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Agro-morphological characteristics of selected sweet potato (*Ipomoea batatas* L.) varieties from organic farming and their genetic background

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ABSTRACT

Sweet potato is one of the most important root crop worldwide. This study aimed to compare agro-morphological characteristics of four sweet potato varieties (Martina, Janja, Lučka, Purple Specllet) from organic farming with additional information about their genetic background. A total of 26 agro-morphological traits were evaluated during vegetation. Pre-grown seedlings were planted in organic fields during the 2021 growing season using the soil ridge cultivation method. The study showed significant differences between varieties in quantitative (except for the extent and intensity of anthocyanin colouration on abaxial veins) and qualitative traits (except for the number and length of primary shoots and internode diameter). **The varieties Lučka and Martina proved to be significantly higher yielding compared to the other two varieties.** The genetic background of the varieties was evaluated on 8 SSR loci using allele polymorphisms with a total number of 34 different alleles and an average polymorphic information content of 0.60. The favourable informativeness of the selected markers was confirmed by the global genetic diversity of 0.68. The assignment of each genotype to two genetic groups agrees well with the varietal distribution in the phylogenetic tree and the results of the analysis of the genetic structure (**Martina/Janja and Lučka/Purple Specllet**). The present study contributes to a better knowledge of the sweet potato varieties considered and their agro-morphological and genetic diversity.

Keywords: Diversity, Organic farming, Plant descriptor, SSR marker, Sweet potato.

INTRODUCTION

Sweet potato (*Ipomoea batatas* L.) is a dicotyledonous angiosperm plant and belongs to the convulvaceae species (Gobena *et al.*, 2022; Cartabiano-Leite *et al.*, 2020). It is native to South and Central America, where its domestication began about > 5,000 years ago. Later, the cultivated types spread throughout the Americas, Asia, and Africa (Escobar-Puentes, 2022; Roullier *et al.*, 2013). **Nowadays**, it is ranked the seventh most important food crop in the world and is grown in 117 countries with a global annual production of nearly 90 million tons with an

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average yield of 12 t ha⁻¹ (FAOSTAT, 2023; Prakash *et al.*, 2018). Sweet potato is grown mainly by smallholders and serves as a staple food in the poorest regions of the world (Andrade *et al.*, 2017) because it can be planted and harvested flexibly in frost-free areas, has a short growing season, uses non-edible parts for planting, does not form trellises, and requires few soil nutrients (Mukhopadhyay *et al.*, 2011). It is usually grown between sea level and 2,300 m altitude in tropical and temperate zones located 40° south and north of the equator (Gobena *et al.*, 2022). Production in Europe, where the largest producers are Spain, Portugal, and Italy, accounts for the smallest share of global production, although the introduction of sweet potato in the central European region has great potential for agriculture and human nutrition due to its variable genetic background potentially suitable for this growing region, including Slovenia (Dinu *et al.*, 2021; Pipan *et al.*, 2017a).

The plant is cultivated for its starchy roots and immature leaves, which are used for human consumption and as animal feed (Gobena *et al.* 2022; Ferreira *et al.* 2022). Sweet potato is an admirable crop because it is the only member of its species capable of developing nutritious tuberous roots that feed a large portion of the world's population, especially in the tropics where most of the crop is grown and consumed (Cartabiano-Leite *et al.*, 2020; Ukom *et al.*, 2009). Tubers are a good source of energy with an abundance of proteins, lipids, fiber, sugars, minerals such as potassium, vitamins A, C, D, E, and B complex, and can be used for various purposes. They are rich in starch, which accounts for more than 50% of carbohydrate components (Hayati *et al.*, 2020; Andrade *et al.*, 2017) and are also a valuable source with anti-cancer, anti-diabetic, and anti-inflammatory properties (Mohanraj and Sivasankar, 2014).

Sweet potato is a vine-like perennial herb that spreads on the soil surface. Morphologically, the plant consists of the following main parts: tubers (enlarged root), stem (also called vine) and leaf, flower, fruit and seed and is grown as an annual plant (Ukom *et al.*, 2009). **Sweet potatoes** can be propagated by seeds, tubers, or vine cuttings. Vegetative propagation is usually done by planting cuttings from the previous season's crop or by raising selected tubers. Vines/shoots **from freshly** harvested crop can also be planted in nursery beds to provide sufficient planting material (Mukhopadhyay *et al.*, 2011). Shoot production is increased by the best selection of storage root sizes to optimize growth and yield. Varieties with different storage root sizes produce a variable number of shoots that vary in length and thickness. Standard characterization of plant genetic resources includes conventional approaches such as the use of descriptor lists for morphological traits or agronomic performance evaluation, complemented by molecular techniques (Maquia *et al.*, 2013). Sweet potato plant diversity can be studied by identifying agro-morphological traits. The purpose of identification is to find out the important

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traits of plant species derived from different clones so that they can be used as a source of genetic diversity to support plant breeding activities. Generally, yields of sweet potato in farmer fields are low due to the use of local genotypes, but could be increased by using improved varieties or new clones (Hayati *et al.*, 2020; Reddy *et al.*, 2018). The success of any genetic conservation and breeding program depends on understanding the distribution of genetic diversity in the gene pool (Zhang *et al.*, 2000). Among the 175 species of *Ipomoea*, *Ipomoea batatas* is the only tuber-forming natural allohexaploid ($2n=6x=90$) species, although many of the species are diploid and tetraploid (Mukhopadhyay *et al.*, 2011, Reddy *et al.*, 2018). There are many varieties of sweet potato known and cultivated worldwide. They have different colours, shapes and sizes of skin and flesh of storage root and differ in taste and texture. The different sweet potato varieties are generally characterized by the skin and flesh color of the storage roots (tubers) and other agronomic traits such as leaf and stem morphology (Amagloh *et al.*, 2021).

The objective of this study was to characterize the agro-morphological variation among four sweet potato varieties grown in organic farming using the soil ridge cultivation method using various **agro-morphological traits** related to overall plant architecture, stem, leaf and tubers, and to determine the main contributors of variation for future selection and breeding programs. In addition, SSR markers were used to investigate the genetic background and relatedness between the four varieties at the molecular level. **Sweet potato is relatively new crop in Slovenia and wider Central European growing conditions. Therefore, agro-morphological and genetic studies on the available varieties creates valuable knowledge for further intensification of cultivation in the region and beyond.**

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MATERIALS AND METHODS

Plant Material and Experimental Design

A set of four sweet potato varieties (Martina – purple skin and white tuber flesh, Janja – white skin and white tuber flesh, Lučka – orange skin and orange tuber flesh, Purple Speplet – purple skin and purple tuber flesh) were grown in the 2021 growing season in the organic fields of the Biotechnical Centre in Naklo, Slovenia (46° 16' 18" N, 14° 18' 56" E, 420 m asl). The varieties Martina, Lučka and Janja were registered as protected varieties in the **Slovenian National List of Varieties** in 2016, while the variety Purple Speplet is commercially available on the European market. A single-factorial field trial was established at the experimental site in a randomised block design with four replicates of 15 seedlings planted 40 cm apart on the soil ridge of each plot. Seedlings were vegetatively propagated in the greenhouse by cuttings from tubers from

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100 previous growing seasons. The seedlings (about 20 cm high) were planted in the field in early
101 June on the ploughed and harrowed soil ridges. Barley straw was used as mulch between plots
102 to prevent roots from growing from each node during vegetation. The soil type is Umbrian
103 planosols with a silty loam texture and a bulk density of 1.61 in the upper 30 cm. Analysis of
104 the upper 30 cm of soil showed a pH of 6.8 and P₂O₅ and K₂O contents of 220 and 500 mg kg⁻¹
105 respectively. The organic carbon content was 5.3%, while the available Nitrate-Nitrogen
106 (NO₃-N) was 0.68%. Basic fertilisation was carried out before tillage with the organic fertiliser
107 Fertigung Stallatico Umificato Pellettato (3-3-1; Fertigest, Fomet, Italy), while the plants were
108 fertilised twice during the growth period with the organic fertiliser Tiger Dung 3:6:12+2MgO
109 (Fomet, Italy). The application rate/dosage was in accordance with the manufacturer's
110 recommendations.

Agro-morphological Characterisation

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112 A total of 26 quantitative and qualitative descriptors related to the architecture of the whole
113 plant, stem, leaves, and tubers were developed by the International Union for the Protection of
114 New Varieties of Plants – UPOV (2010) and the International Board for Plant Genetic
115 Resources – IBPGR (1991) for *Ipomoea batatas* were used for the agro-morphological
116 characterisation. All qualitative descriptors were assessed visually, while quantitative
117 descriptors were measured using a digital calliper (to 0.1 mm), a tape measure (to 1 cm) and a
118 laboratory balance (to 0.5 g). Data on agro-morphological characteristics were collected
119 according to the descriptor list summarised in Table 1.

Molecular Analysis

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122 Young leaf tissue was frozen and stored at -20°C for further genetic analysis. DNA was
123 extracted from the leaves of four individual plants of each variety. The DNA extraction protocol
124 and genotyping procedure followed the methods described in Pipan et al. (2017a, b) using a set
125 of eight Simple Sequence Repeat (SSR) markers (Buteler et al., 1999; Veasey et al., 2008).

Data Analysis

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128 Different univariate and multivariate approaches were applied to the data of the 26 agro-
129 morphological qualitative and quantitative traits using the statistical programming environment
130 version 3.4.4 R Core Team (2021) to investigate the patterns of variation within and among the
131 four sweet potato varieties analysed in this study. First, the “diverse” package (Guevara et al.,
132 2016) was used to calculate the frequency of distribution and estimate the Shannon-Weaver
133 diversity index (H') (Shannon and Weaver, 1949) and Pielou's evenness index (J) to assess the
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130 diversity of the 11 qualitative traits. The package “*ggstatsplot*” (Patil, 2021) was used to plot
136 the frequencies of the different classes of the 11 qualitative traits within and between the four
137 varieties, and the differences within and between varieties were tested using Fisher’s exact test
138 implemented in the package “*rstatix*” (Kassambara, 2023), with $P \leq 0.01$ as the significance
139 threshold. For the 15 quantitative traits, a two-way Analysis Of Variance (ANOVA) was first
140 performed to determine the effects of variety, block effect, and their interaction on the variation
141 of each trait. Then, a one-way ANOVA was performed, followed by a Tukey HSD at the
142 $P < 0.01$ significance level for the comparison of means among the four varieties. ANOVA and
143 the Tukey HSD test were performed using the “*aov*” and “*TukeyHSD*” functions, respectively,
144 implemented in the “*R-stats*” package of the R programming environment.. In addition, the
145 package “*TraitStats*” (Nitesh *et al.*, 2021) was used to calculate the Genotypic Coefficient of
146 Variation (GCV), the Phenotypic Coefficient of Variation (PCV) according to Burton (1951),
147 the broad-sense Heritability (H^2) according to Lush (1940), and the Genetic Advance over Mean
148 (GAM). The latter was calculated as $GAM = (GA/\mu) \times 100$, where GA is the genetic advance and
149 was calculated as $GA = k \times (H^2/100) \times \sigma_g$, and μ was the overall mean of the trait, k was the
150 standardized selection differential at a selection intensity of 5% ($k = 2.06$) and σ_g was the
151 genotypic standard deviation (Johnson, 1955). **Furthermore**, the package “*CorrPlot*” (Taiyun
152 and Viliam, 2017) was used to examine the correlation among the 26 agro-morphological traits
153 using the Spearman correlation coefficient (ρ). Finally, Multifactorial Analysis (MFA) was
154 performed for all analysed traits using “*FactoMiner*” (Lê *et al.*, 2008) and “*Factoextra*”
155 (Kassambara and Mundt, 2020) to examine the differentiation patterns among the four sweet
156 potato varieties and estimate the contribution of each trait to differentiation.

157 Genetic diversity parameters and observations of codominant data were evaluated using
158 various population genetics programs. Marker variability and allele patterns of varieties were
159 calculated in MS Toolikit (Park, 2001) and GenAIEx (Peakall and Smousse, 2006). Allelic
160 richness (Ar) was calculated using Fstat (Goudet, 2005). Genetic distances between varieties
161 were calculated using the standard genetic distance of Nei (Nei, 1972) and the UPGMA
162 (unweighted pair group method with arithmetic mean) clustering method in the software
163 Populations (Langella, 2002).

164 **RESULTS AND DISCUSSION**

165 **Agro-Morphological Variability and Trait Associations**

166 In this study, sweet potato cultivation of four varieties (Martina, Janja, Lučka, Purple Speplet)
167 was tested in organic fields under subalpine continental climate conditions. Sweet potato
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169 varieties are generally distinguished based on agro-morphological characteristics and show
170 great variability in botanical traits related to plant architecture, leaves, stems, and tubers, and
171 productivity among varieties may differ even under the same environmental conditions
172 (Vazhacharickal et al. 2022). Here, analysis of the 11 qualitative traits showed considerable
173 variability among the four varieties studied, with mean values for the Shannon-Weaver
174 diversity index (H') and Pielou's evenness index (J) of 0.69 and 0.62, respectively (Table 2).

175 As revealed by Fisher's exact test, the four varieties differed significantly in all qualitative
176 traits ($P < 0.01$), Except for the extent (EACAV) ($P = 0.049$) and Intensity (IACAV) ($P = 0.063$)
177 of anthocyanin coloration on the abaxial veins of the leaf blade (Figure 1). In terms of plant
178 architecture, Ground Cover (GC) was the most variable trait ($H' = 1.14$ and $J = 0.82$) among
179 those studied. Individual plants of the three varieties Janja, Martina and Purple Speklet had a
180 complete ground cover, with a few plants having a ground cover that varied from low to high,
181 while the ground cover of Lučka plants was mainly medium and some individuals had low
182 ground cover. Growth Habit (GH) ($H' = 1.01$ and $J = 0.78$) was mostly semi-upright in Lučka
183 and Purple Speklet varieties, spreading in Janja, and upright in Martina. In stem-related traits,
184 a relatively large variation was observed in Anthocyanin Coloration of the Internode (ACI)
185 ($H' = 1.02$ and $J = 0.93$), Tip (ACT) ($H' = 0.67$ and $J = 0.61$), and Node (ACN) ($H' = 0.66$ and
186 $J = 0.60$). In the variety Janja, coloration was absent or weak in the internode and the tip and
187 node, in the varieties Lučka and Martina, anthocyanin coloration was mostly medium in the
188 internode and absent or weak in the tip and node, while in Purple Speklet, strong coloration was
189 predominant in the internode and medium coloration in the tip and node. In leaf characteristics,
190 the greatest diversity was observed in Leaf Blade Lobe Depth (DOL) ($H' = 1.08$ and $J = 0.78$)
191 and Leaf Blade Lobes (LBL) ($H' = 0.56$ and $J = 0.81$). Except for Purple Speklet, which had five
192 lobes, the other three varieties had three lobes. The depth of lobing was mostly moderate in
193 Purple Speklet, very shallow in Janja, and shallow in Lučka and Martina. The four varieties did
194 not differ significantly in the extent and intensity of anthocyanin coloration in the abaxial veins
195 (EACAV and IACAV) ($H' = 0.10$ and $J = 0.15$) and in Anthocyanin Coloration of the Petiole
196 (PAC) ($H' = 0.38$ and $J = 0.27$), and coloration was absent or very weak.

197 In addition, analysis of variance for the 15 quantitative traits showed significant differences
198 among sweet potato varieties for all traits except Number of Primary Shoots (PSN), Lngth of
199 Primary Shoots (LPS), and Diameter of Internodes (DI) (Table 3), with an average of explained
200 genetic variance (variety component) of 65.38% for all traits. For the significantly different
201 traits, a comparison of means using Tukey's test showed that variety Janja had a significantly
202 higher Number of Internodes (NI) and Leaves (NL) and significantly lower yield (NTP), as it

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203 had significantly lower values for all tuber traits compared to the other varieties. However, the
204 varieties Lučka and Martina proved to be significantly higher yielding compared to the other
205 two varieties. Nevertheless, Lučka and Martina differed significantly from each other in some
206 traits, such as Internode Length (LI), Number of Leaves (NL), Mature Leaf Size (MLS), Haulm
207 Fresh Weight (HFW), Number of Tubers per Plant (NTP), and Marketable Tuber Weight
208 (WMT). The variety Purple Specklet was in an intermediate position in terms of tuber production
209 (Figure 2). However, the variance explained by the block and variety×block components was
210 relatively small, averaging 12.87 and 16.64%, respectively, and was not significant for most
211 traits analysed. The residual effect was also small, averaging 5.09% for all traits (Table 3).
212 These results indicate that the agro-morphological variability is mainly due to the genetic
213 differences among varieties, indicating the possibility of improving the agro-morphological
214 traits of the studied sweet potato varieties through genotypic selection. Agro-morphological
215 traits that are generally stable and unaffected by environmental factors include leaf shape, leaf
216 and petiole colour, tuber skin and flesh colour, while traits that changed under environmental
217 influence include petiole length, leaf size, and tuber yield (Hayati *et al.*, 2020). In addition,
218 variability in sweet potato agro-morphology may be related to factors such as seasonality, crop
219 farming management, climatic conditions, and natural plant characteristics (Leite *et al.*, 2022).
220 According to Ochieng (2019), sweet potato genotypes grown at two locations differed in terms
221 of internode length and primary shoot (vine) growth rate, petiole length and leaf size, and tuber
222 yield at both locations, with a significant correlation between shoot growth rate and internode
223 length and mature leaf size at one location. At the other side, there was a significant correlation
224 between shoot growth rate and internode length. In our study, there was a correlation between
225 stem length of primary shoots and internode length, between stem length of primary shoots and
226 mature leaf size, the correlation coefficient was low. In the study by Ilodibia *et al.* (2018),
227 similarities were found in plant shape, leaf type and colour, leaf arrangement shape, leaf margin,
228 veining, tips, shoot shape, texture, and tuber type. Differences were noted in shoot length,
229 colour and diameter, leaf size and colour, and petiole length. Phenotypic characterization of
230 sweet potatoes is done by evaluating variations in plant, shoot, leaf, flower, and storage root
231 traits and is traditionally used to identify sweet potato varieties (Vazhacharickal *et al.*, 2022).
232 Patterns of agro-morphological variability in quantitative traits were calculated using
233 Phenotypic and Genotypic Coefficients (PCV and GCV). As shown in Table 4, PCV was higher
234 than GCV for all traits analysed, with average values of 46.16 and 29.08%, respectively. The
235 highest PCV and GCV values were observed for tuber-related traits such as Number (NMTP)
236 (PCV = 91.47% and GCV = 63.85%) and Weight (WMT) (PCV= 93.87% and GCV= 68.35%)

of marketable tubers, while the lowest values were recorded for mature leaf size (MLS) (PCV= 16.49% and GCV= 10.86%) and Internode Length (LI) (PCV= 17.47% and GCV= 8.43%). This higher GCV in tuber traits suggests that these traits can be more easily improved by genotypic selection. Although CVG estimation provides information on genetic variation in quantitative traits, it cannot determine the extent of heritable variability. This was estimated in our study using heritability in a broader sense, which ranged from low ($H^2 < 30\%$) to medium ($30\% \leq H^2 < 60\%$), with an average of 35.57% for the 15 quantitative traits (Table 4). Among the analysed traits, the Number of Internodes (NI) ($H^2 = 55.75\%$) and tuber-related traits had the highest Heritability ($H^2 > 50\%$), except for Haulm Fresh Weight (HFW) ($H^2 = 17.99\%$). These results indicated that, although PCV performed better than GCV, this substantial amount of heritable variation suggested that environmental factors did not strongly influence phenotypic variation in these traits. Of the contracts, the least heritable variation was found for Number of Primary Shoots (PSN) ($H^2 = 2.54\%$) and Internode Diameter (DI) ($H^2 = 16.93\%$). In addition, Genetic Advance as a percentage of the Mean at a selection intensity of 5% (GAM) showed almost the same trends as PCV, GCV, and H^2 , with values ranging from 0.91% for PSN to 102.51% for WMT (Table 4). This pattern indicates that the mean values for most of the analysed traits can be strongly modified at a selection intensity of 5%.

Analysis of **the association** between pairwise traits showed moderate to strong positive correlations were found between leaf- and stem-related traits at the vegetative level (Figure 3). However, relatively low but significant correlations were found between traits characterizing plant architecture and all other traits. On the other hand, strong positive correlations were found at the reproductive level between traits characterizing tuber size (TD and TL) and traits related to marketable tubers (TWTP, NMTP, WMT, TD, and TL) ($\rho > 0.65$). However, the Number of Tubers per Plant (NTP) was negatively correlated with the other tuber traits, except for a moderate positive correlation with Total Tuber Weight per Plant (TWTP) ($\rho = 0.34$), indicating that the plant produced tubers with different sizes. On the other hand, haulm fresh weight (HFW) showed very low but significant positive correlations with the other tuber traits, except for its positive correlation with Number of Tubers per Plant (NTP) ($\rho = 0.45$) and Number of Leaves (NL) ($\rho = 0.51$). It should also be noted that Growth Habit (GH) and Ground Cover (GC), both of which characterize plant architecture, had negative correlations with tuber traits (Figure 3).

To investigate the patterns of agro-morphological differentiation **between varieties** (inter-variety), the data of the 26 traits were analysed using Multifactorial Analysis (MFA). The results of MFA showed that the first two dimensions explained 16.3 and 14.6% of the total

variation, respectively. The plot formed by these two dimensions clearly separated the variety Purple Speklet from the other three varieties on the positive side of the second dimension (Figure 4). The contribution to variation among varieties was much higher for qualitative traits than for quantitative traits (10.77% versus 5.43%) (Table 5). The most important traits that distinguished this variety from the other varieties were mainly qualitative traits related to Anthocyanin Colouration in the Internode (ACI) (16.41%), Node (ACN) (13.11%) and Tip (ACT) (11.51%), traits related to leaf morphology (LBL and DOL) (16.27 and 12.75%, respectively) and Growth Habit (GH) (10.74%) (Table 5). On the other hand, despite some overlap with the variety Martina, the variety Janja seems to differ from the varieties Lučka and Martina on the negative side of the first MFA dimension, which in turn tend to differ from each other on the positive side of the first MFA dimension (Figure 4). The major contributors in the differentiation among varieties were the tuber-related traits including WMT (12.5%), NMTP (11.45%), TL (11.99%), and TD (10.48%) (Table 5).

Agro-morphological quality, agricultural management, and productivity of sweet potato plants are important factors directly related to increasing the supply potential of the crop. Thus, the use of selected high-quality plants and good agricultural practices could improve the physical and morphological characteristics of sweet potato plants (Leite *et al.*, 2022). Koussao *et al.* (2014) reported that the greatest differentiation is between the predominant tuber flesh colour and the number of leaf lobes. Flower shape is very important for breeding, as are other visible traits such as plant type, mature leaf colour, immature leaf colour, general outline of leaves, and predominant shoot colour.

Genetic Background

The SSR markers used in the molecular analysis yielded 34 alleles, with N_e ranging from 2 in Ib255 to 6 in Ib297, with an average of 4.25 alleles per locus (Table 6). The highest level of genetic diversity ($H_e > 0.75$) was found for loci Ib318, Ib248, and Ib297, which were also identified as the most Polymorphic loci ($PIC > 0.7$), while the average PIC value was = 0.60. Deviations from Hardy-Weinberg equilibrium were statistically significant for loci Ib255F1, Ib255, and Ib318. The highest allelic richness was for loci Ib248 and Ib297 ($A_r \geq 1.77$) (Table 6). Diversity parameters among varieties showed that variety Martina had the highest number of alleles (3.250), while the number of locally common alleles with a frequency higher than 5% found in 50% or fewer varieties was calculated for variety Janja. Genetically, the most uniform variety was Purple Speklet, in which the U_{He} was the lowest (0.488) when comparing four varieties (Table 7). The UPGMA clustering showed that varieties Janja and Martina are

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305 genetically closer to each other; both are associated with the variety Lučka to Purple Speplet,
306 which is not strongly associated with them, as shown in Figure 5.

307 As for the genetic background, two genetic clusters (Martina/Janja and Lučka/Purple Speplet)
308 were identified based on the distribution of 16 genotypes within four varieties. The stable
309 genetic structure and uniformity of the already established varieties are reflected in the diversity
310 parameters between loci and among varieties (Tables 6 and 7). The SSR markers were
311 moderately informative as indicated by the PIC value (0.60). Similar results were obtained by
312 Pipan *et al.* (2017a) with the same markers (PIC= 0.69).

313

314 CONCLUSIONS

315 Sweet potato is a tropical crop, but it can be successfully grown on organic fields in Central
316 Europe using the soil ridge cultivation method. This study is the first in Slovenia to use general
317 morphological traits and genetic evaluation of promising sweet potato varieties of different
318 origins as a basis for discovering relationships between and within genotypes. Clustering
319 analysis showed that varieties Janja and Martina are genetically closer to each other. **The**
320 **varieties Lučka and Martina proved to be significantly higher yielding compared to the**
321 **other two varieties.** From a practical point of view, the results are important for the
322 development and improvement of agro-morphological traits, which are becoming increasingly
323 important for breeding.

324

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Table 1. Agro-morphological characteristics considered in the study.

Type of trait	Organ	Abb	Descriptor	Scores
	Whole plant architecture	GH	Growth habit	2 Upright; 3 Semi-upright; 5 Spreading
		GC	Ground cover	3 Low (< 50%); 5 Medium (50-74%); 7 High (75-90%); 9 Total (> 90%)
	Stem	ACI	Anthocyanin coloration of internode	1 Absent or weak; 2 Medium; 3 Strong
		ACT	Anthocyanin coloration of tip	1 Absent or weak; 2 Medium; 3 Strong
		ACN	Anthocyanin coloration of node	1 Absent or weak; 2 Medium; 3 Strong
		PT	Pubescence of tip	1 Absent or sparse; 2 Medium; 3 Dense
Qualitative	Leaf	LBL	Leaf blade lobes	1 Absent; 2 Three lobes; 3 Five lobes; 4 Seven lobes
		DOL	Only varieties with leaf blade lobes present: Leaf blade: depth of lobing	1 Very shallow; 3 Shallow; 5 Moderate; 7 Deep; 9 Very deep
		EACAV	Leaf blade: extent of anthocyanin coloration on abaxial veins	1 Absent or very small; 3 Small; 5 Medium; 7 Large; 9 Very large
		IACAV	Leaf blade: intensity of anthocyanin coloration on abaxial veins	1 Very weak; 3 Weak; 5 Medium; 7 Strong; 9 Very strong
		PAC	Petiole anthocyanin coloration	1 Absent or very weak; 3 Weak; 5 Medium; 7 Strong
Quantitative	Whole plant architecture	PSN	Primary shoot number	
		NI	Number of internodes	
		LPS	Length of primary shoots (cm)	
		LI	Length of internode (cm)	
		DI	Diameter of internode (mm)	
	Leaf	NL	Number of leaves/plant	
		PL	Petiole length (cm)	
		MLS	Mature leaf size (cm)	
		HFWS	Haulm fresh weight (g/plant)	
		NTP	Number of tubers/plant	
		TWTP	Total weight of tubers /plant (g)	
Tuber	NMTP	Number of marketable tubers (≥ 150 g)/plant		
	WMT	Weight of marketable tubers (g)		
	TD	Tuber diameter (cm)		
	TL	Tuber length (cm)		

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Abb, abbreviation.

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Table 2. Shannon-Weaver diversity index and Pielou's evenness index of the 11 qualitative traits.

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Trait	H'	J
GH	1.02	0.93
GC	1.14	0.82
ACI	1.02	0.93
ACT	0.67	0.61
ACN	0.66	0.60
PT	0.81	0.74
LBL	0.56	0.81
DOL	1.08	0.78
EACAV	0.10	0.15
IACAV	0.10	0.15
PAC	0.38	0.27
Average	0.69	0.62

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H', Shannon-Weaver diversity index; J, Pielou's evenness index.

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Table 3. ANOVA showing the effects of variety, block, variety×block and residuals on variation in the 15 quantitative traits.

Trait	Variety		Block		Variety×Block		Residuals Explained variance (%)
	Explained variance (%)	P	Explained variance (%)	P	Explained variance (%)	P	
PSN	17.09	0.375	46.55	0.094	19.94	0.305	16.42
NI	53.61	5.26E-05	0.00	0.989	39.55	7.88E-04	6.84
LPS	0.83	0.593	66.03	0.000	31.83	9.54E-14	1.31
LI	80.42	4.32E-12	10.30	0.102	5.46	0.236	3.82
DI	15.32	0.350	13.57	0.325	57.18	0.007	13.94
NL	89.43	<2E-16	3.16	0.275	4.78	0.145	2.64
PL	90.39	7.40E-08	0.33	0.827	2.31	0.803	6.97
MLS	94.26	<2E-16	0.85	0.527	2.76	0.275	2.13
HFW	77.15	2.53E-07	1.11	0.678	15.30	0.071	6.44
NTP	41.34	0.006	4.68	0.486	44.38	0.004	9.60
TWTP	79.35	<2E-16	17.09	0.000	2.74	0.020	0.82
NMTP	82.77	<2E-16	11.11	0.005	4.70	0.020	1.42
WMT	79.33	<2E-16	12.45	0.001	7.02	0.001	1.20
TD	88.40	<2E-16	1.16	0.394	8.85	0.001	1.59
TL	91.05	<2E-16	4.79	0.050	2.92	0.072	1.24

Table 4. Estimates of phenotypic and genotypic coefficients of variation for 15 quantitative traits.

Trait	PCV	GCV	H ²	GAM
PSN	17.52	2.79	2.54	0.92
NI	54.57	40.74	55.75	62.67
LPS	32.04	20.04	39.11	25.81
LI	17.48	8.43	23.26	8.38
DI	27.46	11.20	16.63	9.41
NL	33.53	20.01	35.63	24.61
PL	21.46	9.24	18.53	8.19
MLS	16.49	10.86	43.40	14.74
HFW	41.49	17.60	17.99	15.38
NTP	47.08	22.43	22.71	22.02
TWTP	41.55	31.95	59.15	50.62
NMTP	91.47	63.85	48.72	91.80
WMT	93.87	68.35	53.01	102.51
TD	79.63	53.03	44.35	72.76
TL	76.70	55.73	52.80	83.43

PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; H², broad sense heritability; GAM, genetic advance as a percentage of the mean.

Table 5. Contribution of the 26 morpho-agronomic traits to the first two dimensions of MFA.

Trait	Dim.1	Dim.2	Dim.1-Dim.2
Explained variance (%)	16.30	14.60	30.90
	10.74	1.95	12.69
	3.46	4.77	8.23
	7.25	16.41	23.67
	1.08	11.51	12.59
	0.80	13.11	13.91
Qualitative traits	3.15	4.27	7.42
	0.11	16.27	16.39
	7.96	12.75	20.71
	0.81	0.29	1.10
	0.81	0.29	1.10
	0.35	0.38	0.73
	0.22	0.02	0.24
	1.62	0.07	1.70
	0.04	0.00	0.04
	1.51	2.84	4.36
	0.13	0.02	0.15
	3.99	0.31	4.30
	0.00	4.81	4.81
Quantitative traits	0.07	8.32	8.39
	0.08	0.38	0.46
	0.46	0.08	0.55
	9.27	0.10	9.37
	11.45	0.29	11.74
	12.15	0.50	12.65
	10.48	0.10	10.59
	11.99	0.14	12.12

The traits with the highest contribution to differentiation between varieties are in bold.

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Table 6. Parameters of genetic variability among loci.

Locus	Range	N	He	PIC	HWE	Ar
Ib242	126-146	4	0.71	0.63	ns	1.71
Ib248	126-190	5	0.79	0.73	ns	1.80
Ib255F1	231-255	5	0.58	0.51	*	1.52
Ib255	172-180	2	0.42	0.32	*	1.31
Ib286	104-120	5	0.74	0.67	ns	1.71
Ib297	104-156	6	0.78	0.71	ns	1.77
Ib316	92-136	3	0.54	0.44	ns	1.53
Ib318	132-138	4	0.83	0.78	*	1.70
Total		34				
Average		4.25	0.68	0.60		1.63

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Range, range of allele lengths; N, number of alleles; He, expected heterozygosity; PIC, polymorphic information content; HWE, Hardy-Weinberg equilibrium; Ar, allelic richness.

Table 7. Diversity parameters between four studied sweet potato varieties.

	Janja	Martina	Lučka	Purple Speclet
No of different alleles	3.000	3.250	2.250	2.250
No of locally common alleles (freq. $\geq 5\%$) found in 50% or less varieties	1.250	1.125	0.125	0.500
Unbiased expected heterozygosity	0.638	0.701	0.656	0.488

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No.: number.



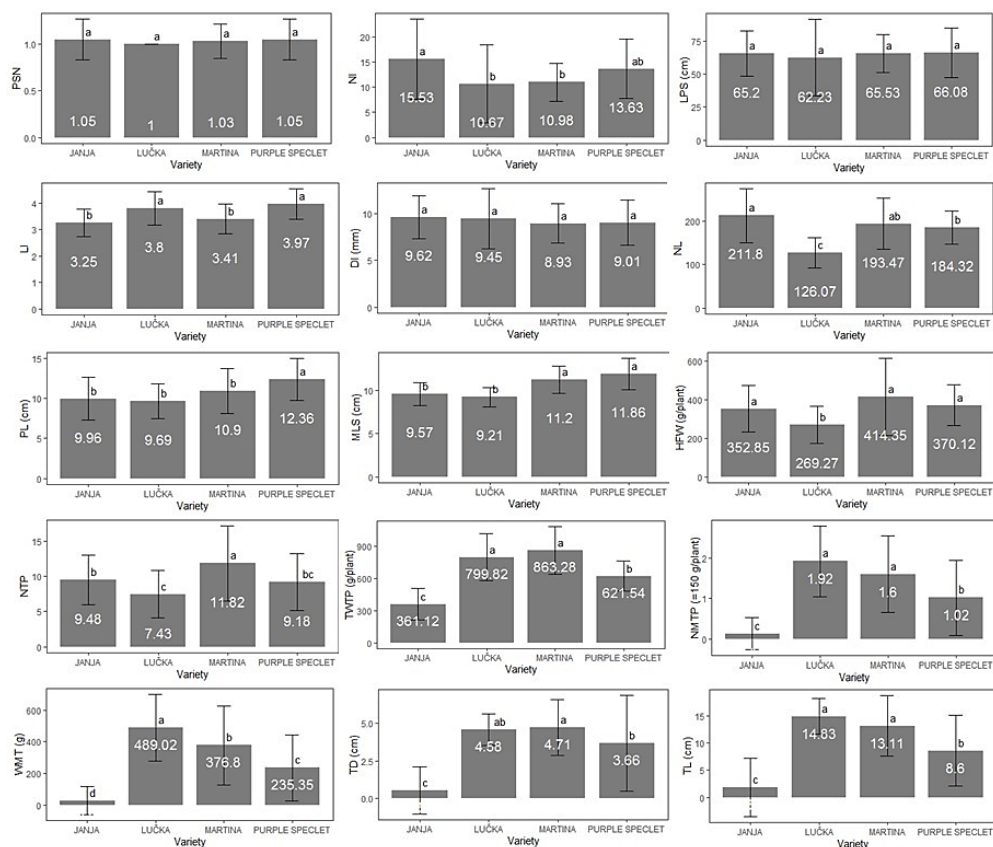
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Figure 1. Patterns of variability among the four varieties based on 11 qualitative traits.

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Figure 2. Comparison of mean values for the 15 quantitative traits. Error bars indicate one standard deviation. Different letters indicate significant pairwise differences at $P < 0.01$.

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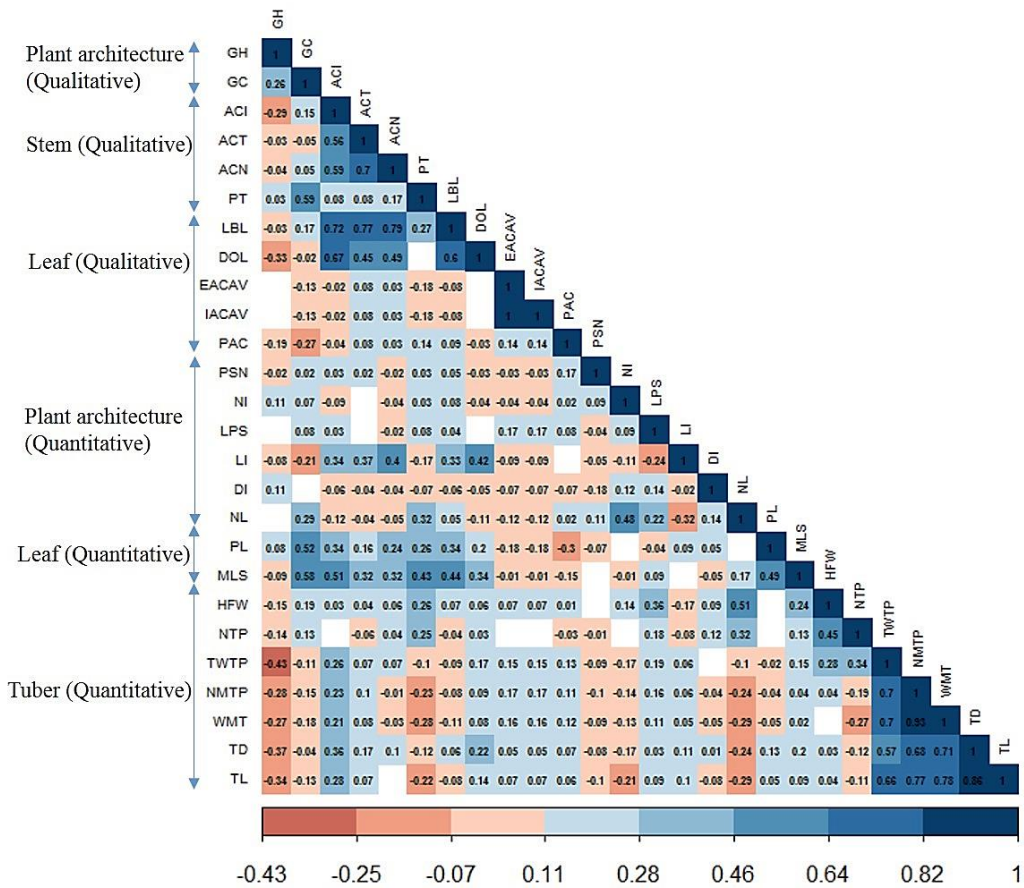


Figure 3. Pattern of correlations among the 26 agro-morphological traits using Spearman's coefficient. Only significant correlations are shown ($P < 0.05$).

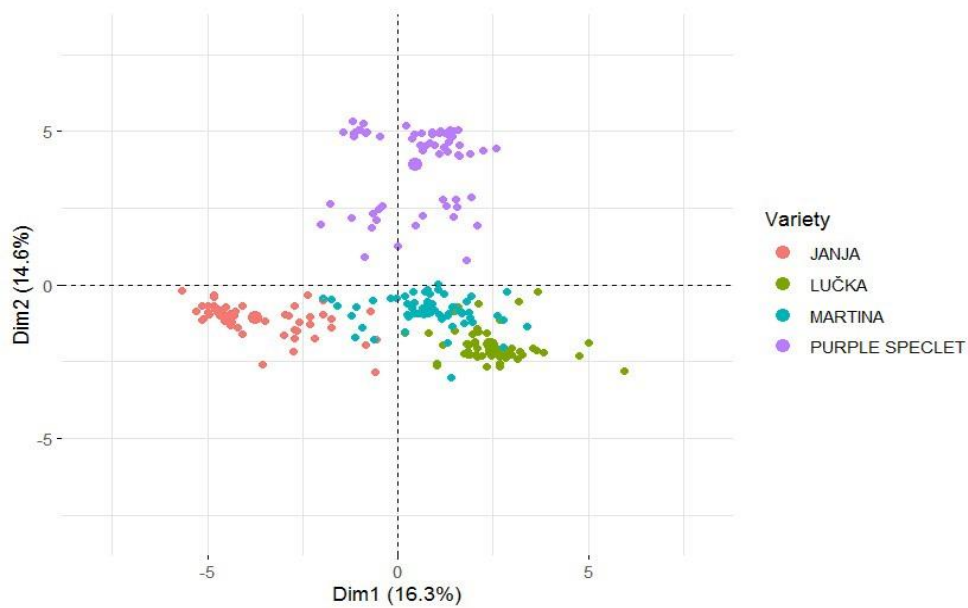


Figure 4. 2D plot of first two dimensions of MFA showing the patterns of differentiation among four sweet potato varieties based on 26 agro-morphological traits.