

The Association between Host and Non-host Basal Resistance

Study on genetics of quantitative resistance to make a contribution to the plant breeding program in a novel way

Hordeum vulgare



Puccinia hordei Orth



Cereals and grasses are hosts for several rust species that may cause economically serious losses. Plants respond to infection of pathogen using innate immune system. Basal resistance is the plant front line defense. The resistance is due to genes with relatively small quantitative effects, located on so called quantitative trait loci (QTL). Quantitative resistance does not provide complete protection, but it is believed to be more durable and effective even after a period of widespread of agricultural use. The knowledge exploited on the genetic characterization and function of basal genes will help breeding for durable resistance in barley and other crops.

This thesis was performed in Laboratory of Plant Breeding of Wageningen UR. Non-host resistance is studied by using the model crop barley. My study contained three different experiments which together contribute important information to one major research project on the association between host and non-host basal resistance.

In first experiment, fine mapping of *Rphq11* and *Rphq16*, two QTLs for host basal resistance of barley to barley leaf rust was to pin point the QTLs into a small and precise region for map based cloning. It was executed in a “fast and dirty” way by using homozygous recombinant lines. The result of the fine mapping is not clear and conclusive; hence more replications are needed to clarify the result. The identification of candidate genes involved in basal resistance will not only enable molecular markers development in the future study, but also to verify responsible genes quickly.

The second experiment intended to generate more molecular markers needed for fine mapping of *Rnhq*, a non-host basal resistance QTL in barley. The peak marker for *Rnhq* is SKT1. To date, not many PCR based marker are saturated around this region. This chapter make use of a premature genome sequencing project of barley which uses 454 sequencing technology. The current attempt failed to develop molecular markers by using the BAC end sequences of the BAC clones spanning the region of our interest. However, more tests are worthy to have another test by searching from

different regions on the BAC clones.

In the third experiment, the specificity of the host and non-host basal resistance QTLs towards homologous and heterologous leaf rusts was tested. Near isogenic lines (NILs) of targeted QTLs were used. The phenotypic and microscopic data showed that host and non-host basal resistance QTLs (*Rphq2*, *Rphq3*, *Rphq11*, *Rphq16* and *Rnhq*) have effects towards homologous leaf rust *P. hordei* 1.2.1 and heterologous rusts, *P. hordei-murini* and *P. hordei-secalini*. Furthermore, a significant positive association was found between the two parameters representing host and non-host basal resistance, indicating possible association between host and non-host basal resistance. Since it is researched at QTL level, at gene level, it could be the same gene or different genes are involved. Thus, the association may not be true.

Study on effect of basal resistance can help to accumulate the effective QTLs into host cultivars, which could be turned into artificial (near) non-host, providing high level of durable resistance against specific pathogen.