

Stress Inducible Gene Expression and its Impact on Seed and Plant Performance

Plants are exposed on a regular basis to a range of environmental stresses. These include **abiotic** insults by extreme temperatures and altered water status (drought) and **biotic** stresses caused by a wide array of plant pathogens, such as bacteria, fungi and viruses. The cellular responses to these environmental challenges are remarkably similar and very often the (induced) resistance to one type of stress is accompanied by resistance to other stresses. This phenomenon is called cross-tolerance. Although cross-tolerance as such has not been studied in seeds there is good evidence that it is also operational in seeds. In fact, the principle is used in the enhancement of seed and seedling quality by the seed industry with a treatment known as seed priming. We aim to gain evidence that exposure of seeds to (abiotic) stresses may lead to a cross-tolerance for other stresses that are experienced during germination and seedling growth. As seen in figure 2 exposure of tomato seeds to osmotic stress (as during priming in PEG and the Seed Conditioner) results in a higher tolerance towards elevated temperatures during germination.

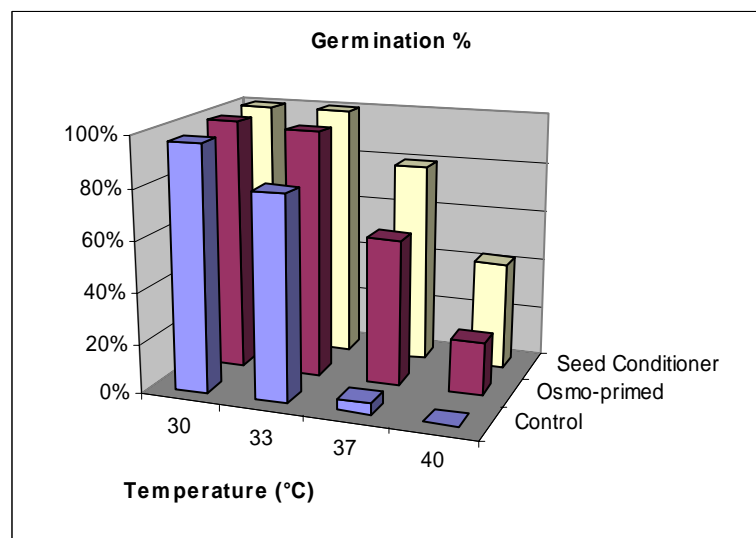


Fig 1. Seeds were primed by -1 MPa PEG for 7 days or by incubation in the Seed Conditioner for 6 days. Germination of these seeds was tested under different temperatures.

We hypothesise that exposure of the seeds to stress induces the expression of (embryonic) genes that are common in the resistance to a variety of biotic and abiotic stresses and that activity of these genes is preserved beyond the seed and seedling stages (fig 2).



Fig 2. Exposure of seeds to stress may induce the expression of genes that are common in the resistance to different stresses and the activity of these genes may be preserved beyond the seed and seedling stage.

In order to identify these genes we make use of tomato microarrays. We have compared the expression profiles of treated versus non-treated dry seeds. In another experiment we analyzed differences in expression profiles between treated and non-treated seeds during germination under normal and stress conditions. The overall expression pattern in these microarray experiments, as analyzed by principle component analysis, show a priming time component on the y-axis and a germination time component on the x-axis (fig 3).

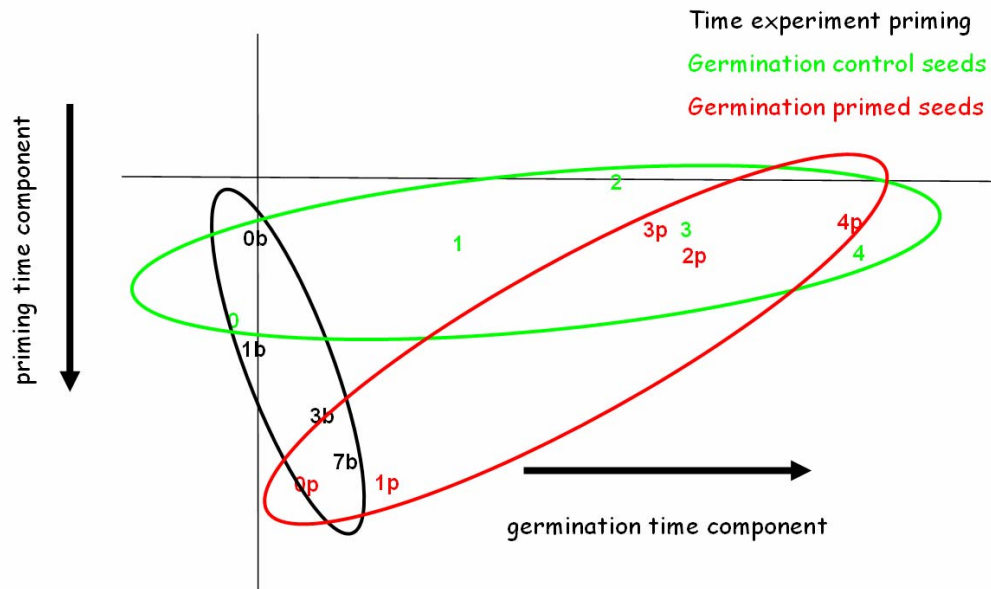


Fig 3. Principle component analysis of different microarray experiments. Shown are the overall expression pattern in 3 different experiments: in black different times of osmo-priming at -1 MPa PEG (0, 1, 3 and 7 days), in green different timepoints from dry seed (0) to almost germinating seed (4) and in red from dry osmo-primed seed (0p) to almost germinating osmo-primed seed (4p).

Genes with an expression pattern that could indicate a possible role in the imposition of cross-tolerance will be further analyzed for their precise role.

Besides the use of microarrays to identify possible interesting genes, we will use a functional complementation approach to identify tomato genes involved in stress tolerance in seeds. For this approach a cDNA expression library will be generated from primed seeds, which will be used for functional complementation of growth of yeast under osmotic and oxidative stress. Genes that are picked up in this screen will be tested for a similar function in tomato seeds.

The practical implications of this study will be two-fold: (i) development of new or modified methods for the improvement of seed quality; (ii) identification of molecular markers that are specific for stress resistance.

Research team

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Collaboration

In the project there is collaboration with several dutch seed companies.

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