

Homogenisation of the old cucumber variety 'Dindoða Zaiie Í ekaru'

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Due to quite a high morphological heterogeneity among plants of the old Latvian cucumber variety 'Dindoða Zaiie Í ekaru', the homogenisation of the variety was started at the Pure Horticultural Research Station in 1994, both by inbreeding and sibling. Genotypes best conforming to the original description of the variety were selected. Five generations of inbreeding and three generations of sibling were evaluated. Particular traits had a different response to selection. For example, fruit development in clusters, which is a characteristic feature of the variety, showed a high response to inbreeding: the percentage of plants with fruits developed in clusters increased from 3.9% to 92.3%. In contrast, such traits as plant length and branching were manifested typically at the beginning of homogenisation and were not changed during inbreeding and sibling. The best lines were selected for seed propagation and included in the Latvian Gene Bank of Cultivated Plants for long-term preservation.

Key words: cucumber, *Cucumis sativus* L., inbreeding, sibling, gene bank

INTRODUCTION

The cucumber variety 'Dindoða Zaiie Í ekaru' was bred by the Latvian breeder Pçteris Dindonis in the period between 1930 and 1960. Three varieties of Russian selection were used as parents of the variety ('Muromsky'/'Borovsky'/'Kulenkampa'). Variety 'Dindoða Zaiie Í ekaru' was registered in 1961 as an open field variety suitable also for growing in hotbeds [1]. The most typical trait of the variety 'Dindoða Zaiie Í ekaru' is fruit development in clusters [2] (Fig. 1), what is reflected in the name of the variety ("í ekari" in Latvian means "clusters").

At the beginning of 1990s plants grown from commercially available seeds of the variety 'Dindoða Zaiie Í ekaru' showed a rather high morphological heterogeneity and weak expression of fruit development in clusters. Due to the problems with including such heterogeneous material into the Latvian Gene Bank of Cultivated Plants, inbreeding and sibling were performed at the Pùre Horticultural Research Station with the aim to produce the homozygotic lines. Genotypes best conforming to the original description of the variety were selected [3].

The aim of the article is to show the changes of some characteristic morphological traits of the cu-

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Fig. 1. Fruit clusters of the variety 'Dindoða Zaiie Í ekaru'

cucumber variety 'Dindoà Zaiie Í ekaru' on the way of inbreeding and sibling.

MATERIALS AND METHODS

In 1994, eight most typical plants of the variety 'Dindoà Zaiie Í ekaru' grown from commercially available seeds were chosen for selfing. Every year, plants best corresponding to the original description of the variety 'Dindoà Zaiie Í ekaru' by all analysed traits were selected for further inbreeding. Before flowering both male and female flowers were isolated with cheese-cloth isolators. For inbreeding, flowers were pollinated within the same plant. Isolators were placed back and kept until the fruits were set. After about 40 days mature seeds were harvested. Seeds of typical plants obtained un-

Table 1. Scale used for scoring the morphological traits

Trait	Score			
	0	1	2	3
Clustered fruits	1 fruit in node	2 fruits in node	3 fruits in node	4 or more fruits in node
Fruit colour	Light green, glossy	Light green	Green	Dark green
Prickle colour	Black	Brown	Yellow	White
Plant length and branching	Bush-like shape	Main shoot is in 0.5–0.7 m long	Main shoot is in 0.7–1.15 m long	Main shoot is above 1.15 m

der controlled pollination were sown the next year. Such procedure was repeated during six generations of inbredlines [3].

In 1997, for creating the sib-lines, plants best corresponding to the variety 'Dindoà Zaiie Í ekaru' were selected from plants grown from uncontrolled pollination in 1996. Next year progenies of

Table 2. Score of morphological traits during homogenisation

Inbredlines	Fruit development in clusters			Fruit colour			Prickles colour		
	Generation								
	3rd	4th	5th	3rd	4th	5th	3rd	4th	5th
1I	0.75	0.67	1.79	2.63	2.89	2.70	2.39	2.57	1.65
2I	0.90	2.64	2.76	2.52	2.83	2.84	2.29	2.50	2.24
3I	0.57	1.51	2.27	2.91	2.58	2.83	2.92	2.89	2.66
4I	0.52	0.26	2.22	2.80	2.33	2.45	2.65	3.00	2.67
6I	0.72	0.26	0.68	2.67	2.62	2.68	2.58	2.94	1.93
7I	0.14	0.22	1.42	2.27	2.08	2.07	2.69	3.00	2.68
8I	0.70	0.67	1.55	2.48	2.03	2.44	2.61	3.00	2.82
Average	0.61	0.89	1.81	2.61	2.48	2.57	2.59	2.84	2.38
LSD between lines	0.53	0.44	1.00	0.36	0.85	0.51	0.39	0.51	1.30
LSD between generations	0.86			NS			0.38		
Siblines	Generation								
	1st	2nd	3rd	1st	2nd	3rd	1st	2nd	3rd
5S	0.71	0.46	2.69	2.79	2.69	2.38	2.58	3.00	2.20
6S	0.39	0.64	1.99	2.50	2.54	2.85	2.87	2.94	2.58
11S	0.78	0.64	2.86	2.83	2.81	2.19	2.83	2.87	2.62
11zS	0.78	0.74	2.74	2.83	2.53	2.55	2.83	2.95	2.32
15S	0.66	0.60	2.50	2.38	2.58	2.73	2.93	2.82	2.11
20S	0.54	1.00	2.82	2.39	2.30	2.61	3.00	2.96	2.98
21(3)zS	0.88	1.33	2.52	2.53	2.74	2.89	2.97	2.86	3.00
21(3)tS	0.88	1.33	2.69	2.53	2.74	2.84	2.97	2.86	2.89
21(3)IVS	0.88	1.33	2.71	2.53	2.74	2.48	2.97	2.86	2.64
Average	0.72	0.90	2.61	2.59	2.63	2.61	2.88	2.90	2.59
LSD between lines	NS	NS	NS	NS	NS	NS	NS	NS	NS
LSD between generations	0.43			NS			0.32		

LSD is for $p = 0.05$; NS – not significant difference.

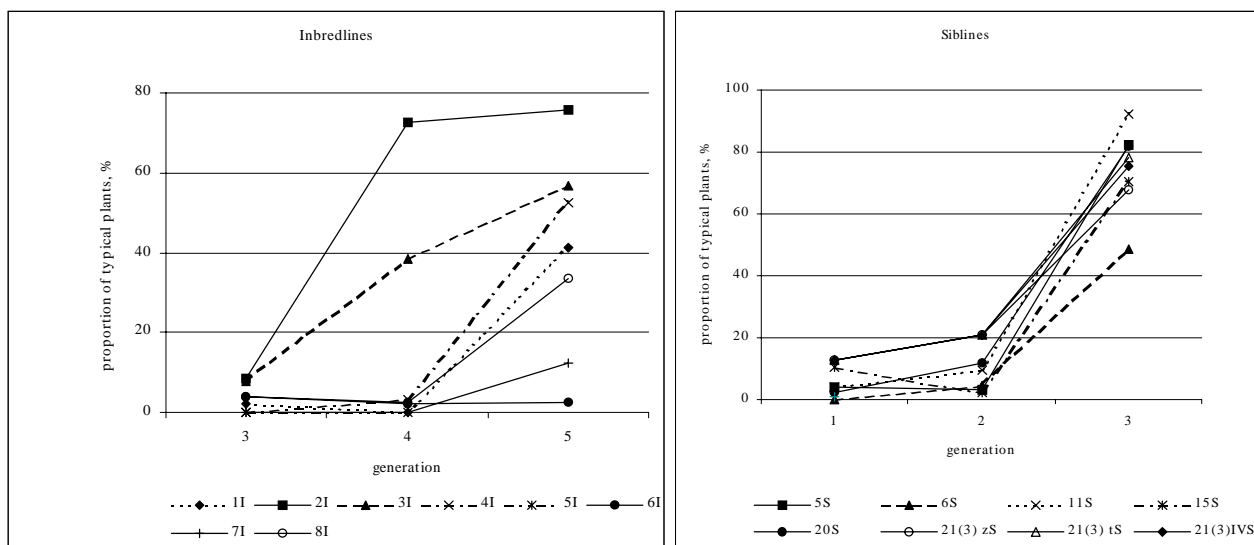


Fig. 2. Proportion of plants with score 3 for clustered fruits during homogenisation of the variety 'Dindoòà Zaiïe Í ekaru'

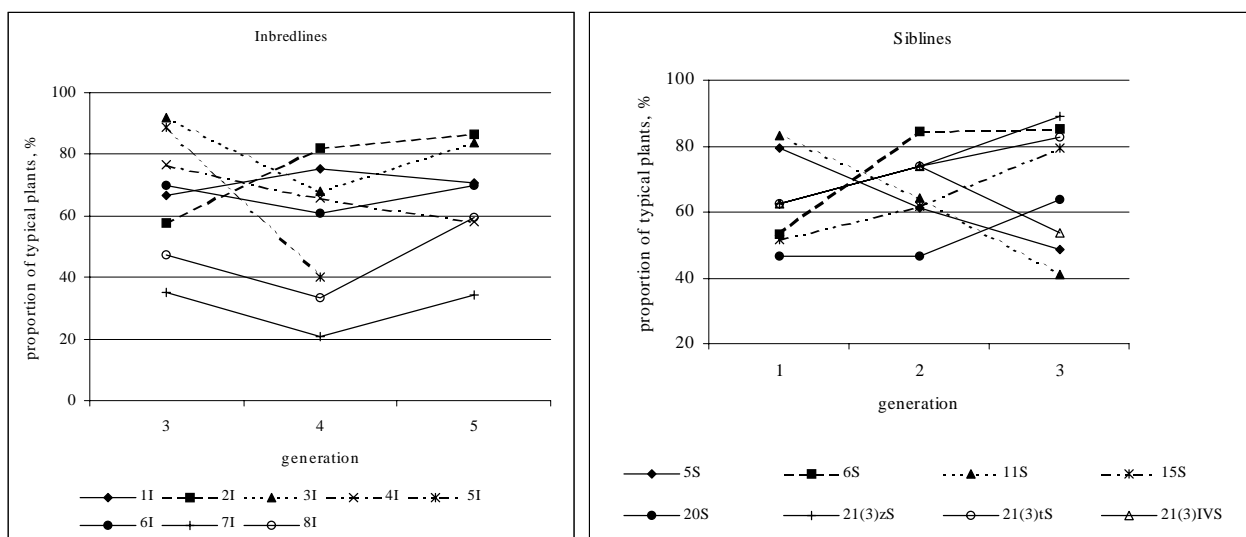


Fig. 3. Proportion of plants with score 3 for fruit colour during homogenisation of the variety 'Dindoòà Zaiïe Í ekaru'

each such plant were recognised as a sibline. Selection of most typical plants and pollination in each following generation were done among those plants within a sibline. Open-pollinated material of the initially used plants of the 'Dindoòà Zaiïe Í ekaru' was included also in the investigation.

Lines were grown in 4 replications, about 20 plants in each replication were evaluated visually on a 4-score scale for plant length and branching, fruit development in clusters, fruit and prickle colour (Table 1). For all traits, score 3 is typical of the variety 'Dindoòà Zaiïe Í ekaru', but 0 is completely atypical.

The average scores were calculated for each line of each trait. LSD was calculated between all lines in three generations (Table 2).

RESULTS

Plant length showed no remarkable changes during inbreeding and sibling up to the 5th generation of inbredlines and 3rd generation of siblines: all plants were of typical length and branching already at the beginning of selection. Main shoots of almost all plants in all generations were evaluated by the score 3.

In Fig. 1–3, changes in the proportion of plants, typical of the variety 'Dindoòà Zaiïe Í ekaru' (scored by 3) are illustrated both for inbredlines from the 3rd to the 5th generations and sib-lines from the 1st to the 3rd generations. In most genotypes, the proportion of plants with *clustered fruits* increased dramatically both during inbreeding and sibling. Up to the 3rd generation of inbredlines the propor-

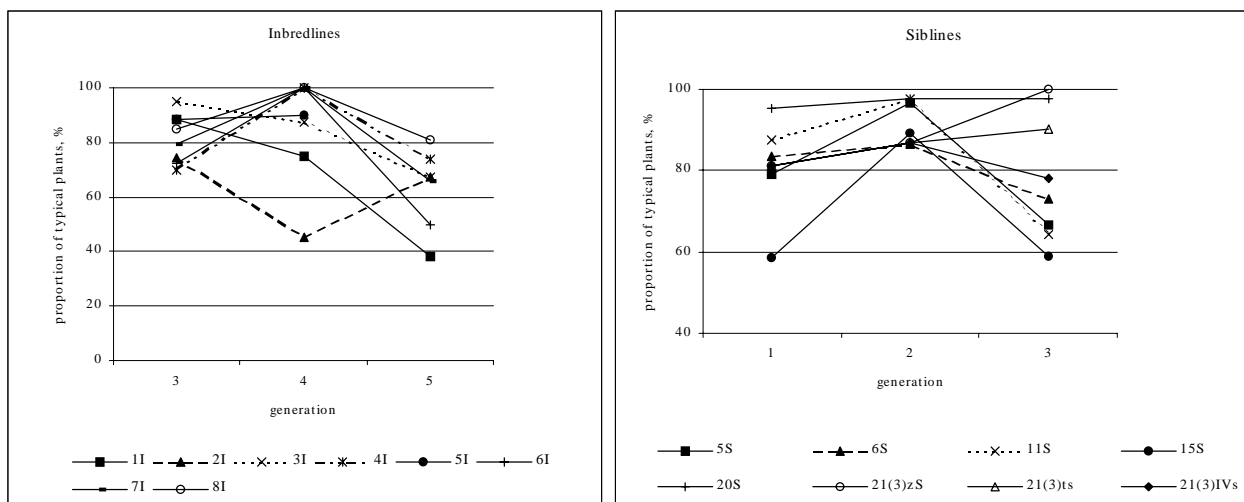


Fig. 4. Proportion of plants with score 3 for prickles during homogenisation of the variety 'Dindoða Zaiie Í ekaru'

tion of the typical plants was low and did not exceed 10%. A rapid increase of the percentage of typical plants was observed for inbredlines 2I and 3I in the 4th generation and was maintained later (Fig. 1). Most of the other inbredlines showed an enhanced proportion of typical plants in the 5th generation. As a result, an increase of the average score for inbredlines was observed (Table 2).

An increased proportion of plants with clustered fruits was registered for all siblines in the 3rd generation (Fig 1). It resulted in a sharp increase of the average score of siblines for this trait in the 3rd generation (Table 2).

Different changes of proportion of typically coloured fruits were observed for particular inbredlines and siblines (Fig. 2). In the 3rd generation, the proportion of typical plants was between 35.3% (inbredline 7) and 92.1% (inbredline 3). In the 5th generation, the proportion of plants with typically coloured fruits was almost in the same range: between 34.1 and 87.8%. Also the score of the fruit colour confirms insignificant changes in inbredlines among generations. At the same time statistically significant differences were observed among the inbredlines in each generation (Table 2).

Siblines had a proportion of typically coloured plants within similar limits as inbredlines (Fig. 2). In all generations, the score for particular lines ranged between 2.19 and 2.89 and showed no significant changes among the generations (Table 2).

The typical colour of prickles for the variety 'Dindoða Zaiie Í ekaru' is white. In most inbredlines and siblines, plants with black-prickled fruits were segregated during inbreeding and sibling. In most inbredlines, even a decrease of the proportion of typical white-prickled fruits was observed (Fig. 3): in the 3rd generation the percentage of typical plants was found between 72.4% and 94.7% but in the 5th generation it was between 38.2% and 81.0%.

The score of prickles colour in inbredlines showed an increasing score of some lines in the 4th generation and a decreasing in the next generation. These changes are significant. Also significant differences were stated among inbredlines in all three generations (Table 2).

The same tendency of the increasing proportion of typically coloured prickles in the 2nd generation and decreasing in the 3rd generation was observed for siblines. Nevertheless, in siblines the percentage of plants with typically coloured prickles was higher than in inbredlines. Also the average score of this trait was higher in siblines. Significant differences in the average score were observed between the sibline generations (Table 2).

DISCUSSION

Particular traits showed a different response to selection during homogenisation. During the process of inbreeding in five generations and sibling in three generations, some characters atypical of the variety 'Dindoða Zaiie Í ekaru' appeared in some lines. On the contrary, some characters were renewed according to the original description of the variety.

The homogeneity of the tested genotypes was checked by using molecular markers (RAPD) [6]. According to the results of marker analysis, some genotypes were quite homogeneous (for example, inbredline 8I), nevertheless, phenotypical traits showed a variation within lines. We assume that it is a result of the genotype and environment interactions.

Fruit development in clusters had a highest response to inbreeding and sibselection. In 1994, when the inbreeding was started, only 3.9% of plants performed clustered fruits. During inbreeding, a significant increase of the proportion of plants with clustered fruits was observed in most of lines, with the only exception for lines 5I and 6I. After five gene-

rations of inbreeding in the best line (2I) fruits were developed in clusters of 75.5% of plants (Fig. 1). Therefore we consider that this characteristic trait was renewed. According to the literature, fruit development in clusters can be determined either by the recessive allele *mp* [4] or by the dominant allele *Mp-2* [5], which has several minor modifiers. In our case, we assume that clustered fruits most likely are determined by the recessive allele *mp* which becomes homozygotic during close-related pollination and therefore is expressed phenotypically.

In contrast, plant length and branching showed no phenotypical changes during the inbreeding and sibling. The variety 'Dindoða Zaiie Í ekaru' was homogeneous for this trait already at the beginning of inbreeding and sibling and maintained this trait in all generations of the close-related crossing. According to Pierce and Wehner [5], plant length is determined by the allele *T*, which is dominant against the short main shoot. As not any other type of plant length and branching has been segregated during inbreeding, we assume that the initial material was homogeneous also genotypically for this trait.

According to Pierce and Wehner [5], dark-green coloured fruits are determined by a dominant allele of unknown location. Therefore we presume that evaluated fluctuations in the fruit colour are determined both by the expression of the homozygous recessive allele which determines light coloured fruits and by the environment and genotype interaction caused, for example, by different light distribution in the case of some dead plants.

The fruit prickles colour was one of the traits most responsive to inbreeding and sibling. Segregation of the initial material of the variety 'Dindoða Zaiie Í ekaru' in so different genotypes for prickles colour can be caused by an inheritance more complicated than monogenic.

Calculation of the LSD confirms that a more close-related pollination (inbreeding) splits the material into more different genotypes according to all the evaluated traits but not crosses among the more distant genotypes (sibling) (Table 2).

As the aim of the research was to split the initial material of the variety into homogeneous genotypes representing the variety for placing it in the gene bank, five lines were chosen as the representatives according to a combination of the morphological evaluation and molecular data. The inbred lines 2I, 3I and 8I in the 5th generation and sibilines 20S and 21(3)zS in the 3rd generation were chosen. All these genotypes have been placed for a long-term conservation in the Latvian Gene Bank of Cultivated Plants.

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