UDK 632.9

YU ISSN 0372-7866

INSTITUT ZA ZAŠTITU BILJA I ŽIVOTNU SREDINU - BEOGRAD
INSTITUTE FOR PLANT PROTECTION AND ENVIRONMENT - BELGRADE

ZAŠTITA BILJA
PLANT PROTECTION

VOL. 49(3),N°225, 1998.

Zaštita bilja, Vol. 49(3), N°225: 191-279, 1998, Beograd

CONTENTS

Review papers

S. Stojanović, J. Stojanović and M. Milovanović
Genetic basis of wheat resistance to parasites 226-227

Original scientific papers

M. Arsenijević and M. Veselić
Possibility of apple fruits utilization for pathogenicity test of the fungi species isolated from necrotic bark and xylem tissues of various fruit trees 243

S. Jasnić, T. Đurić and J. Sabo
Rhizoctonia solani hop pathogen in Yugoslavia 254-255

I. Dulić-Marković, M. Ranković, B. Ćuljković, O. Stojković and S. Romac
Detection of viruses associated with strawberry mild yellow edge disease in Yugoslavia 265

I. Dulić-Marković, B. Ćuljković, S. Romac, S. Vukosavić, O. Stojković and M. Ranković,
Application of polymerase chain reaction for plum pox virus detection 275

GENETIC BASIS OF WHEAT RESISTANCE TO PARASITES

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Summary

The paper showed the review of genetic basis of wheat resistance to diseases. The basis of this investigations was determined according to Flor's (1942, 1956) gene-for-gene hypothesis. The review of the following problems is given in this article, such as:

Inheritance of resistance. – Numerous investigations have shown that the inheritance of resistance may be dominant, recesive or intermediate. Dominant inheritance of resistance (complete or incomplete) was found out in most cases caused by one, two or more genes. Interactions between genes, their complementar, suplementar or additive effects of genes are very important. The additive gene effects were the most important and predominant. Concerning the degree of efficiency, some authors classified the genes of resistance as those with great effects (major) and those with small effects (minor). The major genes had race specific nature, while minor genes usually had additive effects and ensured horizontal resistance.

Location of resistance genes. - Special cytogenetic stocks have been used to locate the resistance genes on the chromosomes of wheat. So far, 23 genes loci for resistance to powdery mildew have been associated with specific chromosomes by aneuploid and nulisomic analysis. The genes Pm4b and combinations of the genes Pm2+Pm6 and Pm5+Pm6 were the most efficient in Yugoslavia. A very detailed review on Sr, Lr and Yr genes and their localization was given by McIntosh *et al.* (1995). Generally, stem rust genes Sr9e, Srll, Sr26, Sr29, Sr3l, r32 and Sr33 and leaf rust genes Lr9, Lrl2, Lrl9, Lr21, Lr24, Lr25 and Lr29 have a high degree of effectiveness. Today, there are the reliable data on the existance of 16 Bt genes of resistance to *Tilletia* spp. and 19 genes to *Ustilago tritici.*

The influence of growth stage and temperature on gene activity. – The genetics of wheat resistance to disease has been studied in different stages of its ontogenetic development. Many authors found out that the resistance of different wheat cultivars to powdery mildew, stem rust, leaf rust, septoria leaf blotch, common bunt etc. was controlled by one or several close-linked genes of different growth stages.The activity of the resistance genes to diseases, greatly depended on enviromental conditions, temperature in particular. Thus, gene Lr20 manifested complete resistance at 20,5°C, partial (incomplete) at 26°C and susceptibility at 30°C (Deverall, 1977). Simple dominant thermosensitive genes, such as Sr6, Srl5, Srl8 and Sr22 gave 0 type of nfection at low temperature and were ineffective at high temperature.

The source of resistant genes. – The best sources of resistance genes originated from wild relatives of soft wheat (Sears, 1969). A translocation between the chromosomes 1B of wheat and 1R of rye has been incorporated into wheat varieties worldwide (Zeller,

1973) and contributed to the stem rust, leaf rust, powdery mildew and septoria leaf blotch resistance. Different species *Aegilops*, *Agropyron* and *Triticum* were the very important sources of resistance genes.

Investigation on molecular level. – The most recent genetic investigations basedon the utilization of molecular markers in identification and mapping of genes resistance and virulency of parasites were conducted. RAPD, RFLP and biochemical markers have been successfully used to develop molecular markers. Liu and Kolmer (1996) found out that RAPD polymorphism was more abundant in the sexual population compared to the asexual field populations.

Today, we can nordly understand how the products of avirulence genes and resistant genes interact to initiate the host:parasite incompatibilities that we exploit in resistant cultivars (McIntosh, 1996). Future molecular research of the genetic basis of wheat resistance and virulency of parasite, and interactions of host: pathogen system are expected to give considerable contribution in that direction.

Keywords: wheat, gene, resistance, parasites, disease.

(Received: October 22.1998.)
(Accepted: March 4.1999.)

Plant Protection, Vol. 49(3), N°225: 195-225, 1998, Belgrade

POSSIBILITY OF APPLE FRUITS UTILIZATION FOR PATHOGENICITY TEST OF THE FUNGUS SPECIES ISOLATED FROM NECROTIC BARK AND XYLEM TISSUES OF VARIOUS FRUIT TREES

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Summary

Apple fruits cv. Golden Delicous were used as a laboratory test to prove the pathogenicity of the fungal species causal agents of dieback diseases on various fruit trees (Table 1).

Artificial inoculation was carried out on mature apple fruits using 7-10 day old culture of the ivestigated fungi developed on PDA.

After the surface desinfection by ethanol (alcohol), the colony fragments about 0,8 cm in diameter were placed into the hole of the apple fruit tissues previously prepared by a scalpel. Having been sprayed by destilated water, the inoculated fruits were placed into the moist chamber 2-3 days and than were removed under the laboratory conditions.

Necrotic process developed around the place on the apple inoculated fruit was indicated as a positive reaction. The degree of the tissue necrosis was evaluated after 5, 8, 15 and 21 days (Table 1).

No tissue necrosis was noticed neitner on control fruits inoculated with PDA fragments without fungal colonies nor on fruits inoculated with *Septocyta ruborum* isolates. Meanwhile, all other isolates, members of the different fungal species and genera caused remarkable tissue necrosis (Table 1). Reisolations of fungi by placing the small fragments of apple necrotic tissues on PDA were successful.

The obtained results indicate that apple fruits could be used as a quick and suitable test of the pathogenicity for the fungal species isolated from necrotic tissues taken from the kancerous branches and trank of the various diseased (pome, stone, kernel and cane berry) fruit trees (Table 1).

Key words: pathogenicity test; fungi isolation of fungi apple fruit inoculation; fungi reisolation of fungi; bark and xylem necrosis; diseased fruit trees.

(Received: September 10, 1998.)
(Accepted: March 4, 1999.)

Plant Protection, Vol. 49 (3), No 225: 227-241, 1998, Belgrade

RHIZOCTONIA SOLANI HOP PATHOGEN IN YUGOSLAVIA

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Summary

During a four-year (1994-1998) survey of hop fields at a number of localities in the Vojvodina province that was conducted as a part of the project "New and Less Known Plant Parasites", we registered various types of hop necrosis. Laboratory tests showed the fungus *Rhizoctonia solani* to be one of the causal agents of this symptoms.

Rhizoctonia solani causes brown necrotic spots on the basal part of the hop stems as well as on the head and root of the hop plants. Necrosis affect not only the bark but also the cortical tissue, causing it to rot and disintegrate. In varieties, necrosis spreads to the vessel elements, while in the case of the root system, the infection is most often only partial and always limited only to those parts of boot that lay closer to the soil surface. Diseased plants have chlorotic leaves, while more severe cases of necrosis result in the wilting of some stems and even entire plants.

Cultural and morphological characteristics of the fungus *R. solani* were studied using isolate H-26 obtained from the variety Bačka. The nutrient medium was potato-dextrose agar. On this medium fungi grow fast - at 25°c, they fill up a 9-cm Petri dishes in four days time. The aeral mycelium is white and cobwebby in the beginning, but after about 10 days they turn light brown. The hyphae are light or dark brown and they branch at right angles to one thother. Their length and width range between 31.0 and 238.0 μm and 7.0 and 11.0 μm, respectively. On the older mycelia, chains of brown cylindrical or pear-shaped moniliform cells with 2-20 nuclei are formed. The fungus form brown to black sclerotia that consist of these moniliform cells. The size of moniliform cells are 10-23 x 25-50 i-μm.

In our study hop cutting and shoots were inoculated to test the pathogenicity of the fungus *R. solani*. When the cuttings were injured necrosis was more severe than in the cases of shoot injury. Necrosis spreads to the shoots from the injured area on the cutting. It affects the base of the shoot and sometimes leads to total plant necrosis and rot and the appearance of cancerous wounds. When shoot injury occurs brown necrosis first affects the base of the shoot and then spreads to its upper parts and sometimes even across the entire cutting. *R. solani* was reisolated from the diseased areas of the inoculated cuttings and shoots.

Based on the cultural, morphological and pathogenic characteristics of the studied isolates, it can be concluded that the necrosis of the basal part of the hop stem and

the hop head and root is caused by the fungus *Rhizoctonia solani*. This fungus has not yet been described as a hop parasite in our country.

Key words: hop; *Rhizoctonia solani;* Yugoslavia; cultural properties; morphological characteristics; pathogenicity.

(Received: December 22. 1998.)
(Accepted: March 4. 1999.)

Plant Protection, Vol. 49 (3), N° 225: 243-253, 1998, Belgrade.

DETECTION OF VIRUSES ASSOCIATED WITH STRAWBERRY MILD YELLOW EDGE DISEASE IN YUGOSLAVIA

by

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Summary

Testing 478 strawberry samples from different areas in Yugoslavia it showed that strawberry mild yellow edge potexvirus (SMVEPV) is spreaded on Leskovac area (38 positive out of 186 samples). At Čačak area, SMYEPV was detected in cv. Čačanska Krupna and in Fruit Research Center strawberry collection in 9 out of 33 cultivars. In Vranje area two positive samples were detected.

dsRNA Mw 6.0, 4.2 and 2.0 Kbp were isolated from the cvs. Belrubi, Čačanska Krupna, Istočnik, Karina, Senga. The same dsRNA pattern was isolated from cv Senga Sengana (Leskovac). Specific PCR products for luteovirus (Hadidi *et* al., 1993) and potexvirus (Kaden-Kreuziger *et al.*, 1995) were amplified from this dsRNA template using random hexamer primers for reverse transcription.

Key words: SMYEV, strawberry, dsRNA, RT PCR

(Received: Juny 30.1998.)
(Accepted: March 04.1999.)

Plant Protection, Vol. 49(3), N°225: 255-263 1998, Belgrade