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STUDIES ON THE BEHAVIOR OF SOME ELITE AND VARIETIES OF PEAR IN THE POLLINATION PROCESS

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Abstract

Fungal plant pathogens belonging to the genus Venturia cause damaging scab diseases of members of the Rosaceae. In terms of economic impact, the most important of these are Venturia inaequalis, which infects apple, and Venturia pirina, which is a pathogen of European pear. Given that Venturia fungi colonise the sub-cuticular space without penetrating plant cells, it is assumed that effectors that contribute to virulence and determination of host range will be secreted into this plant-pathogen interface. The use of resistance varieties in the pollination process is an important way to obtain varieties with genetic resistance to disease. In this paper were used as mother genitors some selections from Pyrus serotina ('9/34-94', '20/1-91' and '5/104-84') with genetic resistance to diseases and pests and as father genitors (pollen) two valuable varieties of the European assortment ('Williams', 'Beuré Bosc') and 'Cristal' cv. - Romanian pear variety registered in 2009 at Research Station for Fruit Growing Voinesti, Dambovita. The selection '9 / 34-94' performed the best results in the pollination process in crossing process with 'Williams' and 'Cristal' cvs., with 21.7%, respectively 32.11% fruit set.

Key words*: pear, resistance, pathogen, scab.*

INTRODUCTION

The *Venturia* pathogen might have originated in Asia and from there spread to Europe and recently to other apple growing countries. Hypervariability and evolution of strains that have overcome host resistance are attributed to the ability of *Venturia* to recombine its genetic material every year (Parisi L. et al., 1993).The conidia and conidiophores, together, give a characteristic velvety appearance to the young lesions of scab. The conidia of *Venturia* are capable of adhesion and germination on nonhost plants such as *Pyrus communis*, however further development to establish infections occurs only on the host plants (Chevalier M. et al., 2004). The isolates of *V. inaequalis* are hypervariable and exhibit differential pathogenicity on apple cultivars (known as differential hosts). Based upon such differences, the pathogen has been categorized into eight physiological races (MacHardy W.E., 1996; Bénaouf G. et al., 2000; Bus V.G.M. et al., 2005). However, some of the isolates of *Venturia* are capable of growing on two different differential hosts and hence it is difficult to classify them to particular race. Understanding the mechanisms of *Venturia* pathogenesis and intricacies of its interaction with apple should provide important insights for developing new strategies to combat the disease (Jha G. et al., 2009). The whole genome mutagenesis screen should be initiated to identify key virulence factors. The availability of standardized transformation methodologies in *V. inaequalis* will facilitate such efforts (Tenzer I. et al., 1997).

MATERIALS AND METHODS

Plant material evaluated included:

Pollen from pear cultivated varieties like 'Williams', 'Cristal', 'Beurré Bosc', was collected in spring 2016.

The resistance selections '9/34-94', '20/1-91', '5/104-84' were used in the controlled crossing process as mother genitors.

The scab source for inoculum was procured from the collection of the Research Station for Fruit Growing Voinesti, Romania.

These breeding progenies will be characterized after screening infections tests. Infection tests will be performed in greenhouse conditions according to Chevalier et al. (1991) will be used for selection of resistant plants. Mixtures of isolates will be used for plantlet inoculation. Seedlings will be spraying with a conidial suspension of *Venturia inaequalis* CKE. Seedlings will be incubating for 48 hours at 18°C and 100% relative humidity. Disease symptoms will be evaluated macroscopically after 21 days of cultivation in a greenhouse. Seedlings will be dividing into 5 classes. Plants in class 0 were without symptoms of infection. Plants of class 4 had lesions with full sporulation.

RESULTS AND DISCUSSIONS

In order to plan an efficient breeding program to obtain cultivars resistant to pear scab, it is important to know the genetic control of this resistance. Although there is controversy about the genetic control of the resistance to pear scab, all authors consider that resistance could be transmitted from resistant progenitors to offspring. However, the descendants from crosses between susceptible and resistant cultivars segregated in a complex way.

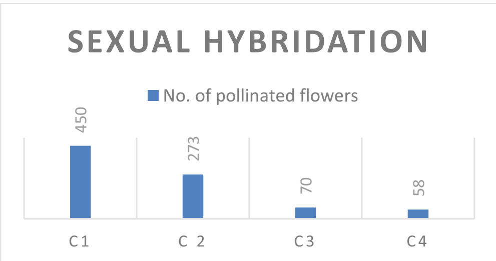

Figure 1. Number of pollinated flowers

In the Table 1 and Figure 1 we observed that the most value combination is C2 with 32.23%, percentage of fruit set, followed by the combination C1 with 21.77% percentage of fruit set:

- the combination C1 of 450 pollinated flowers, 98 fruits were bound, with a fruit set percentage of 21.77%
- the combination C2 of 274 pollinated flowers, 88 fruits were bound, with a fruit set percentage of 32.23%
- the combination C3 of 70 pollinated flowers, 5 fruits were bound, with a fruit set percentage of 7.14%
- the combination C4 of 58 pollinated flowers, 4 fruits were bound, with a fruit set percentage of 6.89%.

Table 1.The percentage of fruits set

No. crt.	Combinations	Genitors ♀ x ♂	No. of polli nated flowers	No. of fruits set	No. of harvested fruits	No. of obtained seeds
1.	C1	9/34-94 x ‘Williams’	450	98	95	650
2.	C2	9/34-94 x ‘Cristal’	273	88	83	535
3.	C3	20/1-91 x ‘Untoasa Bosc’	70	5	5	30
4.	C4	5/104-84 x ‘Untoasa Bosc’	58	4	4	32

In the Figure 2, it is noted that in the hybrid combination, C1% of the linked fruit did not produced hybrid fruit, and in the hybrid combination C2 is noted 6% of the linked fruit did not produce hybrid fruit. At C3 and C4 combinations, the linked fruits had a 100% success rate.

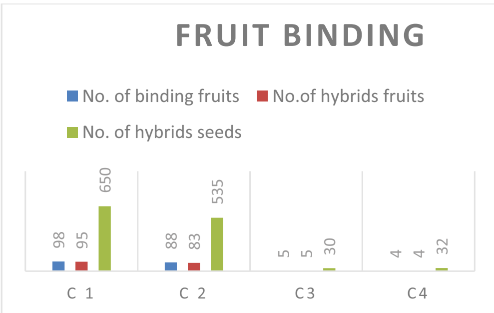

Figure 2. The fruits after pollination

From Table 2 and Figure 3 and 4 we see a success of 44% for Hybrid Combination C1, the 31% for Hybrid Combination C2, and for Hybrid C3 we have a success rate of 83% and for C4 we have a 100% success rate.

The resistant maternal progenitor (`9/34-94`, `5/104-84`, `20/1-91`) was able to transmit the scab resistance to the descendants, in agreement with previous results observed by other authors (Chevalier M., 2004).

Figure 3. Hybrids seeds

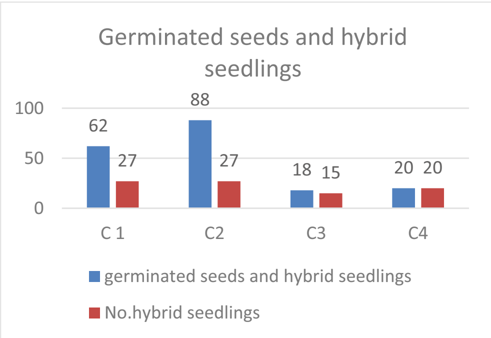

Figure 4. The percentage of germinated seeds and number of hybrid seedlings

Table 2.The percentage of germinated seeds and number of hybrid seedlings

No. crt.	Combinations	Hybrid combinations	No. of seeded seeds	No. hybrid seedlings	Percentage of rooting
1.	C1	9/34-94 x 'Williams'	62	27	44%
2.	C2	9/34-94 x 'Cristal'	88	27	31%
3.	C3	20/1-91 x 'Untoasa Bosc'	18	15	83%
4.	C4	5/104-84 x 'Untoasa Bosc'	20	20	100%

During the course of coevolution, pear has evolved mechanisms to prevent the severity of scab. The matured leaves of pear demonstrate ontogenic resistance because of which the pathogen growth is suppressed immediately after cuticle penetration and appearance of disease symptom gets delayed. The strengthened cell wall and cuticular membrane along with sub-cuticular pH of such leaves are speculated to play a role in governing such resistance. A breakdown of ontogenic resistance revealed by restored growth of the pathogen is observed in the old senescing leaves of apple. Detailed studies are needed to elucidate the functionality of such resistance and understand its breakdown mechanism.

Figure 5. Aspects of pollinations

CONCLUSIONS

It might be evident from this review that *Venturia. Sp.* is an important plant pathogen because it causes huge economic losses and also has a very interesting lifestyle. It is an appropriate time to sequence whole genome of the pathogen. The availability of genome sequence will not only stimulate research in the field of *Venturia* pear interactions and contribute to the basic understanding of this pathosystem but can also revolutionize the understanding of pathogenesis of other obligate pathogens. Understanding the mechanisms of *Venturia* pathogenesis and intricacies of its interaction with apple should provide important insights for developing new strategies to combat the disease. The whole genome mutagenesis screen should be initiated to identify key virulence factors. The availability of standardized transformation methodologies in *V. inaequalis* will facilitate such efforts.

The resistant elite progenitors (9/34-94, 5/104-84, 20/1-91) are an important step on the pear breeding program.The scab conidia could germinate on pear leaves undergoing defense responses, formation of primary hyphae is delayed and growth of subcuticular stroma is suppressed resulting in reduced conidiation. Phenolic produced in response to *V. inaequalis* infections in pear are known to inhibit pathogen growth and are ascribed to be associated with defense mechanisms of scab resistant cultivars.

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