

## Host Resistance:

Two major types:

### 'Specific recognition'

race specific  
qualitative  
major  
monogenic  
differential  
'R-gene'  
vertical

### 'Concert' of defense responses

non-race specific  
quantitative  
minor  
polygenic  
general  
field resistance  
horizontal

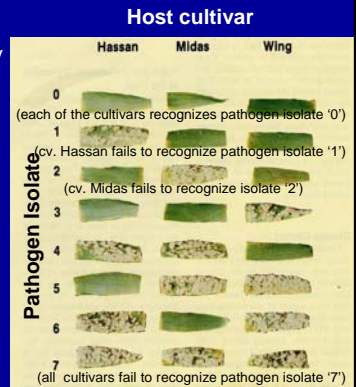
## Genetics of resistance continued:

### Race-specific resistance:

Resistance characterized by **specific recognition** (genetic interactions) between host genotypes and pathogen genotypes.

The ranking of cultivars from least to most resistant depends on the pathogen genotype (race) used.

This type of resistance is commonly 'all or nothing' (qualitative)



## Genetics of resistance continued:

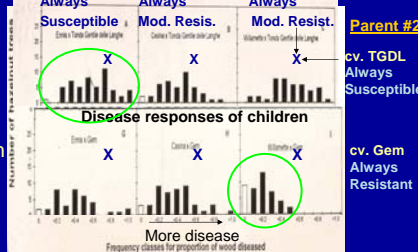
### Non race-specific ('horizontal') resistance:

Host cultivars show the same relative level of resistance to all pathogen isolates

When effective, this type of resistance commonly involves multiple genes, each with a small effect (quantitative)

Example: Parent #1: cv. Ennis, cv. Casina, cv. Willamette

Disease responses in 2-yr-old seedlings of European hazelnut where the parent cultivars (crossed with each other) varied in level of non-race specific resistance



### Genetics of resistance continued:

**Race-specific resistance:**  
Resistance characterized by **specific recognition** (genetic interactions) between host genotypes and pathogen genotypes.

The ranking of cultivars from least to most resistant depends on the pathogen genotype (race) used.

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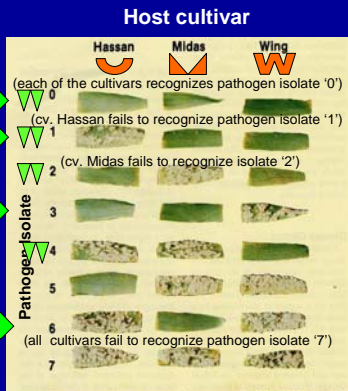


Fig. 1. The seven possible race combinations corresponding to the three resistance phenotypes—Hassan (R<sub>1</sub>), Midas (R<sub>2</sub>), and Wing (R<sub>3</sub>)—include three simple races, three intermediate races, and one complex race.

Race-specific resistance is based on the

### Gene-for-Gene Hypothesis :

The product of a single gene in the host **specifically recognizes** the product of a gene in the pathogen.

During an infection event, an interaction between these products results in incompatibility (i.e., a hypersensitive response and programmed cell death).

### Gene-for-Gene Hypothesis

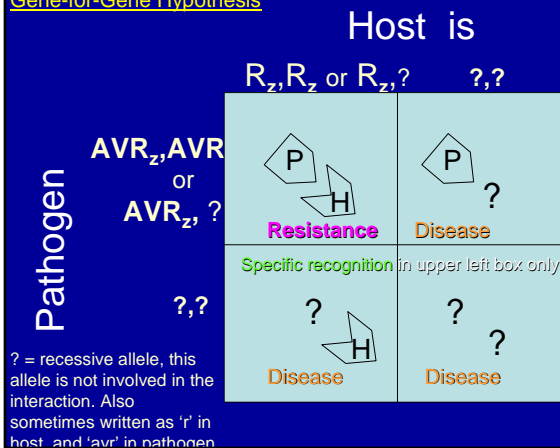
**Host: 'R'-gene = recognizer**  
this gene produces a product that 'recognizes'

usually an R-gene is a dominant gene  
'dominant' means that receiving a copy of the gene from only one parent is sufficient to trigger the recognition response in the plant

**Pathogen: 'AVR' gene = avirulence gene**

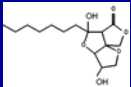
this gene produces an elicitor - 'elicits the HR'  
an AVR-gene is dominant  
dominant means that receiving a copy of the gene from only one parent is sufficient to elicit a recognition response in the host

### Gene-for-Gene Hypothesis

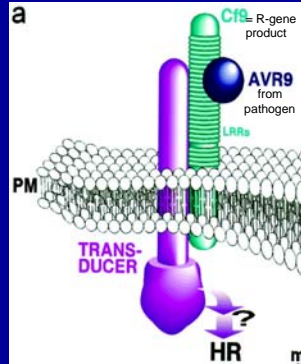


Hypothesized physical model for how R-gene and Avr-gene products interaction on plasma membrane of host cells

Pathogen protein (AVR) interacts with host R-gene protein (Cf9), which triggers the cell death response (hypersensitivity)



Example of AVR gene product from bacterial pathogen



From: MHAJ Joosten and PJGM de Wit Annual Review of Phytopathology Vol. 37:335

What if the pathogen is a necrotrophic fungus that produces a host selective toxin?

		Host	
		S,S or S,?	?, ?
Pathogen	Tox, Tox OR Tox, ?	Disease!! 	 Resistant
	?, ?	 Resistant	 Resistant

Gene-for-gene II  
Tox = gene for toxin  
S = gene for receptor  
Specific recognition in upper left box only

### How many races?

Three cultivars, each with a different R gene yields 8 races ( $2^3$ )

Ten cultivars, each with a different R gene could discern a possible 1024 races ( $2^{10}$ ) !!

The set of cultivars used to characterize races is called a 'differential set'

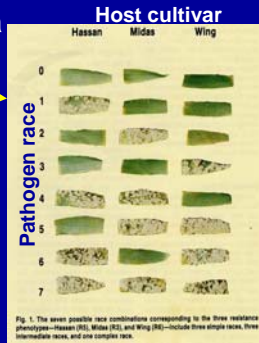


Fig. 1. The seven possible race combinations corresponding to the three resistance phenotypes—Hassan (H), Midex (M), and Wing (W)—include three single races, three intermediate races, and one complete race.

### A common test question: 😊

For each of the boxes, indicate whether or not the races of a rust pathogen will succeed in infecting the host cultivars

Avirulence (A) or lack-of-avirulence (? or 'a') genes possessed

		Race: A <sub>1</sub> A <sub>2</sub> A <sub>3</sub> A <sub>4</sub> A <sub>1</sub> a <sub>2</sub> A <sub>3</sub> A <sub>4</sub> a <sub>1</sub> A <sub>2</sub> A <sub>3</sub> A <sub>4</sub> a <sub>1</sub> a <sub>2</sub> A <sub>3</sub> A <sub>4</sub> a <sub>1</sub> a <sub>2</sub> a <sub>3</sub> a <sub>4</sub>				
Resistance (R) or lack-of-resistance (? or 'r') genes in each cultivar	r <sub>1</sub> r <sub>2</sub> r <sub>3</sub> r <sub>4</sub>					
	R <sub>1</sub> r <sub>2</sub> r <sub>3</sub> r <sub>4</sub>					
	r <sub>1</sub> R <sub>2</sub> r <sub>3</sub> r <sub>4</sub>					
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	R <sub>1</sub> R <sub>2</sub> R <sub>3</sub> R <sub>4</sub>					

'R', 'A' = active product present   '?', 'a', 'r' = active product absent

## A common test question: 😊

For each of the boxes, indicate whether or not the races of a rust pathogen **will succeed** in infecting the host cultivars

Avirulence (A) or lack-of-avirulence (? or 'a') genes possessed

Resistance (R) or lack-of-resistance (? or 'r') genes in each cultivar	Race:					
	A <sub>1</sub> A <sub>2</sub> A <sub>3</sub> A <sub>4</sub>	A <sub>1</sub> a <sub>2</sub> A <sub>3</sub> A <sub>4</sub>	a <sub>1</sub> A <sub>2</sub> A <sub>3</sub> A <sub>4</sub>	a <sub>1</sub> a <sub>2</sub> A <sub>3</sub> A <sub>4</sub>	a <sub>1</sub> a <sub>2</sub> a <sub>3</sub> a <sub>4</sub>	
	r <sub>1</sub> r <sub>2</sub> r <sub>3</sub> r <sub>4</sub>	yes	yes	yes	yes	yes
	R <sub>1</sub> r <sub>2</sub> r <sub>3</sub> r <sub>4</sub>	no	no	yes	yes	yes
	r <sub>1</sub> R <sub>2</sub> r <sub>3</sub> r <sub>4</sub>	no	yes	no	yes	yes
	R <sub>1</sub> R <sub>2</sub> r <sub>3</sub> r <sub>4</sub>	no	no	no	yes	yes
R <sub>1</sub> R <sub>2</sub> r <sub>3</sub> R <sub>4</sub>	no	no	no	no	yes	

'R', 'A' = active product present 'r', 'a', '?' = active product absent