1	ACCEPTED ARTICLE:
2 3 4 5	Determination of markers associated with important agronomic traits of watermelon ( <i>Citrullus lanatus</i> L.)
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12 13	Abstract
14	Association analysis using phenotypic information and molecular markers may provide
15	valuable information for molecular breeding and marker-assisted selection. The objectives of
16	this study were to determine markers associated with sugar parameters and important
17	agronomic traits of watermelon and to estimate the level of genetic diversity. Ninety-six
18	watermelon lines were genotyped by combining SSR (Simple Sequence Repeat), ISSR (Inter-
19	Simple Sequence Repeat) and iPBS (Inter-Priming Binding Sites) marker data. These
20	genotypes were also assessed for population structure, linkage disequilibrium (LD), and
21	association mapping (AM) of sugar parameters and other important agronomic traits. In the
22	analysis, 583 markers had LD values to a certain degree. A general linear model using only the
23	Q matrix showing the population structure in association mapping, a complex linear model
24	using a kinship matrix, and a complex linear model using both the Q and K matrix linear models.
25	The regression model explanation rates for the 26 characters varied from 11.3% to 81.3%. The
26	highest rates of regression model explanation were measured for fruit firmness (81.3%) and
27	fruit height (78.2%). It might be e possible to determine the genes associated with these studied
28	characteristics, to contribute to future genetic and breeding studies, and to be used in marker-
29	assisted selection (MAS) studies.
30	Keywords: Watermelon, sugar parameters, SSR, ISSR, iPBS, association mapping.
31	

## 32 Introduction

Watermelon, a member of the Cucurbitaceae family, is an economically important vegetable.
Its production in the world was 101.634.720 tons on an area of 3.031.544 ha in 2021
(FAOSTAT, 2021). Watermelon yield and quality are the main parameters assessed in

36 combination in breeding programmes. The horticultural industry generally focuses on yield.
37 However, in recent years, consumers worldwide have become increasingly interested in the
38 quality of vegetables. Some phytochemicals in watermelon provide significant health benefits
39 (Fraser and Bramley, 2004). Sweetness is one of the most important quality parameters of
40 watermelon fruit. The total sugar content and ratios of glucose, fructose, and sucrose determine
41 the sweetness of watermelon (Brown and Summers, 1985).

42 Morphological and molecular characterization of watermelon and identification of markers 43 associated with important agronomic traits are valuable for breeding studies. In molecular plant 44 breeding, different marker systems are used for genetic characterization to create genetic maps 45 and linkage groups. Molecular markers are effective method to identify varieties and study their 46 genetic relationships (Du et al., 2019; Zhang et al., 2020; Coskun, 2022; Ebadi et al., 2022; 47 Morilipinar et al., 2022; Sudha et al., 2022; Coskun., 2023). SSR, ISSR, and iPBS markers are 48 effective methods with several advantages, including high levels of polymorphism. SSR and ISSR marker techniques have been used to identify genetic diversity in watermelons (Verma 49 50 and Arya, 2008). Using iPBS markers, the effectiveness of retrotransposon-based marker 51 techniques in watermelon can be determined, and the possibility of finding new association 52 markers can be increased. The inheritance or high correlation between agricultural traits and 53 molecular markers can be used to predict the phenotypic traits of individuals in the population. 54 This increases the efficiency of the breeding program as it allows the selection of the desired 55 individual before planting in the field.

56 Molecular characterization, linkage disequilibrium and genetic mapping are critical tools for 57 further genomic studies, as well as for genetic breeding of economically important horticultural 58 species. To create linkage maps, it is necessary to develop mapping populations by 59 crossbreeding between parents with sufficient morphological and molecular polymorphisms. 60 The association mapping approach has an advantage over that obtained using only two parents. 61 Using this technique, all alleles present in a given germplasm can be detected. Linkage 62 disequilibrium studies have been conducted in watermelons (Ocal et al., 2014; Reddy et al., 63 2014). Association mapping in watermelon is limited, and no markers associated with sugar 64 parameters have been determined. The aim of this study was to determine the genetic diversity of watermelon using different marker techniques, identify markers associated with sugar 65 parameters and other important characteristics of watermelon, and develop regression models. 66 It will be possible to determine the genes associated with these studied characteristics, to 67 68 contribute to future genetic and breeding studies and to be used in marker-assisted selection 69 (MAS) studies.

#### 71 Materials and Methods

### 72 Material used

73 In this study, 96 genotypes selected from the watermelon genetic resource collection of 74 Cukurova University, Faculty of Agriculture, Department of Horticulture were used. The 75 samples mainly included selfed (4-6 times) lines of the genotypes. A total of 96 lines consisting 76 of 94 cultivated watermelon (C. lanatus var. lanatus landrace, a wild form of C. lanatus var. 77 citroides and one Praecitrullus fistulosus line as an outgroup. Morphological and sugar 78 parameter data obtained previously (Coskun and Gulsen, 2023) were used in the association 79 mapping studies. A total of 26 parameter data were used, including two general plant-related 80 traits, three ovary-related traits, eleven fruit-related traits, four seed-related traits, five sugar 81 parameter traits, and additionally yield.

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## 83 Molecular analysis

DNA extraxtion was performed with the DNA isolation method developed by Doyle and Doyle (1990). The total volume for the PCR reaction was prepared as 15 µl: 7.15 µl distilled water, 1.5 µl 10 x DNA polymerase buffer, 2.5 mM dNTPs, 5 mM primer, 1 U Taq Polymerase, and 20 ng DNA. The prepared PCR mix was analysed using 36 iPBS and 12 ISSR primers. Agarose gel was used to display the band profiles of ISSR and IPBS marker studies. Additionally, scoring data for the SSR band profiles were obtained from previous study (Coskun and Gulsen, 2023).

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### 92 Determination of linkage disequilibrium (LD) and associating mapping (AM)

93 The LD level between a pair of loci was obtained in Tassel 5.2 program using marker data. 94 Analysis were performed after removing loci with a low number of alleles (f < 0.10). In the 95 association mapping study, 26 character-related traits were analysed in 96 watermelon 96 genotypes. General linear model (General Linear Model- GLM+(Q)) using only Q matrix 97 showing population structure in associating mapping, complex linear model using kinship 98 matrix (Mixed Linear Model+K- MLM+(K)) and complex linear model using both Q matrix 99 and K matrix linear model (Mixed Linear Model- MLM+(K+Q)) was used. The web-based 100 Structure Harvester (Earl and Vonholdt, 2012) software was used with the result file to calculate 101 the  $\Delta K$  value of the populations. The significance level between the marker and phenotypic 102 traits was determined using the Tassel 5.2 program (Bradbury et al. 2007) based on the P values 103 and the F test. The Q matrix showing the population structure used in the mapping was obtained

using the Structure program. The kinship matrix was obtained by analysing 583 polymorphic
DNA bands with the A.mat function using the 'rrBLUP'R package (Endelman 2011). The model
with the best results was determined by obtaining the QQ (quantile quantile plot) graphs.

#### 108 Statistic analysis

109 NTSYS 2.1 and Tassel 5.2 programs were used for molecular analysis. In addition, the 110 estimated allele frequency, effective allele number (Ne), Shannon's information index (I), 111 expected heterozygosity (He), and unbiased expected heterozygosity (uHe) values were 112 determined using the GenAlEx 6.5 program. The amount of polymorphic information (PIC) was determined using Microsoft Excel. For association mapping, quantile quantile plots and 113 114 Manhattan plots were obtained using Tassel 5.2. Regression analysis were performed on the 115 related markers obtained using three different statistical methods. For this purpose, backward 116 and forward regression models were used in the SPSS 22.

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#### 118 **Results and discussion**

119 Analysis of molecular characterization were performed with a total of 110 primers, 36 iPBS, 120 12 ISSR and 62 SSR in 96 genotypes. The total number of bands obtained was 1397 and the 121 number of bands per primer was 12.7. A total of 1364 of the 1397 bands obtained were 122 polymorphic, the polymorphism rate was determined to be 97.6% and the band sizes vary is 123 between 45-2100 bp. By combining the iPBS, ISSR and SSR primers into 96 genotypes, 124 similarity coefficients based on the DICE index were determined using the NTSYS package 125 program. The similarity coefficients ranged from 0.25-0.99. The most distant genotypes were 126 147 and 331, with a similarity coefficient of 0.25. The genotype of the 331 P. fistulosus species 127 was closest to the 86, 36 and 62 genotypes, with a similarity ratio of 0.32. There were 87 128 genotypes in the first main group and 4 (53, 114, 203 and 151) genotypes in the second main 129 group. The similarity coefficient for the genotypes in the first main group was 0.8 and above. 130 The genotypes closest to each other in the UPGMA dendrogram were 45 and 48 genotypes, 131 respectively (Figure 1).

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Figure 1. UPGMA dendrogram constructed with iPBS+ISSR+SSR primers using the DICE
 similarity index in ninety-six watermelon genotypes.

In the principal component analysis obtained using 96 genotypes, the cumulative sum of the first three eigenvalues for the two- and three-dimensional graphs was determined as 89.1. In the three-dimensional PCA graph, the 85 genotypes took place together and formed the first cluster. Genotypes 331, 234, 342, 303, 354, 229, 96, 350, 34, 62 and 36 were located separately and independently of the others. Genotypes 331 and 234 were located the farthest away (Figure 2).

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Figure 2. Three-dimensional graph obtained as a result of principal component analysis with 146 iPBS+ISSR+SSR primers in 96 watermelon genotypes. 147

148 Considering the K values obtained with iPBS+ISSR+SSR data using the Structure Harvester

149 program, it was determined that the 96 watermelon genotypes consisted of two subpopulations.

150 There were 8 pure individuals in the first subpopulation and 73 pure individuals in the second

151 population. Fifteen genotypes had mixed genetic structures. Genotypes included in the first

152 population were ETAE origin 53, Divarbakir origin 96, Mardin origin 114, Usak origin 203,

153 USA origin 234 and C. lanatus var. citroides, Hatay origin 229, India origin 331, P. fistulosus,

154 and Antalya origin 342 (Figure 3).





The number of bands obtained per primer (12.7) was higher than Alsohim and Motawei (2014), 161 162 Elias (2016), Soghani et al. (2018). In this study, the polymorphism rate (97.6%) obtained from 163 the 96 genotypes was lower than that detected by Elias (2016) and Dje et al. (2010). This was 164 found to be higher than those of Alsohim and Motawei (2014) and Soghani et al. (2018). 165 Although similarity coefficient values (0.29-0.99) obtained in 96 genotypes in this study 166 showed a wider variation than the values determined by Dje et al. (2010), similarity coefficients 167 were higher. The biggest reason for the current differences is the number and diversity of genetic resources examined. Retrotransposon-based marker systems have been successfully 168 169 used in genetic diversity studies of some plants (Mardi et al., 2011; Nasri et al., 2013). This 170 marker technique has been studied in some cucurbit species (Khoei et al., 2014; Khoei et al., 171 2015) but not in watermelon. In this study, the genetic characterization efficiencies of iPBS 172 primers for watermelon genotypes were determined. In this study, 96% of the polymorphisms 173 were obtained. The obtained polymorphism rate and similarity coefficient values show that this 174 primer technique is suitable for genetic characterization of watermelon genotypes. In this study, 175 the average effective allele numbers in iPBS analysis were found to be 1.706 and Shannon's 176 knowledge index was 0.602.

177 The expected value (He) averages obtained in this study were 0.412, 0.416 and 0.415 for iPBS, 178 ISSR and SSR primers, respectively. The expected values of the three marker primers were 179 higher than those reported in other studies on watermelon (Mujaju et al., 2013; Mujaju and 180 Nybom, 2011) and others (Mashilo et al., 2016; Mashilo et al., 2017). Mujaju et al. (2011) and 181 Singh et al. (2017) obtained expected values similar to those obtained in this study. The 182 polymorphic information amount (PIC) averages obtained in this study were 0.679, 0.498 and 183 0.638 for iPBS, ISSR and SSR primers, respectively. The PIC values determined by Mujaju et 184 al. (2013) and Kwon et al. (2010), working with SSR primers, were found to be lower than the 185 values obtained from iPBS and SSR primers and higher than the values obtained from ISSR 186 primers. The data obtained in this study were high (Elias, 2016; Singh et al., 2017). Only 10 of 187 the 110 primers had PIC value <0.5. Differences in PIC values may be partly due to 188 polymorphism of the primers used and partly due to genetic differences between the studied 189 materials.

In the analysis conducted using the Tassel 5.2 program, it was determined that 583 markers had LD values at certain degrees. Out of a total of 103927 marker pairs, 28795 showed LD at the 0.05 level (27.7%), 17782 at the 0.01 level (17.1%), and 7915 at the 0.001 level (7.6%). The mean LD value (D') among the loci showing a statistically significant LD was 0.54. LD is usually evaluated using  $r^2$ , which summarizes both recombination and mutation histories (Flint195 Garcia et al., 2003). The mean  $r^2$  value (square of the correlation coefficient between the two

loci) for all marker pairs was 0.105. Approximately 16.2% of the  $r^2$  values were above 0.2, whereas 28.7% were above 0.1. The LD blocks obtained for the 583 markers are shown in

198 Figure 4 as "heat map".

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Figure 4. LD measurements (values above the diagonal,  $r^2$ ) and probability values (values below the diagonal, P) for the iPBS, ISSR and SSR markers.

In the association mapping study, 26 important characteristics, including morphological and sugar parameters, were used for 96 watermelon genotypes. To eliminate false-positive results, the results were compared according to the models using a model containing three different statistical approaches. The Kinship matrix was obtained by analysing 583 polymorphic DNA bands with the A. mat function using the "rrBLUP" R package (Endelman 2011). Considering the Q-Q plot graphs for associating mapping in five characters, it was determined that MLM (K) and MLM (K+Q) analysis were appropriate for all characters.

211 In the model obtained with ovarian height values, nine significant independent variables at p<0.05 level (iPBS-2277.1400, iPBS-2277.1500, iPBS-2217.1600, iPBS-2228.350. iPBS-212 213 2244.920, iPBS-2249.220, ISSR-DBDACA7.440, SSR-CGB4767.175 and SSR-214 CMTp46.360). The rate of explanation of the ovarian height of the model based on these 215 markers was 63.4%. The model obtained using ovarian diameter values included six 216 independent variables (ISSR-DBDACA7.540, iPBS-2239.1130, iPBS-2393.660, SSR-CI.1-217 120.185, SSR-CGB4767.175 and iPBS-2074.530). The rate of explanation of the ovarian 218 diameter of the model based on these markers was 46.3%. In the model obtained with ovarian 219 hairiness values, there were four independent variables at p < 0.05 level (iPBS-2217.450, iPBS-220 2239.950, iPBS-2249.420 and ISSR-GACA4.720). The rate of explanation of the hairiness 221 value in the ovary of the model based on these markers was 37.4%. In the model obtained from 222 the hermaphrodite flower status data, there were 2 independent variables at the p < 0.05 level 223 (SSR-CSTA050.560 and SSR-CMTp125.600). The hermaphrodite flower state of the model 224 based on this marker was explained 47%. In the model obtained with the main stem number 225 data, there were two independent variables at p < 0.05 level (SSR-CMTp182.120 and iPBS-226 2381.1280). The rate of explaining the number of main bodies of the model depending on this 227 brand was 27.2%.

228 In the model obtained with fruit weight values, there were three independent variables (p < 0.05) 229 (iPBS-2389.350, SSR-CMTm207.350, and SSR-CMTmC67.500). The rate of explaining fruit 230 weight variation in the model based on these markers was 47.8%. In the model obtained with 231 fruit diameter values, there were four independent variables at p < 0.05 level (iPBS-2074.290, 232 iPBS-2384.750, iPBS-2393.820 and SSR-CMTmC67.500). The rate of explanation of the fruit 233 diameter of the model based on these markers was 52.4%. In the model obtained with fruit 234 height values, there were four independent variables at p < 0.05 level (iPBS-2384.500, SSR-235 ASUW2.170, iPBS-2077.460 and iPBS-2400.1350). The rate of explanation of the fruit height 236 of the model based on these markers was 78.2%. In the model obtained with fruit peel thickness 237 values, there were four independent variables at p < 0.05 level (SSR-CGB4767.170, iPBS-238 2228.500, ISSR-DBDACA7.490 and iPBS-2383.720). The rate of explanation of the fruit peel 239 thickness of the model based on these markers was 29.8%. In the model obtained with fruit 240 firmness values, there were four independent variables at p < 0.05 level (iPBS-2074.290, iPBS-241 2217.1450, SSR-CMTp182.120 and SSR-CMTm207.350). The rate of explaining the fruit 242 firmness of the model based on these markers was 81.3%. In the model obtained with TSS values, there were three independent variables at p < 0.05 level (ISSR-AG8T.500, SSR-243 244 CGB5009.200 and SSR-CMTp182.160). The rate of explanation of the TSS value of the model 245 based on these markers was 23.9% (Table 1).

In the model obtained with fruit color L\* values, there were three independent variables at 246 247 *p*<0.05, that is (iPBS-2074.290, SSR-CMTiPBS-2077.4609.500, ISSR-CAC6.220). The rate of explanation of the fruit color L\* value of the model based on these markers was 45.7%. The 248 249 model obtained with fruit color a\* values included six independent variables at p < 0.05 level 250 (ISSR-CT8TG.860, iPBS-2375.750, ISSR-CAC6.220, ISSR-HVHCA7T.480, SSR-251 CMTp182.160 and SSR-CMTC160.600). The rate of explanation of the fruit color a\* value of 252 the model based on these markers was 38.8%. In the model obtained with fruit color b\* values, 253 there were five independent variables at p < 0.05 level (ISSR-AG8T.560, iPBS-2391.1150, 254 iPBS-2400.405, iPBS-2226.250 and ISSR-TAA8.1450). The rate of explaining the fruit color 255 b\* value of the model based on these markers was 32.5%. In the model obtained with fruit 256 number values, there were five independent variables at p < 0.05 level (iPBS-2217.1450, iPBS-257 2217.1600, ISSR-CAC6.220, SSR-CMTiPBS-2077.4609.500 and SSR-CMTm207.350). The 258 rate of explanation of the number of fruits in the model based on these markers was 59.9%. The 259 model obtained with the yield values included two independent variables (p < 0.05) (iPBS-2077.490 and iPBS-2383.1250). The rate of explanation of the efficiency values of the model 260 261 based on these markers was 68.6% (Table 1).

- In the model obtained with seed number values, there were two independent variables at p < 0.05262 263 level (SSR-CMTm144.550 and SSR-CMTp158.1050). The rate of explanation of the number 264 of seeds in the model based on these markers was 11.3%. In the model obtained with seed width 265 values, there were two independent varies at (p < 0.05) (iPBS-2217.450 and SSR-CGB4767.170). The seed-width disclosure rate of the model based on these markers was 266 267 29.2%. In the model obtained with seed height values, there were two independent variables at p < 0.05 level (SSR-CSJCT 191.240 and SSR-CMTm207.350). The seed size explanation rate 268 269 of the model based on these markers was 34.1%. In the model obtained with seed thickness 270 values, there were four independent variables at p < 0.05 level (ISSR-GACA4.350, iPBS-271 2074.53043, SSR-CMTp182.160 and ISSR-CAC6.1250). The rate of explanation of the seed 272 thickness of the model based on these markers was 37.4%. In the model obtained with seed 273 weight values, there were 4 independent variables at p < 0.05 level (ISSR-GACA4.350, SSR-CGB4767.170, SSR-CSJCT 191.230 and ISSR-TAA8.920). The rate of explanation of the seed 274 275 weight of the model based on these markers was 49.2% (Table 1).
- 276 According to the fructose character and MLM (K+Q) model, there were 2 independent variables 277 at the p < 0.05 level (ISSR-AG8T.1140 and iPBS-2387.480). The rate of explanation for the 278 fructose value of the model based on these markers was 41.5%. In the model obtained according 279 to the MLM (K+Q) model with the glucose character, there were five independent variables at 280 *p*<0.05 level (iPBS-2226.1600, iPBS-2077.740, iPBS-2376.470, iPBS-2376.1060 and SSR-281 CMTp174.850). The rate of explanation of the glucose value of the model based on these 282 markers was 61.1%. In the model obtained according to the MLM (K+Q) model with the 283 sucrose character, there were five independent varies at (p < 0.05) (SSR-CSJCT 191.230, iPBS-284 2076.900, ISSR-HVHTCC7.500, ISSR-DBDACA7.600 and iPBS-2239.950). The rate of 285 explanation of the sucrose value of the model based on these markers was 47.2%. In the model 286 obtained according to the MLM (K+Q) model with total sugar character, there were 2

- independent variables at the p < 0.05 level (SSR-CMTm252.1150 and iPBS-2387.480). The rate of explaining the total sugar value of the model based on this marker was 41.9%. In the model obtained according to the MLM (K+Q) model with fructose/glucose character, there were four independent variables at p < 0.05, that is (ISSR-GACA4.720, iPBS-2077.740, ISSR-DBDACA7.780 and ISSR-DBDACA7.1080). The rate of explaining The fructose/glucose ratio
- of the model based on this marker was 46.1% (Table 1).
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294	Table 1. Marker	counts and a	innotation rates	associated with	th important	agronomic traits.
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Character	Method	Number of	Number of Markers	Model
		Associated	Remaining in the Model	Description
		Markers	-	Ratio
Ovary height	GLM (Q)	29	9	% 63.4
Ovary diameter	GLM (Q)	19	6	% 46.3
Fruit weight	MLM (K+Q)	22	3	% 47.8
Fruit width	MLM (K+Q)	8	4	% 52.4
Fruit size	MLM (K+Q)	46	4	% 78.2
Fruit skin thickness	MLM (K+Q)	19	4	% 29.8
Fruit firmness	MLM (K+Q)	64	4	% 81.3
TSS	GLM (Q)	32	3	% 23.9
Fruit color L*	MLM (K+Q)	18	3	% 45.7
Fruit color a*	MLM (K+Q)	13	6	% 38.8
Fruit color b*	MLM (K+Q)	10	5	% 32.5
Number of fruits	MLM (K+Q)	13	5	% 59.9
Yield	MLM (K)	69	2	% 68.6
Number of seeds	MLM (K+Q)	16	2	% 11.3
Seed width	MLM (K+Q)	36	2	% 29.2
Seed size	MLM (K+Q)	20	2	% 34.1
Seed thickness	MLM (K+Q)	16	4	% 37.4
Seed weight	MLM (K+Q)	13	4	% 49.2
Ovarian hairiness	GLM (Q)	16	4	% 37.4
Hermaphrodite flower status	MLM (K+Q)	67	2	% 47
Number of main body	MLM (K+Q)	18	2	% 27.2
Fructose	MLM (K+Q)	66	2	% 41.5
Glucose	MLM (K+Q)	78	5	% 61.1
Sucrose	MLM (K+Q)	31	5	% 47.2
Total sugar	MLM (K+Q)	92	2	% 41.9
Fructose/glucose	MLM (K+Q)	36	4	% 46.1

296 AbdoliNasab and Rahimi (2020) determined the number of markers associated with important 297 traits in watermelon to be 13 for 2015 data and 12 for 2016 data. A higher number of associated 298 markers were determined in this study. The number of markers related to fruit weight, fruit diameter, fruit height, fruit skin thickness, fruit firmness and fruit number and the regression 299 300 model explanation rate were found to be higher than those determined by Yagcioglu's (2016) 301 GLM method. The model with two markers associated with the number of seeds explained the 302 number of seeds by 11.3%, and the model with two markers associated with seed width 303 explained the seed width at a rate of 29.2%. In some other studies, linkage mapping studies 304 were conducted on seed characteristics (Prothro et al., 2012). The model with two markers

- related to seed size explained 34.1% of the seed size. The significance level of the markers associated with seed and fruit characteristics in this study was higher than that determined by AbdoliNasab and Rahimi (2020). In this study, the number of related markers determined by the MLM (K) method was lower than that determined by the GLM method by Yagcioglu (2016). The reason for determining a larger number of markers and having a higher significance value in this study in relation to some morphological features may be the differences in the number and types of analysed markers and genotypes.
- Association mapping has not been previously performed with sugar parameters in watermelons. However, three studies have done link mapping. Ren et al. (2014) nine and Cheng et al. (2016) identified four QTLs for sugar parameters. In our study, 18 markers remained in the model for all sugar parameters. The relationship rates varied from 41.5% to 62.8%. The detection of sugar parameters, one of the most important criteria in terms of quality, and markers related to this level will be important in terms of shortening the breeding period. The use of DNA markers associated with important agronomic traits can increase the efficiency and accuracy of classical
- 319 plant breeding through marker-assisted selection (MAS).
- 320 The regression model explanation rates for the 26 characters varied from 11.3% to 81.3%. This 321 could be due to the choice of markers. The highest rates of regression model explanation were 322 measured for fruit firmness (81.3%) and fruit height (78.2%). The lowest regression disclosure 323 rates were determined for the number of seeds (11.3%) and main stems (27.2%) of the SSC 324 (23.9%). In previous studies, some genetic mapping studies related to fruit characteristics in 325 watermelon have been carried out. Genetic mapping studies are generally conducted in the form 326 of linkage mapping. Therefore, fewer characteristics were examined than those determined in 327 the present study. In this study, markers associated with 26 characteristics were identified. Chi 328 et al. (2017) six, Sandlin et al. (2012) six, Li et al. (2018) three, Cheng et al. (2016) seven, Ren 329 et al. (2014) twelve characters The QTL has been determined. Compared to other watermelon 330 linkage maps in this study, other researchers identified fewer associated markers because other 331 studies used populations with different genetic diversity. Populations obtained by crossover 332 have a much more limited genetic diversity than natural populations. This reduces the number 333 of associated markers identified.
- These findings suggest that there is narrow genetic variation among watermelon genotypes. Within the scope of this study, DNA markers associated with important characteristics were determined by association mapping analysis using different marker techniques in watermelon. The results obtained in this study showed the importance of association mapping in terms of determining marker-trait relationships in watermelon breeding. This study combined different

- mapping models and provided information on the suitability of watermelon genotypes for association mapping analysis. It is possible to determine the effect of genetic variation on the results of the associating mapping study with the data obtained from the study to determine the genes associated with these studied characters, to contribute to future genetic and breeding studies, and to be used in marker-assisted selection (MAS) studies.
- 344

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- 347

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