

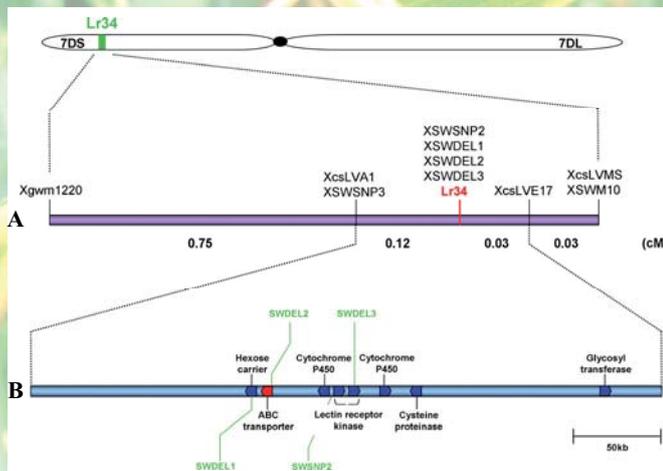
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## Introduction

- The bread wheat (*Triticum aestivum* L.) gene *Lr34* confers durable, partial, and race non-specific resistance against the three devastating biotrophic fungal diseases leaf rust (caused by *Puccinia triticina*), stripe rust (*P. striiformis*), and powdery mildew (*Blumeria graminis*).
- Flag leaves of many wheat cultivars containing *Lr34* develop a necrotic leaf tip, a morphological marker described as leaf tip necrosis.
- Three breeding lineages of *Lr34* have been identified: (i) Far East germplasm, (ii) spring wheat lines from North and South America, and (iii) winter wheat material in Europe.

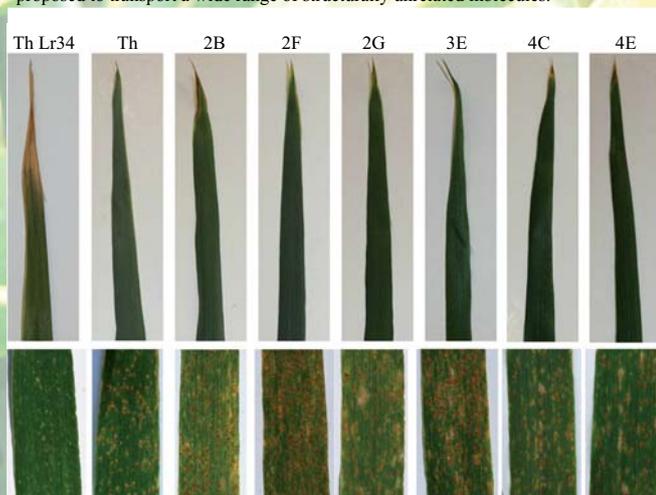
### 1. Map-based cloning of *Lr34* identified a PDR-like ABC transporter



**Fig.1.** (A) Choosing a map-based cloning approach, we localized *Lr34* to a genetic interval of 0.15 cM on wheat chromosome 7D. (B) The 363 kb physical interval contained eight candidate genes represented by arrows. The position of the four co-segregating markers is indicated in green. Analysis of eight independent *Lr34* mutants revealed that the durable resistance is conferred by a pleiotropic drug resistance (PDR)-like ATP-binding cassette (ABC) transporter.

### 2. The *Lr34* mutants were more susceptible to leaf rust, stripe rust, and powdery mildew and they did not show the leaf tip necrosis

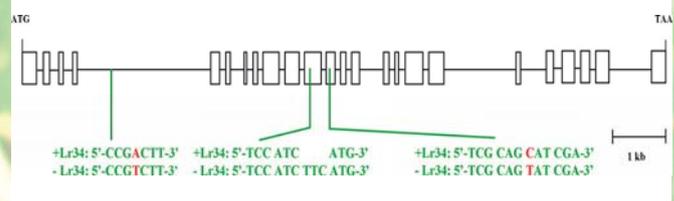
PDR-like ABC transporters have a conserved structural organization consisting of nucleotide-binding domains and transmembrane domains. They have been proposed to transport a wide range of structurally unrelated molecules.



**Fig.2.** Leaf tip necrosis and leaf rust infection of six of the eight *Lr34* mutants. Th *Lr34* = 'Thatcher *Lr34*', resistant wild type / Th = 'Thatcher', susceptible wild type / 2B, 2F, 2G, 3E, 4C, and 4E = sodium azide-induced *Lr34* mutants derived from 'Thatcher *Lr34*'. Each mutant carried a sequence alteration in the ABC transporter.

### 3. Resistant and susceptible haplotypes differ by only three sequence polymorphisms

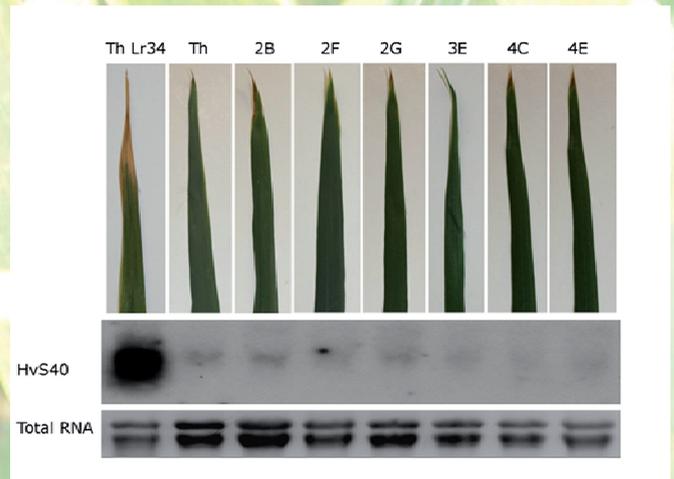
The coding sequence of *Lr34* spans 11'805 bp. Alleles of the resistant cultivar 'Chinese Spring' and the susceptible cultivar 'Renan' differed by only three sequence polymorphisms. Two of them were located in exons. The same resistance haplotype was found in the three breeding lineages indicating that a single progenitor was likely to account for the origin of *Lr34*.



**Fig.3.** Gene structure of *Lr34*. Open boxes indicate exons, while introns are shown as adjoining lines. The three conserved sequence polymorphisms between susceptible and resistant haplotypes are indicated in green. Both haplotypes may encode for a functional protein.

### 4. *Lr34* may regulate senescence-like processes in flag leaves

Results from Northern blots and measurement of chlorophyll degradation products suggested that *Lr34* may regulate senescence-like processes in wheat flag leaves. During senescence, nutrients are reallocated to growing seeds. Premature leaf senescence, starting from the leaf tip, may therefore retard growth of biotrophic pathogens.



**Fig.4.** Northern blot probed with the barley cDNA Hvs40 that is known to be highly upregulated during leaf senescence (Krupinska *et al.* (2002) *Plant Physiol.* 130, 1172). Th *Lr34* = 'Thatcher *Lr34*', resistant wild type / Th = 'Thatcher', susceptible wild type / 2B, 2F, 2G, 3E, 4C, and 4E = sodium azide-induced *Lr34* mutants.

**Concluding remark:** The observation that a multi-pathogen resistance in wheat is controlled by the same gene demonstrates the existence of single genetic factors in plants which act durably against several diseases.