

Possibilities of Using Wild Lettuce Forms Originating from the Spontaneous Yugoslav Flora in the Selection for Virus Diseases of *Lactuca sativa* L

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Abstract

An investigation was carried out with aims to create lettuce cultivars (*Lactuca sativa* L.) resistant to pathogens, such as the causal agents of plant diseases, and especially that of virus diseases. The spontaneous flora in the localities of Pomoravlje and Sumadija were investigated for this propose where resistant genotypes of the species *Lactuca sp.* could be found. The interspecies hybrids *Lactuca virosa* L. x *Lactuca sativa* L., *L. saligna* L. x *L. sativa* L., were investigated as a possible source of genetic variability. *L. saligna* L. and *L. virosa* L. represented only a part of the population related to *L. sativa* L. Wild varieties of this species belong to the weed flora.

After crossings, variable achenes were obtained only between *L. sativa* L. x *L. saligna* L. In the first crossings, as many as two populations of *L. saligna* L. were used, one with and the other without anthocyanin, but the seedlings of *L. saligna* L. without anthocyanin decayed after being taken out in the field. In the process of the selection of F₁ generation, 31 plants emerged. However, only 19 plants survived after transplanting in the field. In 9 plants the fertility was provoked by colhicyn, but the percentage of fertile achenes was low as compared to the number of achenes that were not viable.

The collection of the genotypes of *Lactuca sp.* for the gene bank and further investigations on the possibilities of crossing them with the cultivated lettuce (*Lactuca sativa* L.), the selection programmes on lettuce could be improved. Eventually, the final aim of obtaining a cultivar with the built-in genes of resistance to virus diseases and acceptable morphological characteristics would be achieved.

INTRODUCTION

The genus *Lactuca* is represented by six species: *L. perennis* L., *L. viminea* L., *L. quercina* L. with its two subspecies subsp. *quercina* and subsp. *chaixii* Vill., *L. saligna* L., *L. sativa* L., with the varieties var. *capitata* L., var. *longifolia* Lam., and var. *crispa* L., *L. serriola* L. with the varieties var. *serriola* L. and var. *integrata* Gren et Godr. (Josifovic, 1975).

Cultivated lettuce takes a special place within the genus *Lactuca* together with the species *L. saligna* L., *L. virosa* L., and *L. serriola* L. They are classified together as the group *serriola* (Tomson 1943; Lindquist, 1960; Feranova, 1976). Concerning the flora of Serbia (1975) *L. virosa* L. was not described but according to the description of the species that were present in our regions, the description of *Lactuca serriola* var. *integrata* Gren et Godr. was identical with the description of *L. virosa* L. according to Lindquist (1960).

When comparing *virosa* and *sativa*, genetic transfer was found between them (Tompson and Ryder, 1961) where *sativa* was a more complex hybrid. This program resulted in creating the cultivar Vanguard characterised by a more vigorous root system than in *L. virosa* L., as well as a dark green leaf colour. Lindquist (1960) in his cytogenetic study, obtained anfidiploids older than F₁ generation among all the representatives of the group *serriola*. Eenink et al. (1982) performed a successive genetic

transfer on resistance to leaf lice crossing *L. virosa* x *L. sativa* by using *L. serriola* L. as a bridge. Eenink et al. (1982) did not succeed in direct crossing *L. virosa* L. and *L. sativa* L. However, Maxon (1984) did succeed by using the two lines of *L. virosa* L. originating from the researches of Ryder (1965) who broke the sterile barrier in F₁ generation by colchicine treatment, and back-crossed the obtained tetraploids with *L. sativa* L.

The species that are crossed with each other in a natural manner make a large part of the gene fund, whereas the isolated species have a smaller chance to exchange the genes but a strong possibility to create divergent lines (Maxon, 1984). By engaging "wild" and "semi wild" varieties from the species *Lactuca* sp. in the selection programmes of cultivated lettuce, there is a great field for increasing the genetic variability of the selected materials, which enables obtaining the new quality lines with incorporated favourable characteristics.

On the basis of the researches of Zdravkovic et al. (1994) on the possibilities of crossing *L. virosa* L. and *L. saligna* L. with the cultivated lettuce *L. sativa* L., some initial results were obtained, i.e. F₁ generation of *L. sativa* L. and *L. saligna* L.. Hybrids could not be obtained between *L. sativa* L. and *L. virosa* L., regardless if the mother or the father was *L. sativa* L. This paper represents further continuation of these researches in the older generations (F₂ and F₃), after controlling sterility in F₁ generation of interspecies hybrids.

MATERIAL AND METHOD

The initial material for crossing actually was the collected one from the region of Sumadija and Pomoravlje, out of which only two populations were chosen. One of them belongs to the species *L. saligna* L. and the other to *L. virosa* L., both of which belong to the weed flora of this region.

The crossing was performed by the method of "mist pollination" which removes the pollen from the stamen with a fine stream of water. The plants obtained by self-pollination were removed after their emergence. After crossing with the cultivated lettuce *L. sativa* L., by applying the reciprocal method, F₁ generation was obtained only with *L. saligna* L. From F₁ generation, F₂ and F₃ generations were obtained by self-pollination.

Sterility in F₁ hybrids was controlled by applying colchicines. Aloploidoids were obtained by wrapping the axial buds with the cotton wool moisturised with 0.4 % colchicines solution of 2-4 hours duration. After the treatment, the treated place was washed with water several times. Testing the level of poliploids was performed by counting the chromosomes with the "squash" method (Folgen "squash" method). The lettuce head with one or more seeds per flower head was considered a fertile head.

RESULTS

After crossing, viable achenes could only be obtained in the crosses between *L. sativa* L. x *L. saligna* L. In the initial crossings, as many as two populations of *L. saligna* L. were used, one with and the other without anthocyanin but the seedlings of *L. saligna* L. without anthocyanin decayed after being taken out in the field. In the process of the selection of F₁ generation, 31 plants emerged. After transplanting in the field, only 19 plants could survive. In 9 plants the fertility was provoked by colchicyn, but the percentage of fertile achenes was low as compared to the number of achenes that were not viable.

The plants from F₂ generation varied much by their morphological characteristics and that is the reason why their general characteristics could be distinguished. On the whole, the most common characteristics can be described as having long leaves, pointed with a small petal and marked nervure. Some alotetraploids are different from these "common" characteristics, by having wide leaves of with a larger area as compared to the majority, and at first sight, they resemble *L. sativa* L.

Not all of the plants had the characteristics of alotetraploids. Two plants showed the characters of a diploid and were therefore excluded from the selection process.

The obtained progeny of the F₂ generation was poorly developed with weak

viability, which resulted in forming the lines in F₃ generation with only four plants out of which four F₃ lines were formed. The formed lines were grouped according to earliness and leaf shape. The lines that phenotypically resembled *L. saligna* L. were late, and reversely, the plants that resembled *L. sativa* L. were earlier. As for the leaf shape, they were grouped according to their phenotypical similarity to *L. saligna* L. and *L. sativa* L. In the selection process, these plants are in F₄ generation.

DISCUSSION

Small percentage of germinated achenes and high sterility of these hybrids represent the constant cause for interrupting the selection process. Maxon (1984) controlled low percentage of pollination by the combination of washing the pollen with classical flower castration, i.e. physical removal of stamen from the flower. In F₁ generation, he performed back crossing, which is not included in this investigation. A fertile F₁ generation was obtained after the application of colchicines, but the number of viable achenes was insufficient for a serious genetic analysis in F₂ generation. As meiotic division was deranged, it was not possible to trace any regularity in segregation by Mandel rules. All the individuals of F₂ generation that were aloploidoids were chosen for further selection process. *L. virosa* L. was the carrier of resistance to the pathogens that are causal agents for plant diseases. Regarding our selection programme, the most important is resistance to virus diseases. Our investigation did not result in obtaining a hybrid of *L. sativa* L. and *L. virosa* L.. However, Eenink et al. (1982) used *L. serriola* L. as a genetic bridge for crossing *L. sativa* L. and *L. saligna* L., and found that *L. serriola* was phylogenetically closer to *L. sativa* L. than to *L. virosa* L. The sterility barrier was up to a certain point controlled, although the number of the obtained aloploidoids was insufficient. Ryder (1965) controlled the sterility barrier by applying the colchicines and backcrosses with *L. sativa* L. By interspecific hybridisation and applying the technique of backcrosses in the selection process aimed to obtain a larger number of individuals in F₂ generation, we could have more results on the regulation of segregation, which will increase the possibility of obtaining lines with resistance carriers.

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