AGRONOMIJAS VĒSTIS (Latvian Journal of Agronomy), No.10, LLU, 2008

HORTICULTURE

GENETIC MATERIAL HOMOGENIZATION OF LATGALES MELONS
LATGALES MELOŅU ĢENĒTISKĀ MATERIĀLA HOMOGENIZĀCIJA

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Kopsavilkums

Pagājušā gadsimta vidū Daugavpils rajona Dvietes pagastā pazīstamais vīnogu selekcionārs Pauls Sukatnieks izveidoja vairākas Latvijas agroklimatiskajiem apstākļiem piemērotas šķirnes. Tomēr neorganizētas sēklaudzēšanas dēļ šīs šķirnes savstarpēji saziedējās ar citām Latvijā ievestām šķirnēm un pakāpeniski izvirta. Pateicoties dārzkopju – entuazistu un pētnieku darbam (Ē. Piļka, U. Dēķens, I. Drudze), šis unikālais ģenētiskais materiāls tika saglabāts. Kopš 2003. gada Pūres dārzkopības Izmēģinājumu Stacijā tiek veikta Latgales meloņu populācijas izvērtēšana un atjaunošana, veidojot tuvradniecisku krustojumu un inbredās līnijas. Tuvradnieciskās krustošanas un inbredizācijas mērķis ir homogenizēt pieejamo ģenētisko materiālu, sadalot to ģenētiski un morfoloģiski atšķirīgos genotipos. 2006. gadā, izmantojot 15 mikrosatelītu marķierus, molekulārajās analīzēs noteikta 3 dažādu Latgales meloņu līniju un 5 Dienvideiropas šķirņu savstarpējā ģenētiskā saistība. Latgales meloņu līnijai 5(2) bija augstākā vidējā augļu masa no auga, lielākie augļi, kā arī biezāks augļa mīkstums. Pārējos mērījumos labāki rezultāti novēroti Dienvideiropas meloņu šķirnēm. Ģenētiski vistuvākā Dienvideiropas meloņu šķirnēm bija Latgales meloņu līnija ‘8’.

Abstract

In the middle of the last century in the region of Daugavpils the well known grape breeder - Pauls Sukatnieks bred several melon (*Cucumis melo* L.) varieties. He also developed the open field growing system for these vegetables in Latvia. These varieties were sustainable for the agroclimatic conditions of Latvia – low night temperature, a short period of high temperatures and high air humidity. During several decades these genotypes were destroyed because of the cross-pollinating of different varieties. This unique genetic material was saved by the gardener Ē. Piļka, and the scientists U. Dēķens and I. Drudze. Since 2003, the renovation of Latgale’s melons was started in the Pūre Horticultural Research Station. Since 2003, inbreeding and sibling has been carried out. The aim of the investigation is to homogenize the genetic material of Latgale’s melons. In 2006, the genetic distance between 3 lines of Latgale’s melons and 5 South European varieties was detected by using 15 microsattelite markers. The highest average fruit weight, the largest fruits, bigger thickness of fruit flesh was observed on Latgales melon line ‘5(2)’. South Europe melons were better in other measurements. Genetically the closest to the South Europe varieties was Latgale’s melons line ‘8!’.

Key words

Cucumis melo, inbred lines, cross-pollination, microsattelites

Introduction

Melons *Cucumis melo* L. are widely cultivated plants originating from South Asia and the central part of Africa. From these regions (mostly from South Asia) melons have spread around the world (Белик, 1998; Лебедева, 2000). Many melon varieties were selected by humans in the since start of melon cultivation (IPGRI, 2003). The melons require high and substrate temperatures. The recommended sum of effective temperatures (temperature ≥ +10°C) for melon growth is 3000-5000°C (Taranovs, 1968). One of the famous melon growers in Latvia was Pauls Sukatnieks. He worked in Dviete, Latgale’s region, and bred such varieties as ‘Dvietes Oranžā’ and ‘Dvietes

Banānu'. P. Sukatnieks also developed the growing systems for melons in Latvia (Sukatnieks, 1954). The varieties bred by him were sustainable for Latvia's agroclimatic conditions. These varieties were of a very short vegetation period, and produced a good yield also in rainy summers (Sukatnieks, 1954). The aim of the research was to determine the morphological and genetic distance between Latgales melon lines and the southern European varieties.

Materials and Methods

The melons were grown in the Pūre Horticultural Research Station in the Tukums region. The research was done in 2006. Three lines ('5(2)', '4(3)!!!', '8!') of Latgale's melon and five South Europe varieties ('Honey Dew Orange Flesh', 'Tendral Verde Negro', 'Jaune Canaris', 'Gros Pecoud', 'Cantaloup de Bellegarde') were included in the investigation. The South Europe varieties were used for comparison with Latgale's melons morphologically and on the molecular level. For these melons we choose IPGRI descriptors for melons as these were best for the comparison of morphological features. For every variety, five plants were evaluated. The melons were sown on April 22 in pots of 8 cm diameter, in peat substrate with pH_{KCl2} 5.5±0.5, N – 100-140 mg kg^{-1}, P_2O_5 – 110-170 mg kg^{-1}, and K_2O – 190-290 mg kg^{-1}. The seedlings were grown in pots in a plastic tunnel till May 28. Plants were planted in a plastic tunnel in a peat substrate with 0.8 m density. During the time of the investigation the melons were regularly watered and every second week fertilized with $Ca\ (NO_3)_2$ (1200 g m^{-3} water) and with 'Kemira' 10:10:20 (1750 g m^{-3} water).

The following parameters were measured to compare Latgale's melons with the South Europe varieties: length and width of the cotyledons (cm), petiole scar diameter (cm), and average fruit weight (kg) from plant, thickness of flesh (cm), average fruit length and width (cm). Genetic relations between genotypes were detected by the use of 15 microsattelite markers (CMCTT144F, CMACC146F, CMGA104F, CMAT141F, CMCCA145F, CMTC13F, CMGT108F, CMCT134bF, CMCT44F, CMTC168F, CMCT170bF, CMAG59F, CMTC47F, CMGA15F, CMTA170aF) in the Latvian State Forestry Research Institute „Silava".

Differences between measurements of lines and varieties were evaluated according to ANOVA. The genetic distance between Latgale's melon lines and the southern European varieties was evaluated using GeneMapper software.

Results

The bigger cotyledons were observed for the South Europe varieties 'Honey Dew Orange Flesh' (6.6 and 3.5 cm), 'Jaune Canaris' (6.1 and 3.1 cm) and 'Tendral Verde Negro' (5.8 and 2.9 cm) (Figure 1). The data of the mathematical analyses showed that there was a significant difference between the genotypes according to cotyledons length and width: between cotyledons length $F=42.28>F_{crit}=2.31$ and between cotyledons width $F=46.89>F_{crit}=2.31$ (with P=95 %).

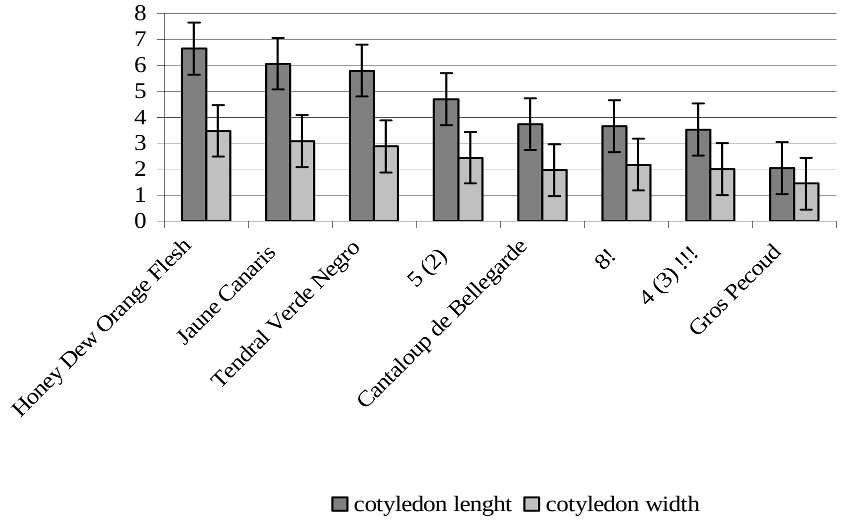


Figure 1. Size of cotyledons, cm

The significant difference of cotyledons length was observed between ‘Honey Dew Orange Flesh’, ‘Tendral Verde Negro’, ‘Jaune Canaris’ and ‘4(3)!!!’, ‘8!’, ‘Cantaloup de Bellegarde’, ‘Gros Pecoud’. For the other variants differences were not significant. The significant differences of cotyledons width was between ‘Honey Dew Orange Flesh’, ‘Tendral Verde Negro’, ‘Jaune Canaris’ and ‘4(3)!!!’, ‘Cantaloup de Bellegarde’, ‘Gros Pecoud’. For the other variants differences were not significant.

The biggest petiole scar diameter was observed in the Southern European variety ‘Gros Pecoud’ (2.1 cm) and Latgale’s melon lines ‘8!’ (1.7 cm), ‘5(2)’ (1.7 cm). (Figure 2) The data mathematical analyses showed that there was a significant difference between the genotype according to petiole scar diameter: $F=9.57>F_{crit}=2.31$ (with P=95 %). The significant difference of petiole scar size was between ‘Jaune Canaris’ and ‘Gros Pecoud’.

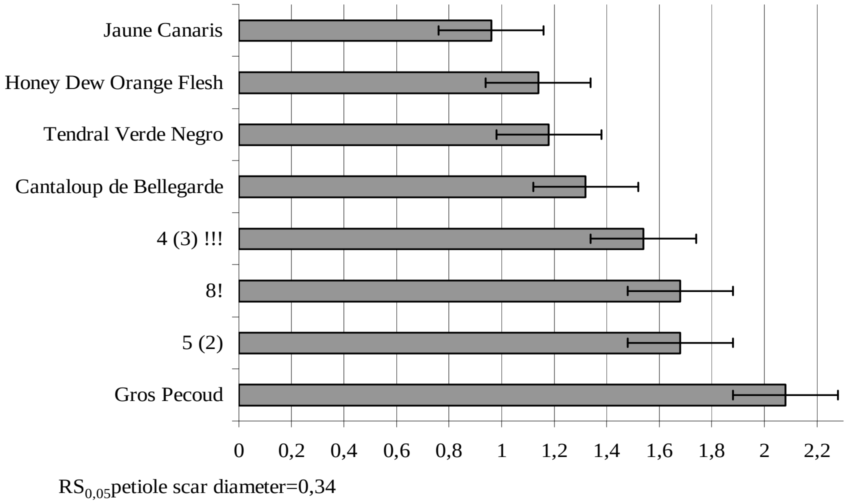


Figure 2. Petiole scar diameter, cm

A higher average fruit weight was observed for all of Latgale’s melon lines. Between fruit weight $F=18.75>F_{crit}=2.31$ (with P=95 %). The mathematical analyses data showed that there was a significant difference between the genotypes according to fruit weight. (Figure 3) The significant difference of fruit weight was between lines ‘5(2)’, ‘4(3)!!!’, ‘8!’ and the varieties ‘Jaune Canaris’ and ‘Gros Pecoud’.

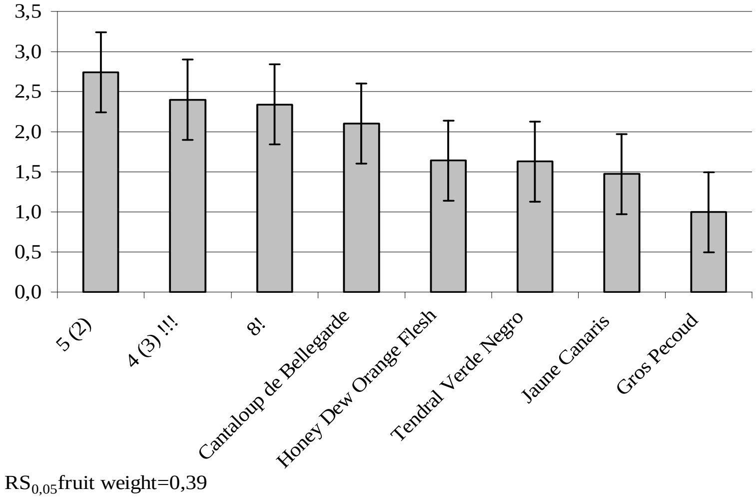
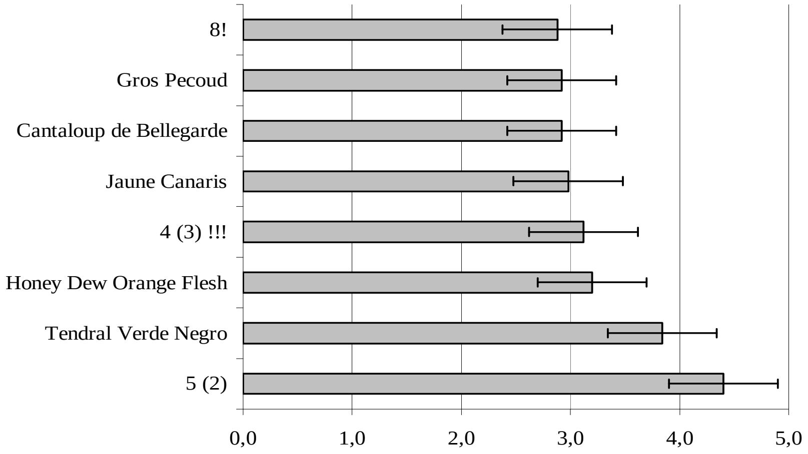


Figure 3. Average fruit weight from plant, kg

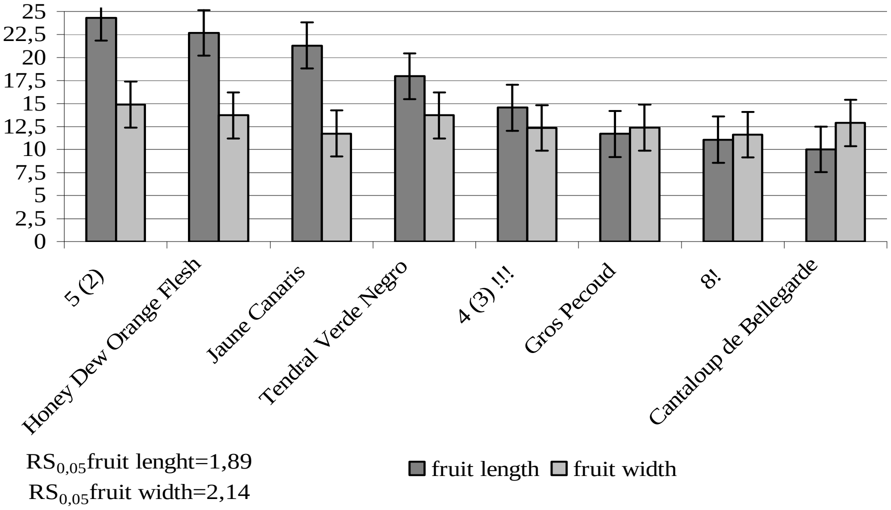
Thicker flesh was observed in the Latgale's melon line '5(2)' (4.4 cm) and the Southern European variety 'Tendral Verde Negro' (3.8 cm). There was a significant difference between the variety or line, and the thickness of the flesh. Fruit thickness of flesh depends on variety or line. Between fruit weight $F=4.76>F_{crit}=2.31$ (with P=95 %). On all occasions essential differences were not observed. (Figure 4)



$RS_{0,05}$fruit thickness=1,19

Figure 4. The fruit thickness of flesh, cm

The average fruit length and width was higher in the Latgale's melon line '5(2)' and Southern European varieties 'Honey Dew Orange Flesh', 'Jaune Canaris'. The mathematical data analyses showed that there was a significant difference between the variety or line, and parameters of fruit. Between fruit length $F=75.17>F_{crit}=2.31$ and between fruit width $F=2.35>F_{crit}=2.31$ (with P=95 %). The significant differences of fruit length was between '5(2)', 'Honey Dew Orange Flesh', 'Jaune Canaris' and '4(3)!!!', '8!', 'Cantaloup de Bellegarde', 'Gros Pecoud'. In all measurements of fruit width significant differences were not observed. (Figure 5)



$RS_{0,05}$fruit lenght=1,89
$RS_{0,05}$fruit width=2,14

Figure 5. The fruit parameters, cm

The experiment used 15 microsattelite markers. The genetic distance between Latgale's melon lines and the South Europe varieties was determined by the use of these markers. If the genetic interrelations coefficient is close to one, then the melons are genetically distinct. If the coefficient is close to zero, then the melons are genetically close. (Figure 6).

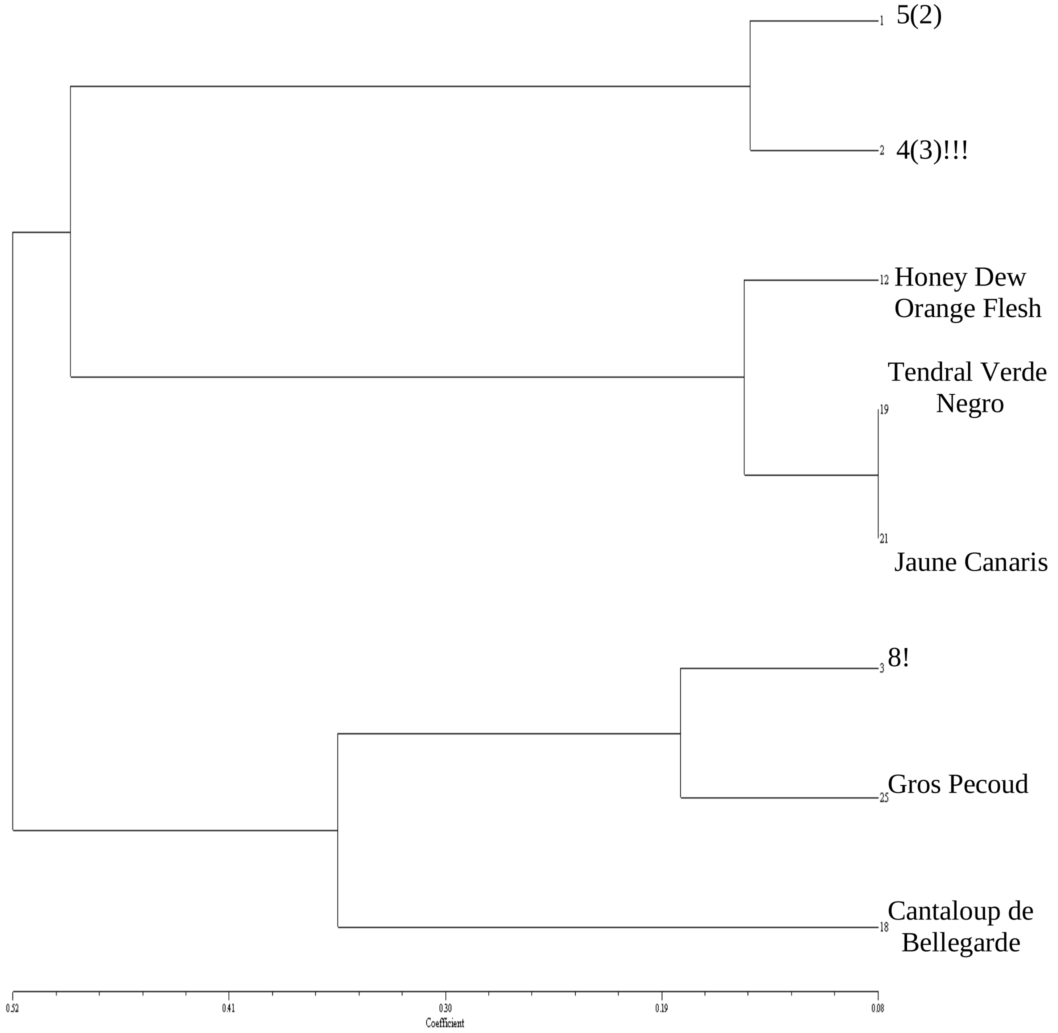


Figure 6. Genetic interrelations between melons

Two lines of Latgale's melons (5(2); 4(3)!!!) are genetically different from other varieties. The line of Latgale's melon '8!' is genetically close to the South Europe variety 'Gros Pecoud'. Lline '8!' also is morphologically distinct from other lines of Latgale's melons.

Discussion

Latgale's melons till now have not been investigated and compared by using molecular markers. Local Latvian genotypes are genetically different from South Europe varieties. According to the molecular data one of Latgale's melons (8!) is relatively close to the 'Gros Pecoud' variety.

In cotyledons plant accumulated nutrients and cotyledon size affects further plant development (Шевелёв, 1996). The South Europe varieties had the bigger cotyledons. Bigger cotyledons create the possibility to give the highest results in plant vegetative evolution and in yield (Шевелёв, 1996). But according to future results Latgales melons show highest measurements.

The storage length of fruits depends on the fruit petiole scar. From the scar it is possible for the fruit to be infected by different fungal diseases. (Борисова, 1984). Latgale's melons are less suitable for storage. The highest average fruit weight was observed for Latgale's melon lines. This trait is important for the commercial growing of melons. The thickness of fruit flesh is also an important morphological parameter. If the cavity of seeds is smaller the weight of fruit will be higher.

Latgale's melons have a bigger fruit petiole scar, smaller in size, but these genotypes have a higher amount of fruits from one plant and higher average fruit weight in comparison to South Europe varieties. Two of Latgale's melon lines are genetically more distinct from South Europe varieties. This confirms the historical origin of Latgale's melons – mostly they were bred by using varieties of Russian origin (Sukatnieks, 1954).

Conclusions

The largest cotyledons were observed for South Europe varieties 'Honey Dew Orange Flesh', 'Tendral Verde Negro' and 'Jaune Canaris'. The smaller fruit petiole scar diameter was observed for the South Europe varieties 'Honey Dew Orange Flesh', 'Tendral Verde Negro' and 'Jaune Canaris'. The highest average fruit weight was found in Latgale's melon lines. The thickness of flesh was bigger for Latgale's melon line '5(2)' and South European variety 'Tendral Verde Negro'. The largest fruits were produced by Latgale's melon line '5(2)' and South European varieties 'Honey Dew Orange Flesh' and 'Jaune Canaris'. According to microsattelite markers the genetically closest variety to South Europe varieties was Latgale's melon line '8!'.

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LATVIJAS MARTAGONLILIJAS (*LILIUM MARTAGON L.*) POPULĀCIJAS NOVĒRTĒJUMS UN IZMANTOŠANA SELEKCIJĀ

ASSESSMENT OF THE POPULATION OF LATVIAN MARTAGONLILY (*L. MARTAGON* L.) AND APPLICATION IN BREEDING

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Abstract

Lily breeders are very interested to find bulbs in the wild, collect them and use them for breeding purposes. The genus *Lilium* L. includes approximately a hundred species distributed throughout the cold and temperate parts of the northern hemisphere. One of the best known of wild lilies is *L. martagon* L. Of all the lily species, it is distributed across the largest growing area – from western Portugal through Europe and Asia. It was discovered in 1839, and is the only wild lily species in Latvia. The stem is erect, up to 200 centimetres, and there are as many as 50 pendent-like turk's-cap flowers on a stem. To evaluate the survival potential of *L. martagon* L., research was carried out in locations at Aizkraukle, Ventspils, Kuldiga and Tukums. Research results indicate that the diversity in genotypes varies according to location and distribution. According to morphological traits, these martagonlilies were classed into three groups: 1) plants found on the left bank of the Daugava near Vigante Park and Staburags (areas which belong to the region of Aizkraukle); 2) plants found in the regions of Ventspils, Kuldiga and Tukums; 3) plants found at Aizkraukle on the right bank of Daugava near Klintaine. Crosses were made between wild martagons with light pink