Verticillium Resistance in Different Crop Species- a Survey

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Introduction

The genus *Verticillium* consists of more than 160 species and subspecies (45). Among these are three important plant pathogens: *Verticillium albo- atrum*, *Verticillium dahliae* and *Verticillium longisporum*. *Verticillium* spp. are soil- borne plant pathogens causing vascular diseases with severe economical losses worldwide. They infect many dicotyledonous crops like lettuce, cauliflower, sugar- beet, melons, hop, oilseed rape, olives, cotton, strawberry, tomato, potato and many more. Altogether, they affect more than 400 plant species in 75 plant families (24).

Verticillium disease symptoms are wilting, discoloration, chlorosis, necrosis, and premature ripening. In cauliflower, cotton, sunflower (10) and hop (2) yield losses of up to 100% have been reported. In certain cropping areas of oilseed rape *Verticillium* is meanwhile the greatest threat (19). Agronomical control means are poor, as fungicides are not effective. Cultivation practices like chemical soil fumigation are very effective, but too expensive, harmful to the environment and therefore not available anymore. Therefore breeding for resistance is a promising alternative to manage Verticillium wilt. Many studies have identified resistance genes to Verticillium wilt in different crops. Here we summarize the knowledge published so far about resistance sources, inheritance and effects of *Verticillium* resistance genes in several crop species (Table 1).

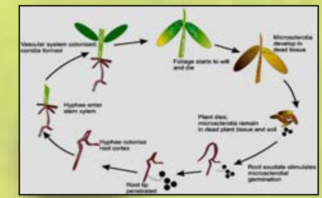
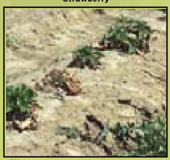


Figure 1: Life cycle of Verticillium dahliae / longisporum
(http://www.hdc.org.uk/files/verticillium-wilt-cycle-pictures-1.jpg)

Strawberry



(32)

Olive

(http://efe.aua.gr/en_gallery_fungal.php)

Hop

(http://www.lfl.bayern.de/publikationen/daten/merkblaetter/p_33873.pdf)

Oilseed rape, premature senescence/ripening — Oilseed rape, normal senescence/ripening

Pepper

(http://hobbykafe.com/forum/viewtopic.php?=15&t=394&start=30)

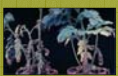
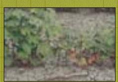
Eggplant

(http://vegetablemdonline.ppath.cornell.edu/PhotoPages/Impt_Diseases/Eggplant/Egg_Vert.htm)

Tomato

(http://vegetablemdonline.ppath.cornell.edu/photopages/Tomatoes/Tom_Vertic/Tom_VerticFS1.htm)

Table 1: host range, sources of resistance, inheritance and effects of Verticillium resistance in different crop species

Crop species	Verticillium species	Source of resistance	Inheritance	Effect
Potato (*Solanum* spp.)	V.albo- atrum	*S.chacoense* (20)	1 dominant gene (Vc)	Race- specific
	V.dahliae	Crosses between *S.tuberosum* and various wild species (16)	2 dominant genes (Vt, Vw)	No information
	V.dahliae	Crosses between diverse wild species (7)	Multigenic, dominant	No information
	V.dahliae + V.albo- atrum	*S. tuberosum* (34, 35, 15)	Multigenic	Quantitative
	V.dahliae + V.albo- atrum	Various solanum wild species (1, 11, 16, 17, 20, 24, 34, 39)	No information	Quantitative and qualitative
Cotton (*Gossypium* spp.)	V.dahliae	*G.barbadense*, *G.arboreum*, *G.herbaceum*, *G.hirsurtum* (24), cv. Sea- island cotton (*G.barbadense*) with highest resistance of all cvs. (4, 40)	*G. hirsurtum*: multigenic (1-2 gene), dominant; *G. barbadense* monogenic	*G. hirsurtum* quantitative, *G. barbadense* qualitative
	V.dahliae	Cross between *G. hirsurtum* and *G. barbadense* (41)	Monogenic, dominant or partial dominant	Qualitative
	V.dahliae	Intraspecific *G.hirsurtum* hybrid (23, 44)	Single dominant gene / multiple genes	Qualitative/ quantitative; controlled by environment
Tomato (*Lycopersicon esculentum*)	V.dahliae + V.albo- atrum	*L. pimpinellifolium* (24)	Ve gene (Ve1+ Ve2), dominant, monogenic	V.dahliae race 1, strains of V.albo- atrum
	V.dahliae + V.albo- atrum	*L. peruvanium*, *L. peruvanium* var. *dentatum*, *L. peruvanium* var. *humifusum*, *L. chilensei*, *L. pimpinellifolium* (24, 25, 26, 38, 39)	Multigenic	No information
Strawberry (*Fragaria ananassa* Duch.)	V.dahliae + V.albo- atrum	*F.chiloensis* (3, 22, 37), *F. yukonensis*, *F. ovalis*, *F. orientalis* (46)	Multigenic, additive and dominant gene effects	Quantitative
Sunflower (*Helianthus annuus*)	V.dahliae	Inbredline HA 89 (28)	1 dominant gene (V1), monogenic	No information
	V.dahliae	*H. annuus* (27)	1 dominant gene (V1), monogenic	No information
	V.dahliae	Wild species: *H. annuus*, *H. petiolaris* (14)	Heterozygous, dominant	No information
	V.dahliae	*H. annuus*, *H. petiolaris*, *H. praecox* (30)	1 dominant gene (V1), monogenic	No information
Olive (*Olea europaea*)	V.dahliae	Various cultivars of *Olea europaea* (5, 6, 13, 18, 31)	No information	Race- specific
Oilseed rape (*Brassica napus* ssp. *oleifera*)	V.longisporum	*B. oleracea*, *B. rapa* (9,12,19,29) *B. cretica*, *B. incana*, *B. insularis*, *B. villosa* (12, 19)	Multigenic	Quantitativ
Hop (*Humulus lupulus*)	V.dahliae + V.albo- atrum	Various wild species of *Humulus lupulus*, e.g. Manitoba wild hop (24), german land races (36)	Multigenic (24)	Race- specific

Verticillium* outgrowth on stem segments of *B. alboglabra

The formation of *V. longisporum* microsclerotia protruding from the vascular strands of an oilseed rape leaf

(19)

Verticillium wilt on lucerne. Necrotic vessels of lucerne roots infected by *Verticillium albo-atrum*

(http://www.inra.fr/hyp3/images/6037411.jpg)

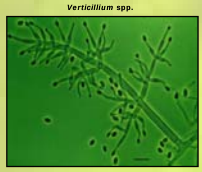
Microsclerotia of *Verticillium dahliae* formed on living tissue

(http://www.apsnet.org/edcenter/intropp/lessons/fungi/ascomycetes/Pages/VerticilliumWilt.aspx)

***Verticillium* in the vascular system of tree branches**

(http://greenspade.com/verticillium-wilt)

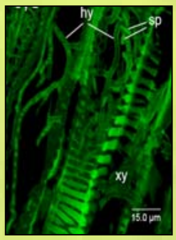
***Verticillium* spp.**



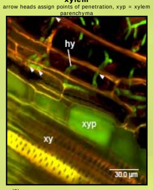
(http://biomikro.vscht.cz/documents/metmiklab/Metmiklab12.pdf)

Fluorescence image of GFP-tagged mycelium of *V. longisporum* on a root of *B. napus* (48 hpi)

(8) **Hyphal growth and production of conidiospores in a xylem element**
hy = hypha, xy = xylem elements, sp = conidiospores



(8) **Directed growth of *V. longisporum* in the root cortex towards the xylem**
arrow heads assign points of penetration, xyp = xylem parenchyma



(8)

Resistance and Defence Mechanisms

In many host species dominant, monogenic resistance genes against Verticillium have been described; only some of these show a race-specific effect. Furthermore, multigenic resistance has also been described for a number of hosts, which is mostly inherited in a dominant manner as well. None of the described resistance sources was inherited in a recessive manner, which was unexpected, as polyphagous pathogens often interact in a quantitative way with their hosts, and frequently resistance against pathogens with broad host range is based on multiple, recessive genes having small effects. Active defence mechanisms might be of greater relevance against Verticillium rather than preformed barriers.

Verticillium wilt is a vascular wilt disease. The fungus is entering the plant via the root before it is colonizing the xylem by hyphae and/ or conidia (Fig. 1). Infected plants have a number of defence mechanisms to limit the spread of the fungus via the xylem into the shoot. These include:

- Deposition of callose
- Accumulation of phenolics like lignin
- Accumulation of unsaturated fatty acids like Suberin
- Production of phytoalexins
- Vessel occlusions by gums, gels and tyloses

(24)

In a resistant plant, the pathogen is restricted to the root and stem base because of the defence responses described above. The effect of these mechanisms on the fungus depends on the timing and rate of their formation. If they occur before conidia are released into the xylem stream, the pathogen may be contained and the plant is resistant.

If to many vessels are blocked by occlusions at the same time and the plant is not able to produce new vessel elements, the water and nutrient transport into the upper parts of the plant is almost completely interrupted and the plant may start to wilt (10).

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