed that this kind of resistance has a broad-spectrum effectiveness against all physiological races of *P. coronata*. Second, it can provide protection even when cultivars are grown for prolonged periods in environments favorable to the spread of the casual agent of crown rust. Although many components of the molecular race-specific resistance mechanisms have being described, few studies have been performed on the molecular mechanisms controlling host PR in any plant pathosystem. Genes involved in this process should be activated in response to the pathogen. Identifying these specific genes would shed light on the molecular basis of PR. Moreover, the availability of their sequences would increase the pool of oat sequences with assigned putative functions that could be used to develop new molecular markers.

We generated a suppression subtractive hybridization (SSH) library enriched for specific transcripts expressed when the PR resistant line MN841801-1 was inoculated with *P. coronata*. The procedure used involves analyzing sequences expressed in leaves of the inoculated line, as well as sequences that were not expressed, or were only expressed at a low level, in leaves of the same oat line that had not been inoculated. Next generation sequencing was used to obtain a good representation of expressed sequences. The annotation of transcripts allowed them to be related to important steps in the overall plant-pathogen interaction. Of special note were transcripts involved in pathogen recognition, cell-wall modification, oxidative bursts, and abscisic acid biosynthesis and signaling. Our findings support the hypothesis that basal defense mechanisms are the main systems operating in oat partial resistance to *P. coronata*.

Moreover, we examined and compared the expression patterns of a set of selected genes in resistant and susceptible genotypes at different times after inoculation with the fungus. We concluded that the partially resistant genotype was much quicker in mounting a defense response than a susceptible genotype. Further work will test whether this response is common in other oat genotypes showing PR.

In conclusion, our research provides evidence of the mechanisms of oat partial resistance to crown rust infection. Further detailed analysis of the relevant genes described in this work in other cultivars and by using different *P. coronata* isolates should contribute to identify those that would be the best potential targets for implementing durable resistance in oat.