Molecular genetic factors controlling plant resistance to diseases

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Quantitative disease resistance (QDR)

- Quantitative disease resistance (QDR) causes the reduction, but not absence, of disease, and is a major type of disease resistance for many crop species. QDR results in a continuous distribution of disease scores across a segregating population, and is typically due to many genes with small effects. It may also be a source of durable resistance.
- because multiple genes underlie QDR, the evolutionary pressure on pathogens is significantly decreased. QDR may therefore be a good source of durable resistance (resistance that remains effective over a long period of time even with wide crop cultivation).
 - QDR provides an effective means of control for both biotrophic and necrotrophic pathogens
- many QDR loci are effective against multiple races of a given pathogen, providing broad-spectrum resistance, or are effective against multiple pathogens
- QDR is effective against a wide range of microbe classes bacteria, fungal, viral and nematodes – and against pathogens that infect different parts or different developmental stages of the plant

Table 1

Genes contributing to QDR.

Gene	Туре	Pathogen(s)	Disease	Host
ZmWAK	wall-associated kinase, non RD	Sporisorium reilianum	head smut	maize
Htn1	wall-associated kinase, non RD	Exserohilum turcicum	Northern Corn Leaf Blight	maize
Yr36	kinase with START domain	Puccinia striiformis	stripe rust	wheat
RF01/WAKL22	Wall associated-like kinase	Fusarium oxysporum f. sp. matthioli	wilt	Arabidopsis
RKS1	atypical kinase	Xanthomonas campestris pv. campestris	black rot disease	Arabidopsis
Lr34	putative ABC transporter	Puccinia striiformis, Puccinia triticina, Blumeria graminis	stripe rust, leaf rust, powdery mildew	wheat
pi21	proline containing protein	Magnaporthe oryzae	rice blast	rice
Rhg4	serine hydroxy-methyl transferase	Heterodera glycines	cyst nematode	soybean
Rhg1	copy number variation for an amino acid transporter, an α-SNAP protein, and a wound-inducible protein	Heterodera glycines	cyst nematode	soybean
Pi35	NBS-LRR	Magnaporthe oryzae	rice blast	rice
RPS4/RRS1	R gene pair: NBS-LRR and NBS-LRR-WRKY	Xanthomonas campestris pv. campestris	black rot disease	Arabidopsis

Developmental stage-specific expression: ZmWAK

Zuo used map-based cloning to identify the causal gene underlying the quantitative resistance locus qHSR. qHSR1 provides resistance to Sporisorium reilianum, a soil-borne fungus and the causal agent of head smut in maize. ZmWAK encodes a receptorlike protein with a domain characteristic of wall-associated kinases (WAKs), and localizes to the plasma membrane in onion epidermal cells and maize protoplasts. Experiments with chimeric receptors demonstrated that the kinase activity of ZmWAK is necessary for its signaling function.



Developmental-stage specific expression 2: Lr34

The wheat Lr34 QTL encodes a putative ABC transporter that confers resistance to multiple diseases, including fungal stripe rust (Puccinia striiformis), leaf rust(Puccinia triticina), stem rust(Puccinia graminis), and powdery mildew (Blumeria graminis). Lr34 results in partial adult plant resistance at 20 °C and seedling resistance at low temperature.

The gene is expressed during the grain-filling stage of wheat in the uppermost (or flag) leaf of wheat, and when pyramided with other adult wheat resistance genes provides near-complete adult resistance levels. Map-based ¢loning and mutant analysis of Lr34 demonstrated that Lr34 is identical to the QTL Yr18 (controlling adult resistance to stripe rust), and Pm38 (controlling resistance to powdery mildew). How Lr34 provides resistance is not well understood, but leaf senescence processes may play a role



Thatcher + Lr34

Thatcher

Environment-specific expression of QDR: Yr36

In wheat, the Yr36 locus for partial resistance to wheat stripe rust (Puccinia striiformis) encodes WHEAT KINASE-START 1 (WKS1), a novel protein consisting of a kinase. Yr36 is effective in adult wheat plants at high temperatures (25–35 °C) but susceptible at lower temperature (~1/5 °C). The kinase domain in WKS1 has similarity to several WAK-like kinases in Arabidopsis, but WKS1 is likely to function somewhat differently as it does not have the extracellular receptor domain or transmembrane domain typical of WAKs





Mechanisms of quantitative disease resistance in plants
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