YIELD AND RESPONSE TO THE MAIN DISEASES ATTACK OF PEAR CULTIVARS AND HERITABILITY OF THE TRAITS

PRODUCTIVITATEA ŞI RĂSPUNSUL LA ATACUL PRINCIPALELOR BOLI ALE UNOR SOIURIDE PĂR ŞI HERITABILITATEA ACESTOR CARACTERISTICI

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Abstract*. In order to identify potential genitors for pear breeding, 17 varieties of European and Asian origin were tested for productivity and their response to pear scab (Venturiapirina) and septoria (Septoriapyricola) attack. During two consecutive years, the highest yields of pear trees were recorded for two Romanian varieties, Adria and Napoca.The best response to the pear scab and septoria diseases was recorded within Asian varieties, most of them being registered with a low degree of attack or without symptoms of attack. Some European varieties (i.e.. Doyenné du Comice, Jubileu 50), or interspecific variety Kieffer Seedling, presented also a good response to diseases.The correlation between pear scab and septoria degree of attack statisticallyconfirmed that the susceptible varieties to scab were also sensitive to septoria, and vice versa.The broad-sense heritability coefficients for yield and response to the diseases attack varied depending on the two algorithms used, but the lowest value was registered for the trees'response to the pear scab attack, this trait being more difficult to manage in pear breeding.*

Key words*:* broad-sense heritability, correlation, genetic resources, inheritance

Rezumat. *În scopul identificării unor potenţi genitori pentru ameliorarea părului, 17 soiuri diferite ca origine, europene şi asiatice, au fost evaluate pentru productivitate şi comportare la rapăn (Venturiapirina) şi septorioză (Septoriapyricola). În decursul a doi ani consecutivi, cea mai mare producţie de fructe s-a înregistrat la două soiuri româneşti, Adria şi Napoca. Cea mai bună comportare la atacul celor două boli s-a înregistrat la soiurile asiatice, acestea având un grad de atac redus sau neprezentând simptome de atac. O bună reacţie la boli au prezentat şi unele soiuri europene (de exemplu Doyenné du Comice, Jubileu 50) sau soiul interspecific Kieffer Seedling. Corelaţia dintre gradul de atac cu rapăn şi septorioză a confirmă statistic faptul că soiurile sensibile la rapăn au prezentat susceptibilitate şi la septoria, şi invers. Coeficienţii de heritabilitate în sens larg, calculaţi pentru producţia de fructe şi răspunsul la atacul celor două boli, au variat în funcţie de algoritmul utilizat, dar cea mai mică valoare a fost înregistrată pentru comportarea pomilor la atacul de rapăn, această caracteristică fiind mai dificil de gestionat în ameliorarea părului.*

Cuvinte cheie*:* heritabilitate în sens larg, corelaţie, resurse genetice, ereditate

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INTRODUCTION

Pear (*Pyrus communis* L.) is an important fruit species in areas recognized for fruit trees cultivation in the temperate climate. In order to maximize the pear culture, through the research of the pear breeding are pursued different objectives, among which are included the obtaining of productive new varieties, resistance to stress factors, especially to the attack of the main diseases (Dondini and Sansavini, 2012; Chatzidimopoulos and Pappas, 2016). The main method of pear breeding remains artificial hybridization, which involves the crossing of varieties that possess the desired characteristics, followed by selection of hybrids according to the proposed desires (Sestras, 2004; Hancock and Lobos, 2008).

In order to increase the chances of getting valuable descendants, as perspectives for the selection of new varieties, the judicious choice of genitors is essential. An appropriate choice is based on the identification of varieties that are distinguished by certain characteristics useful in pear breeding, as well asthe heritability of these traits. If some adequate genitors are used in artificial pollination and if they have the ability to transmit the desired characters, the efficiency of selection in the descendancy increases considerably (Sestraş, 2004; Sestraş, 2018).

In the presentresearch, 17 pear cultivars were analyzed to identify those with high productivity and properly response to the attack of two common diseases in Transylvania, Romania: pear scab (*Venturia pirina*) and septoria (*Septoria pyricola*). Although there are different information about the monogenic or polygenic inheritance of the two pear diseases (Brewer *et al*., 2009; Liu *et al*., 2009; Won *et al*., 2014), in experience these characters were considered to have a polygenic determinism, so that their heritability was calculated by two algorithms, as heritability in broad-sense.

MATERIAL AND METHOD

The biological material was represented by different varieties of pear, located in the Didactic-Experimental Collection (micro collection), from the Faculty of Horticulture, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca. The plantation was established in 2013, in a modern system, with drip irrigation and anti-hail net; the trees wereconducted as slender spindle. The soil maintenance system followed the grazing interval method, a strip processed along the line, whilethe planting distance was 3.5 × 0.9 m. The fruits yields were analyzed, as well as the response of the trees to the main pear diseases attack: scab (*Venturia pirina*) and septoria (*Septoria pyricola*), in the third and fourth years aftertrees were planted, under natural conditions of infection and fewphytosanitary treatments.

The statistical processing of the experimental data was performed by analysis of variance (ANOVA). When the null hypothesis was rejected, the Duncan's Multiple Range test (DMRT) was applied as a post hoc test, in order to make direct comparisons between the pairs of means of the genotypes.

In addition of statistical variance, there was performed also the genetic variance analysis. The overall (phenotypic) variance decomposition model was applied for micro-collection genotypes using a model adapted after Falconer and Mackay (1996),Sestras (2018), in which the variance between clones was considered being induced by the genotypes, while among trees (individuals) within clones was influenced by the environment (tab. 1).

Table1

Decomposition of overall variance (phenotypic variance)in its components (genetic and environmental variance)for apple cultivars

Source of variation	Degree of freedom (DF)	Variance - mean sum of squares (MS)	Parameter components
Between clones - C (varieties)	C - 1	S_C^2	$\sigma_E^2 + n\,\sigma_G^2$
Within trees among clones (varieties)	C(n - 1)	S_c^2	σ_E^2
Total	C · n - 1	-	-

In table 1, the symbols used are the following:C = number of clones;n = number of individuals (analyzed trees) in a clone (here, 10 trees/cl);S_C^2 = variance between clones(varieties), which can be equated withσ_G^2 - genotypic variance (between varieties, because due vegetative propagation, each variety is a clone);s_c^2 = variance within trees among clones (varieties), which can be equated withσ_E^2 - environmental variance (within trees among clones/varietiesvariation, respectively errors variation).

Based on the model, the influence of the hereditary dowry (inheritance) of the studied traits and the phenotypic expression of the analyzed characters were evaluated, illustrated by the broad-sense heritability coefficients, computed by two formulas (H_a^2 and H_b^2)(Sestras*et al*., 2018).The heritability in the broad-sense was calculated using H_a^2formula (1):$H_a^2 = s_C^2/(s_C^2+s_c^2) = s_G^2/(s_G^2+s_E^2)$. For the H_b^2formula (2), there was computed a genetic variance $s_{G'}^2$, as $s_{G'}^2 = (S_C^2 - s_c^2)/n$, and phenotypic variance as $s_P^2 = S_c^2 + s_{G'}^2$, then the heritability in the broad-sense was calculated as $s_{G'}^2$(the variance attributed to the genotype, i.e. clones, respectively varieties), divided by s_P^2($s_P^2 = s_{G'}^2 + s_c^2$),the variance attributed to the phenotype (which is composed of the variance of genotype and variance of environment - errors).Simply, the algorithm represents the ratio of genetic variance to the overall or phenotypic variance ($H_b^2 = s_{G'}^2 / s_P^2$), i.e. highlighted the genotype participation in the phenotypic expression of a quantitative trait.

RESULTS ANDDISCUSSIONS

There were registered significant differences among the studied pear varieties, both for the production of fruits (fig.1) and for the response to the attack of the main diseases (figs.2 and 3).

The largest productions of pears were recorded at two Romanian varieties,

Adria and Napoca, obtained at Fruit Research Station Cluj (both with an average on two years of evaluation, of approximately 8.5 kg/tree). The smallest fruit production was obtained at varietiesKieffer Seedling, GieserWildeman and Nijisseiki, at the first two being obtained just a bitover 2 kg of fruit per tree. Because the amplitude of yields among cultivars was high, the coefficient of variability for fruit production within the 17 varieties revealed also a large variation of the trait (CV% =42.8).

The cultivar Primadona, created at FRS Cluj, showed a serious susceptibility to pear scab attack, not only as the highest level of AD%, but as significance compared to all other genotypes (fig. 2).

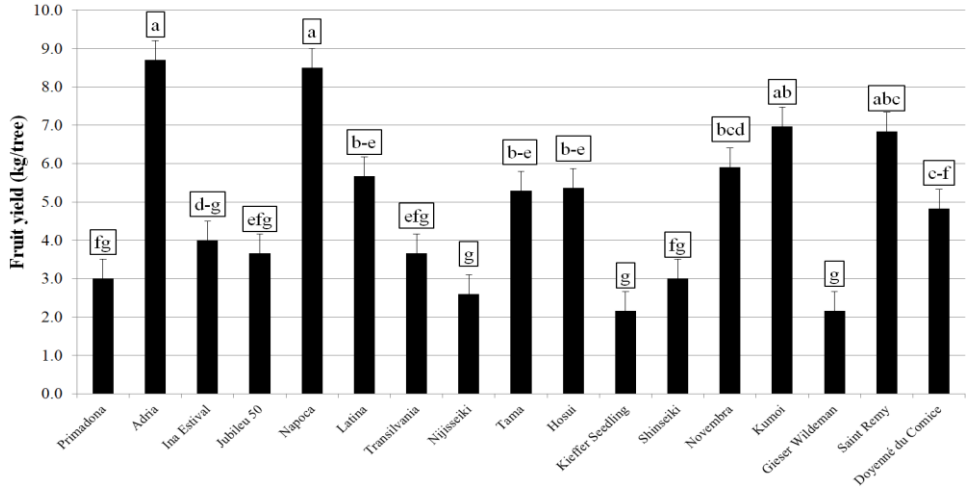

Fig. 1 Average fruit production in kg/tree at different pear varieties, in the third and fourth years after plantation

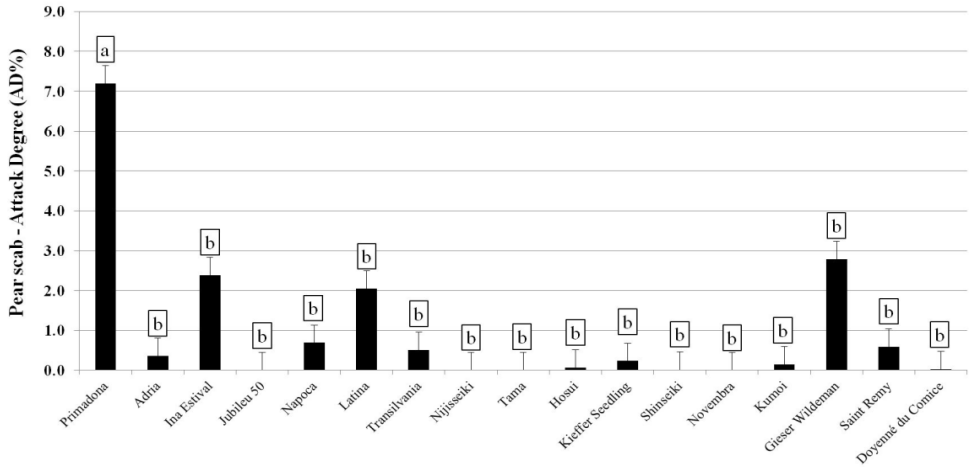

Fig. 2 The response of pear varieties to pear scab attack (as Attack Degree - AD%)

Asian varieties were recorded with a low degree of attack or were recorded without symptoms of attack. Even if the varieties GieserWildeman, Ina Estival and

Latinapresented an AD between 2-3%, they did not registered significant differences compared with the cultivars with the lowest attack.

Also for the septoria attack, the most susceptible variety was proved Primadona, followed by another variety created at FRS Cluj, namely Adria (fig. 3). Both European and Asian cultivars, i.e. Jubileu 50, Latina, Nijisseiki, Tama, Shinseiki, Kumoi, Gieser Wildeman, Doyenné du Comice, or hybrids between different species as origins (Kieffer Seedling), were registered without septoria symptoms during the two years survey.

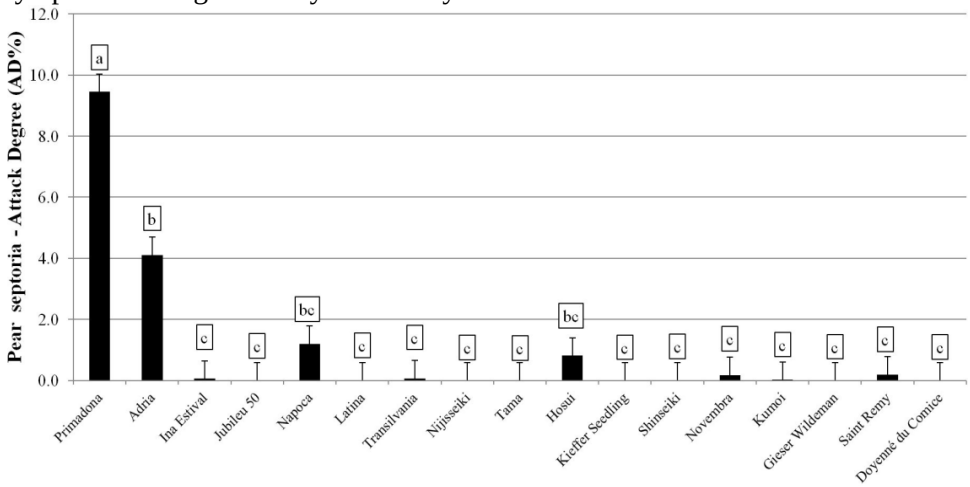

Fig. 3 The response of 17 pear varieties to pear septoria attack (as Attack Degree - AD%)

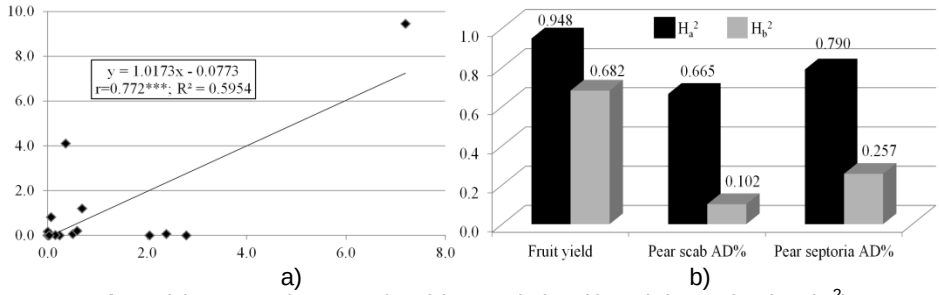

Fig. 4 (a) Regression equation (y), correlation (r) and determination (R^2) coefficientsbetween response of the cvs. to pear scab and septoria attack; b)broad-sense heritability coefficients for the analyzed traits, obtained by two formulas,H_a^2 and H_b^2

It is worth to notice that between pear scab and septoria attack there was registered a strong positive correlation (r=0.772***, fig. 4 a), which denote that, amongthe 17 pear varieties analyzed, the response to the attack of the two diseases was directly proportional (i.e. the susceptible varieties to scab were also susceptible to septoria, and vice versa). In addition, 59.5% from proportion of the variable variance represented by the scab response is predictable from the septoria response variance.

The broad-sense heritability coefficients for yield and response to the diseases attack of the analyzed pear cultivars, obtained by thetwo formulas (fig.4b) have oscillated between 0.665-0.948 (H_a^2) and 0.102-0.682(H_b^2). Between the coefficients of heritability calculated for the same trait there were differences depending on the formula used. Nevertheless, regardless of the algorithm, the heritability values illustrate the lowest inheritance for the response of the trees to pear scab attack. Compared to the hereby trait, which is more difficult to use in pear breeding, fruit production seems to be more inherited, and consequently more easily to manage, in pear breeding by a proper choice of appropriate genitors.

CONCLUSIONS

1. The existing variability among the 17 pear varieties studied allows the selectionof those with the desired characteristics in order to improve the productivity or tolerance (resistance) to the two diseases: pear scab (*Venturia pirina*) and septoria (*Septoria pyricola*).

2. The heritability of the traits illustrate that pear scab seems to be more difficult to be transferred to the descendants, due to a lower contribution of additive effects in the ensemble of polygenic inheritance.

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