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Research

Comparison of the Sweet Taste Receptor (TAS1R2) Polymorphism and Nutrient Intakes in Adults

Yetişkinlerde Tatlı Tat Reseptör (TAS1R2) Polimorfizmi ile Besin Ögesi Alımlarının Karşılaştırılması

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ABSTRACT

Objective: It is known that genetic variations in the mechanism of taste perception play an essential role in food intake. In this study, we investigated the SNP rs35874116 polymorphism in the sweet taste receptor (TAS1R2) gene and nutrient intakes of adults.

Methods: The study conducted with 95 volunteers. Food consumption records of participants obtained by 24-h recall method, and analyzed by Computer-Aided Nutrition Software, Nutrition Information Systems 8.1 Package Software (BeBiS). Venous blood samples of the participants were collected to determine genotype distribution, and genotype distributions were determined using the Kompetitive Allele-Specific PCR (KASP) method.

Results: The genotype examination of participants revealed that the percentage of individuals with GA, AA, and GG genotypes were 67.3%, 26.3%, and 6.3% respectively. Daily total carbohydrate and sucrose intakes were found as the highest in individuals with GG genotype (145.55±56.69 g and 28.66±26 g, respectively), but without statistical difference.

Conclusion: According to our knowledge the study is the first to examine TAS1R2 polymorphism and nutrient intake in the Turkish population. We did not find any difference between TAS1R2 (rs35874116) polymorphism and nutrient intake; however, the study may serve as a preliminary result. Studies with a wider sample may help to enhance our understanding of the TAS1R2 and nutrient intake.

Keywords: TAS1R2, nutrient intake, carbohydrate, polymorphism

ÖZ

Amaç: Tat algısı mekanizmasındaki genetik varyasyonların besin alımında önemli rol oynadığı bilinmektedir. Bu çalışmada tatlı tat reseptörü (TAS1R2) SNP rs35874116 polimorfizmi ve yetişkin bireylerin besin ögesi alımı incelenmiştir.

Gereç ve Yöntem: Mevcut çalışma 95 gönüllü birey ile yürütülmüştür. Katılımcılardan 24 saatlik geri çağırma tekniği ile besin tüketim kayıtları toplanmış ve ilgili veriler bilgisayar destekli beslenme programı, Beslenme Bilgi Sistemi (BeBiS), 8.1 Paket programında analiz edilmiştir. Genotip dağılımı Kompetitif Allel-Spesifik PCR yöntemi ile belirlenmiş olup, bunun için araştırmaya katılan bireylerden venöz kan örnekleri toplanmıştır.

Bulgular: Katılımcılar genotiplerine göre incelendiğinde GA, AA ve GG genotiplerine sahip bireylerin yüzdesi sırasıyla %67,3, %26,3 ve %6,3'tür. Günlük toplam karbonhidrat ve sükroz alımları GG genotipli bireylerde daha yüksek (sırasıyla 145,55±56,69 g ve 28,66±26 g) bulunmuştur, ancak sonuçlar istatistiksel olarak anlamlı farklılık göstermemiştir.

Sonuç: Bilgimiz dahilinde mevcut çalışma, Türk popülasyonunda TAS1R2 polimorfizmi ve makro besin alımını inceleyen ilk çalışmadır. TAS1R2 (rs35874116) polimorfizm ve makro besin alımı arasında herhangi bir fark bulunamamış olmakla birlikte mevcut sonuçlar bir ön sonuçtur olarak literatüre katkıda bulunabilir. Daha geniş örneklemli çalışmalar, TAS1R2 ve gıda alımı konusundaki rolünün anlaşılmasında yardımcı olabilir.

Anahtar Kelimeler: TAS1R2, besin ögesi alımı, karbonhidrat, polimorfizm

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INTRODUCTION

Taste is considered the primary determinant of food preference and intake. Given that taste can affect nutritional preferences, understanding the factors that mediate differences in taste function and their effect on food preference and consumption is important (1). Many factors affect individuals' food choices, including physiological, nutritious, environmental, socio-cultural, and genetic factors (2). The number of studies on taste genetics and biology is increasing day by day as the genetic factors underlying individual differences in the ability to perceive tastes, which can affect eating behavior and food intake (3).

Taste perception in the taste sensory system occurs through specialized taste receptor cells (TRCs) found in the taste buds of the tongue (4). TRCs are indirectly or directly stimulated, detecting different tastes. G protein-coupled receptors (GPCRs) trigger indirect stimulation, whereas ion channels trigger direct stimulation (5). GPCRs mediate the perception of sweet, bitter, and umami taste, whereas the specific membrane channels mediate sour and salty taste (6). The GPCR protein family consists of 3 different taste receptor type 1 (T1R) and approximately 30 different taste receptor type 2 (T2R) members. Sweet taste ligands are bound to heterodimeric T1R2/T1R3 receptor, umami tastes ligands with heterodimeric T1R1/T1R3 receptor, and bitter taste ligands with T2R receptors to detect different flavors (7-9).

The T1R protein family that detects sweet and umami flavors are encoded by the *TAS1R1*, *TAS1R2*, and *TAS1R3* genes (10). T1R2, a sweet taste receptor protein, is synthesized from the *TAS1R2* gene discovered in 1999 (11,12). The *TAS1R2* gene is located on chromosome 1p36.13 and consists of six exons and produces a protein with 839 amino acids (2,13). Genetic diversity of sweet taste receptor genes has been shown to have a role in sweet taste sensitivity in adults (9,14,15).

Studies reported that the single nucleotide polymorphisms (SNP) of these chemosensory genes of the taste-sensing mechanism may be associated with food preferences and consumption (9,16). TAS1R2 is a highly polymorphic gene, and this high polymorphic ratio is assumed to be associated with variations in sweet taste perception. One of the *TAS1R2* gene SNPs occurs by nucleotide replacement of Adenine/Guanine (A571G, rs35874116) in the base 571 of the exon 3. This change alters the triplet codon sequence, causing the isoleucine/valine amino acid conversion in position 191 (3,17). A study investigated the relationship of the Ile191Val variations with carbohydrate intake and revealed that individuals with Val/Val genotype were associated with high carbohydrate intake (17). Another study investigated the relationship between sugar consumption of individuals with and without diabetes and variations of Ile191Val and reported that this variation may affect sugar consumption habits (9). Another study revealed that children with TT genotype in the TAS1R2 rs35874116 locus (Ile191Val) mostly preferred sweet foods and consumed desserts mostly in the evening (18). Additionally, according to another study, variation in TAS1R2 affects food consumption including cruciferous vegetables and foods with an umami taste (19).

The genetic background of food consumption has been widely evaluated, but individual food choices could be affected by genetic variations. Thus, we investigated the effect of SNP rs35874116 polymorphism in the sweet taste receptor (*TAS1R2*) gene on the nutrient intake to contribute to the enlightenment of factors involved in food preference and consumption.

METHODS

Study Group

This study included 95 volunteers between 21 and 60 years old. Our study was approved by Istanbul Aydın Universiry Non-Interventional Clinical Research Ethics Committee on 09/10/2019 with the decision number 2019/115. Volunteers were included in the research by obtaining written and oral consent.

Food Consumption Record/Nutrient Intake Analysis

The daily energy and food intakes of individuals were evaluated by a 24-hour recall food consumption record. The food consumption records of participants were analyzed using the "Computer-Aided Nutrition Software, Nutrition Information Systems 8.1 Package Software (BeBiS)," and nutrient intake was calculated.

Blood Sample Collection and Deoxyribonucleic Acid (DNA) Isolation

Venous blood samples of the participants were stored into tubes containing 2 mL of ethylene diamine tetraacetic acid. DNA isolation from the samples was performed using a commercial kit (EZ-10 Spin Column Genomic DNA Kit, Bio Basic Inc., Markham, Canada) using the spin column method. The purity and quantity determinations of DNA samples were spectrophotometrically performed (Thermo Scientific Multiskan Go, Thermofisher, USA), and samples with a measurement rate of A260/A280 ≅ 1.8 at 260 and 280 nm absorbency were considered pure. DNA amounts for the Kompetitive Allele-Specific PCR (KASP) method were ensured to be 10 ng/µL. Of each sample, 2 µL, whose purity

and quantity was determined, were used for the KASP genotype reaction mixture.

KASP Genotyping

The KASP™ method was used for TAS1R2 (rs35874116) genotyping. The KASP reaction mixture (10 µL) contained 5 µL of 2× KASP master mix, 0.14 µL of KASP primer assay mix, and 5 µL of DNA template (1 µL of PCR product/DNA extract + sterile water of 4 µL). There were Primer Allele A (FAM) (CAGCTGCACCATGGCCTCGAT) and Primer Allele G (HEX) (GCTGCACCATGGCCTCGAC) and primer common (CACCCAGCGCCGACCACCA) sequences specific to SNP rs35874116 within the KASP primer assay. KASP conditions were 1 cycle of 30 °C/1 min and 1 cycle of 94 °C/15 min, followed by 10 cycles of 94 °C/20 s and 61 °C/1 min, and 26 cycles of 94 °C/20 s and 55 °C/1 min. Finally, fluorescent endpoint readings were performed at 30 °C/1 min using the Applied Biosystems Step One Plus Real-Time PCR Systems (Foster City, CA, USA).

Statistical Analysis

Data were analyzed using the Statistical Package for the Social Sciences 25.0 software. The relationship between genotypes and categorical variables was evaluated using the Fisher's exact test. The Kruskal-Wallis test was used to compare the values of genotypes that did not match the normal distribution. Binary comparisons of statistically significant variables were evaluated using the Mann-Whitney U test and Bonferroni correction. Additionally, p-values of <0.05 were considered statistically significant.

RESULTS

The genotype and allele frequency distributions of participants are summarized in Table 1.

According to the dominant model, the average energy and nutrient intake of participants were summarized in Table 2. No statistically significant difference was found between the median values of measurements according to the dominant model (p>0.05). The odds ratio could not be calculated because the number of samples in the dominant model was insufficient (Table 2).

Participants' energy and nutrient intake are presented in Table 3. No statistical difference was found between genotypes and median values (p>0.05).

DISCUSSION

This study aimed to investigate the TAS1R2 rs35874116 (A > G, Ile191Val) sweet taste receptor polymorphism, and nutrient intake of adult individuals.

Taste perception plays an important role in determining individual food preferences and eating habits. Genetic diversity of sweet taste receptor genes has played a role in sweet taste sensitivity in adults (9,14,15). TAS1R2 is a highly polymorphic gene and this high polymorphism is assumed to be associated with variations in sweet taste perception (3,17). Therefore, genetic variations in the TAS1R2 receptor may contribute to the differences between individual dietary intake (17,20). Eny et al. (9) investigated the effect of TAS1R2 Ile191Val (rs35874116) polymorphism on sugar intake with two different populations including 1,037 individuals without diabetes and 100 individuals with type 2 diabetes. They found a significant relationship between Ile191Val and body mass index (BMI) in terms of sugar consumption in 1,037 individuals without diabetes, and individuals with the Val allele (103±6 g sugar/day) in at least one locus consumed less sugar than individuals with homozygote Ile/Ile genotype (122±6 g sugar/day). A study that investigated the effects of polymorphisms in TAS1R2 receptor (rs9701796, rs35874116) on chocolate powder consumption and dietary fiber intake in obese children revealed that the rs9701796 variant in obese children was associated with high chocolate powder consumption and rs35874116 variant was associated with low dietary fiber intake. They revealed that the daily carbohydrate consumption was 258±36 g for Ile homozygotes and 248±41 g for the Val carriers. Daily sugar intake was determined as 58 g in Ile homozygotes and 51 g in Val carriers. Val allele in the variant rs35874116 was found to be associated with low fiber consumption in children and adolescents with obesity (2). Ramos-Lopez et al. (17), investigated the polymorphism of the TAS1R2 (Ile191Val) gene and revealed that Val/Val carriers consumed

Table 1. Genotype and allele frequency distributions of participants

TAS1R2 rs35874116	n	%
GG genotype	6	6.3
GA genotype	64	67.4
AA genotype	25	26.3
Allel frequency		
G	76	40
A	114	60
Dominant model		
AA + GA vs	89	93.7
GG	6	6.3
Recessive model		
GG + GA vs	70	73.7
AA	25	26.3

Table 2. Amount of nutrients and energy intake of individuals according to the dominant model

	Dominant model	n	Median	p-value		Dominant model	n	Median	p-value
Energy	AA + GA	89	1228.37 (518.08-3734.30)	0.32	Vit E (mg)	AA + GA	89	8.67 (1.5-53.57)	0.963
	GG	6	1374.235 (1125.09-2386.64)			GG	6	8.815 (3.08-19.35)	
Protein (g)	AA + GA	89	49.44 (15.26-153.32)	0.215	Vit B1 (mg)	AA + GA	89	0.67 (0.2-3.02)	0.233
	GG	6	69.81 (31.31-102.40)			GG	6	0.795 (0.5-1.21)	
Protein (%)	AA + GA	89	17 (9-29)	0.89	Vit B2 (mg)	AA + GA	89	1.08 (0.29-2.68)	0.869
	GG	6	16.00 (11-28)			GG	6	1.485 (0.96–2)	
Fat (g)	AA + GA	89	55.82 (13-248.52)	0.375	Vit B6 (mg)	AA + GA	89	1.03 (0.20-3.15)	0.4
	GG	6	67.75 (33.29-116.01)			GG	6	1.09 (0.59-2.85)	
Fat percentage (%)	AA + GA	89	42 (21-75)	0.824	Folate (µg)	AA + GA	89	228.81 (70.6-795.05)	0.963
	GG	6	43 (26-47)			GG	6	176.375 (107.7-480.8)	
CHO (g)	AA + GA	89	119.18 (8.12-289.6)	0.543	Vit C (mg)	AA + GA	89	64.32 (1.11-246.94)	0.624
	GG	6	136.04 (87.86-249.55)			GG	6	68.765 (41.71-329.59)	
CHO (%)	AA + GA	89	41 (6-66)	0.963	Sodium (mg)	AA + GA	89	2339.9 (435.3-53137.75)	0.818
	GG	6	40 (28-57)			GG	6	2878.68 (924.67-5602.04)	
Fiber	AA + GA	89	15.4 (1.88-49.1)	0.951	Potassium (mg)	AA + GA	89	1972.68 (354.95-5101.6)	0.463
	GG	6	13.51 (6.27-29.17)			GG	6	2191.24 (922.7-4188.43)	
Alcohol (g)	AA + GA	89	0.00 (0-52.27)	0.278	Calcium (mg)	AA + GA	89	504.74 (84.2-1255.26)	0.491
	GG	6	0.00 (0-0)			GG	6	595.65 (199.76-991.64)	
Alcohol (%)	AA + GA	89	0.00 (0-19)	0.513	Magnesium (mg)	AA + GA	89	201.86 (50.74-644.6)	0.223
	GG	6	0.00 (0-0)			GG	6	246.265 (129.5-600.25)	
MUFA (g)	AA + GA	89	19.97 (4-92.41)	0.571	Phosphorus (mg)	AA + GA	89	816.1 (267.3-2431.65)	0.284
	GG	6	22.735 (13.45-39.44)			GG	6	1057.15 (530.46-1387.18)	
SFA (g)	AA + GA	89	22.91 (6.39-65.27)	0.641	Iron (mg)	AA + GA	89	7.24 (1.6-20.98)	0.071
	GG	6	25.26 (11.38-59.21)			GG	6	9.47 (5.73-18.6)	
PUFA (g)	AA + GA	89	7.5 (1.45-76.28)	0.482	Zinc (mg)	AA + GA	89	7.6 (1.95-26.24)	0.15
	GG	6	10.69 (4.83-27.43)			GG	6	10.66 (4.86-19.69)	
Cholesterol (mg)	AA + GA	89	232 (9-1079.4)	0.233	Sucrose (g)	AA + GA	89	13.03 (0.41-76.61)	0.32
	GG	6	376.025 (35.8-859.1)						
Carotene (mg)	AA + GA	89	1.93 (0.1-32.16)	0.379		GG	6	23.81 (2.71-84.76)	
	GG	6	1.275 (0.33-12.34)						

Mann-Whitney U test, CHO: Carbohydrate, MUFA: Monounsaturated fatty acids, SFA: Saturated fatty acids, PUFA: Polyunsaturated fatty acids

332.7±102.6 g of carbohydrates, Ile/Ile carriers consumed 273±102.4 g, and Ile/Val carriers consumed 265.2±98.1 g of carbohydrates daily. The difference in carbohydrate intake between genotypes was found to be statistically significant (p=0.01), and Val/Val genotype of TAS1R2 was associated with higher carbohydrate intake. Chamoun et al. (18) investigated the effect of taste genetics on snack consumption habits in preschoolers and revealed that children with the TT genotype TAS1R2 rs35874116 consumed more sugary and high-calorie snacks than children with the C allele. Additionally, children with TT genotypes were significantly more likely to opt for sugary snacks in the evening. Han et al. (16) evaluated the relationship between TAS1R2 rs38574116 polymorphism and carbohydrate intake and found that C alleles (CC and CT) were associated with higher sugary food consumption than TT allele. Contrarily, Hwang et al. (21) found no association between sugar/sweet food intake and TAS1R2 (rs35874116). Our study revealed that daily total carbohydrate and sucrose intakes were the highest in individuals with GG genotype (145.55±56.69 g and 28.66±26 g, respectively) but results were not statistically different between daily carbohydrate and sucrose intake (p>0.05) according to the genotypes of participants (Table 2).

Dias et al. (1) investigated the relationship of TAS1R2 sweet taste receptor polymorphisms (rs12033832, rs12137730, rs35874116, rs3935570, rs4920564, rs4920566, rs7513755, and rs9701796) with sweet taste threshold and sugar intake and revealed that individuals with the GG/GA genotype consumed more sugar compared to individuals with the AA allele in a BMI of ≥25, and individuals with the GG/GA genotype with BMI of <25 consume less sugar compared to individuals with the AA genotype (1). Accordingly, TAS1R2 rs12033832 polymorphism was found to be associated with individuals' sweet taste threshold and sugar consumption, but this relationship differed according to the BMI. Additionally, the association of the polymorphism of rs35874116 with the BMI and the threshold of sweet taste was not found. However, the polymorphism rs35874116 was found to be associated with differences in carbohydrate and sugar intake, regardless of taste perception. This difference was assumed to be related to the expression of TAS1R2 in the small intestine, and this effect can be created by a post-digestive mechanism (1). We also investigated the relationship of sugar and carbohydrate consumption with BMI, thus we divided the participants into two groups, BMI of <25 kg/m^2 and BMI of ≥25 kg/m^2, but no difference was found between the groups' sugar and carbohydrate intake (data not shown).

In the literature, studies on TAS1R2 variations mainly focused on carbohydrate and sweet consumption. However, some studies also provide a perspective on TAS1R2 and other nutrient intakes. Of which, one study that evaluated TAS1R2 (rs7534618) and dietary intake revealed that genetic variation had an association with food intake, including total grain and bread consumption. Additionally, the authors revealed that in the Korean female population, compared to those with the rs7534618 A allele, (AA and AC genotypes), having the CC genotype, which corresponds to the rs12033832 AA genotype, seemed to be associated with decreased carbohydrates but increased fat intake (22). Choi et al. (19) found that TAS1R2 polymorphisms affected cruciferous vegetables, citrus fruit, fatty, and umami food intake. The TAS1R2 rs9701796 variant allele was associated with decreased cruciferous vegetable consumption in males. TAS1R1 rs34160967, diplotype, and TAS1R2 rs35874116 exhibited differential umami foods intake by genotype (19). In the studies that investigated the TAS1R2 rs38574116, some studies also examined the relationship between participants' food consumption records and TAS1R2 rs38574116 genotypes GA (Ile/Val, CT), AA (Ile/Ile, TT), and GG (Val/Val, CC). Ramos-Lopez et al. (17) revealed no difference between the daily average calorie, protein (%), protein (g), fat (%), and fat (g) consumption of individuals with Ile/Ile, Ile/Val, and Val/Val genotypes. Contrarily, daily carbohydrate (g) and fiber (g) consumption of individuals with the Val/Val genotype was significantly higher than Ile/Val and Ile/Ile genotypes (17). Similar to that study, Han et al. (16) found no differences between total energy, carbohydrate (g), protein (g), and fat (g) consumption according to the TT and CC/CT genotypes. Sweet (g) consumption was significantly higher in CC/CT genotype and dietary protein (%) was higher in the TT genotype (16). Our study revealed no significant difference in the participants in terms of energy, protein (g), protein (%), carbohydrate (g), carbohydrate (%), fat (g), fat (%), and sucrose consumption according to their genotypes (Table 3).

CONCLUSION

Elucidating the relationship between individuals' food consumption and genetic basis will contribute to creating individual-specific nutrition programs and maintaining and improving health. We investigated the effect of SNP rs35874116 polymorphism in the sweet taste receptor (*TAS1R2*) gene on the nutrient intake to contribute to the enlightenment of factors food preference and consumption. Contrary to the literature, we found no difference between genotypes and nutrient intake, especially in sweet/sugar

Table 3. Amount of nutrients and energy intake of individuals according to the genotype

	Genotype	n	Median (min-max)	p-value		Genotype	n	Median (min-max)	p-value
Energy	AA	25	1138.52 (562.36-3734.30)	0.533	Alcohol (g)	AA	25	0.00 (0.00-1.20)	0.400
	GA	64	1258.06 (518.08-3273.24)			GA	64	0.00 (0.00-52.27)	
	GG	6	1374.24 (1125.09-2386.64)			GG	6	0.00 (0.00-0.00)	
Protein (g)	AA	25	46.20 (15.26-153.32)	0.269	Alcohol (%)	AA	25	0.00 (0-1)	0.645
	GA	64	51.98 (16.54-112.99)			GA	64	0.00 (0-19)	
	GG	6	69.81 (31.31-102.40)			GG	6	0.00 (0-0)	
Protein (%)	AA	25	17.00 (9-26)	0.515	MUFA (g)	AA	25	19.58 (4.00-92.41)	0.851
	GA	64	17.00 (11-29)			GA	64	20.29 (5.52-75.65)	
	GG	6	16.00 (11-28)			GG	6	22.74 (13.45-39.44)	
Fat (g)	AA	25	52.87 (13-248.52)	0.650	SFA (g)	AA	25	22.57 (6.60-61.26)	0.660
	GA	64	56.54 (18.09-191.30)			GA	64	23.24 (6.39-65.27)	
	GG	6	67.75 (33.29-116.01)			GG	6	25.26 (11.38-59.51)	
Fat percentage (%)	AA	25	41.00 (21-59)	0.948	PUFA (g)	AA	25	9.56 (1.45-76.28)	0.644
	GA	64	42.00 (21-75)			GA	64	7.08 (2.28-60.34)	
	GG	6	43.00 (26-47)			GG	6	10.69 (4.83-27.43)	
CHO (g)	AA	25	118.85 (58.36-221.11)	0.744	Cholesterol (mg)	AA	25	201.80 (9.0-670.35)	0.397
	GA	64	121.28 (8.12-289.60)			GA	64	253.20 (10.98-1079.40)	
	GG	6	136.04 (87.86-249.55)			GG	6	376.02 (35.80-859.10)	
CHO (%)	AA	25	41.00 (24-66)	0.966	Carotene (mg)	AA	25	2.97 (0.50-32.16)	0.083
	GA	64	40.50 (6-60)			GA	64	1.81 (0.10-23.35)	
	GG	6	40.00 (28-57)			GG	6	1.28 (0.33-12.34)	
Fiber	AA	25	14.91 (5.17-42.45)	0.992	Vit E (mg)	AA	25	7.57 (1.85-53.57)	0.935
	GA	64	15.56 (1.88-49.10)			GA	64	8.84 (1.50-50.46)	
	GG	6	13.51 (6.27-29.17)			GG	6	8.82 (3.08-19.35)	
Vit B1 (mg)	AA	25	0.63 (0.29-3.02)	0.484	Calcium (mg)	AA	25	421.45 (84.20-1134.15)	0.321
	GA	64	0.68 (0.20-2.68)			GA	64	557.06 (94.40-1255.26)	
	GG	6	0.78 (0.50-1.21)			GG	6	595.65 (199.76-991.64)	
Vit B2 (mg)	AA	25	1.02 (0.31-1.86)	0.113	Magnesium (mg)	AA	25	179.05 (110.00-644.60)	0.424
	GA	64	1.11 (0.29-2.68)			GA	64	206.88 (50.74-606.85)	
	GG	6	1.48 (0.96-2.00)			GG	6	246.26 (129.50-600.25)	
Vit B6 (mg)	AA	25	1.04 (0.32-3.15)	0.695	Phosphorus (mg)	AA	25	810.89 (290.30-2056.10)	0.361
	GA	64	1.02 (0.2-2.55)			GA	64	891.18 (267.30-2431.65)	
	GG	6	1.09 (0.59-2.85)			GG	6	1057.15 (530.46-1387.18)	

Table 3. Continued

	Genotype	n	Median (min-max)	p-value		Genotype	n	Median (min-max)	p-value
Folate (µg)	AA	25	211.85 (70.60-639.80)	0.836	Iron (mg)	AA	25	7.63 (2.72-16.36)	0.196
	GA	64	243.10 (71.30-795.05)			GA	64	7.22 (1.60-20.98)	
	GG	6	176.38 (107.10-480.80)			GG	6	9.47 (5.73-18.60)	
Vit C (mg)	AA	25	64.58 (12.25-215.66)	0.714	Zinc (mg)	AA	25	7.35 (2.53-20.25)	0.354
	GA	64	63.84 (1.11-246.94)			GA	64	7.61 (1.95-26.24)	
	GG	6	68.76 (41.71-329.59)			GG	6	10.66 (4.86-19.69)	
Sodium (mg)	AA	25	2827.80 (543.30-5744.20)	0.971	Sucrose (g)	AA	25	14.83 (1.06-54.81)	0.601
	GA	64	2292.06 (435.30-53137.75)			GA	64	11.84 (0.41-79.61)	
	GG	6	2878.68 (924.67-5602.04)						
Potassium (mg)	AA	25	1864.90 (897.30-5101.60)	0.763					
	GA	64	40.50 (6-60)			GG	6	23.81 (2.71-84.76)	
	GG	6	40.00 (28-57)						

Kruskal-Wallis test, CHO: Carbohydrate, MUFA: Monounsaturated fatty acids, SFA: Saturated fatty acids, PUFA: Polyunsaturated fatty acids, min: Minimum, max: Maximum, vit: Vitamin

consumption. Considering the interpretation of these results, our sample size was small and food consumption is affected by cultural and individual perceptions. Thus, this study may serve as a preliminary result for our country.

ETHICS

Ethics Committee Approval: Our study was approved by Istanbul Aydın University Non-Interventional Clinical Research Ethics Committee on 09/10/2019 with the decision number 2019/115.

Informed Consent: Volunteers were included in the research by obtaining written and oral consent.

Authorship Contributions

Concept: S.A.Ö., A.S., Design: K.K., S.A.Ö., A.S., Data Collection or Processing: K.K., S.A.Ö., A.S., Analysis or Interpretation: K.K., S.A.Ö., A.S., Literature Search: K.K., S.A.Ö., A.S., Writing: K.K., S.A.Ö., A.S.

Conflict of Interest: No conflict of interest was declared by the authors.

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REFERENCES

1. Dias AG, Eny KM, Cockburn M, Chiu W, Nielsen DE, Duizer L, et al. Variation in the TAS1R2 Gene, Sweet Taste Perception and Intake of Sugars. J Nutrigenet Nutrigenomics 2015;8:81-90.
2. Pioltine MB, de Melo ME, Santos AS, Machado AD, Fernandes AE, Fujiwara CT,et al. Genetic Variations in Sweet Taste Receptor Gene Are Related to Chocolate Powder and Dietary Fiber Intake in Obese Children and Adolescents. J Pers Med 2018;8:7.
3. Chamoun E, Mutch DM, Allen-Vercoe E, Buchholz AC, Duncan AM, Spriet LL, et al. A review of the associations between single nucleotide polymorphisms in taste receptors, eating behaviors, and health. Crit Rev Food Sci Nutr 2018;58:194-207.
4. Bachmanov AA, Beauchamp GK. Taste receptor genes. Annu Rev Nutr 2007;27:389-414.
5. Roper SD, Chaudhari N. Taste buds: cells, signals and synapses. Nat Rev Neurosci 2017;18:485-497.
6. Spaggiari G, Di Pizio A, Cozzini P. Sweet, umami and bitter taste receptors: State of the art of in silico molecular modeling approaches. Trends Food Sci Technol 2020;96:21-9.
7. Habberstad C, Drake I, Sonestedt E. Variation in the Sweet Taste Receptor Gene and Dietary Intake in a Swedish Middle-Aged Population. Front Endocrinol (Lausanne) 2017;8:348.
8. Melo SV, Agnes G, Vitolo MR, Mattevi VS, Campagnolo PDB, Almeida S. Evaluation of the association between the TAS1R2 and TAS1R3 variants and food intake and nutritional status in children. Genet Mol Biol 2017;40:415-20.
9. Eny KM, Wolever TM, Corey PN, El-Sohemy A. Genetic variation in TAS1R2 (Ile191Val) is associated with consumption of sugars in overweight and obese individuals in 2 distinct populations. Am J Clin Nutr 2010;92:1501-10.
10. Treesukosol Y, Smith KR, Spector AC. The functional role of the T1R family of receptors in sweet taste and feeding. Physiol Behav 2011;105:14-26.

11. Joseph PV. Sucrose thresholds and genetic polymorphisms of sweet and bitter taste receptor genes in children [dissertation]. University of Pennsylvania; 2015.
12. Reed DR, McDaniel AH. The human sweet tooth. BMC Oral Health 2006;6 Suppl 1:S17.
13. Kim UK, Wooding S, Riaz N, Jorde LB, Drayna D. Variation in the human TAS1R taste receptor genes. Chem Senses 2006;31:599-611.
14. Fushan AA, Simons CT, Slack JP, Drayna D. Association between common variation in genes encoding sweet taste signaling components and human sucrose perception. Chem Senses 2010;35:579-92.
15. Fushan AA, Simons CT, Slack JP, Manichaikul A, Drayna D. Allelic polymorphism within the TAS1R3 promoter is associated with human taste sensitivity to sucrose. Curr Biol 2009;19:1288-93.
16. Han P, Keast RSJ, Roura E. Salivary leptin and TAS1R2/TAS1R3 polymorphisms are related to sweet taste sensitivity and carbohydrate intake from a buffet meal in healthy young adults. Br J Nutr 2017;118:763-70.
17. Ramos-Lopez O, Panduro A, Martinez-Lopez E, Roman S. Sweet Taste Receptor TAS1R2 Polymorphism (Val191Val) Is Associated with a Higher Carbohydrate Intake and Hypertriglyceridemia among the Population of West Mexico. Nutrients 2016;8:101.
18. Chamoun E, Hutchinson JM, Krystia O, Mirotta JA, Mutch DM, Buchholz AC, Duncan AM, Darlington G, Haines J, Ma DWL; Guelph Family Health Study. Single Nucleotide Polymorphisms in Taste Receptor Genes Are Associated with Snacking Patterns of Preschool-Aged Children in the Guelph Family Health Study: A Pilot Study. Nutrients 2018;10:153.
19. Choi JH, Lee J, Choi IJ, Kim YW, Ryu KW, Kim J. Variations in TAS1R taste receptor gene family modify food intake and gastric cancer risk in a Korean population. Mol Nutr Food Res 2016;60:2433-45.
20. Bachmanov AA, Bosak NP, Floriano WB, Inoue M, Li X, Lin C, et al. Genetics of sweet taste preferences. Flavour Fragr J 2011;26:286-94.
21. Hwang LD, Lin C, Gharahkhani P, Cuellar-Partida G, Ong JS, An J, et al. New insight into human sweet taste: a genome-wide association study of the perception and intake of sweet substances. Am J Clin Nutr 2019;109:1724-37.
22. Choi JH. TAS1R2 sweet taste receptor genetic variation and dietary intake in Korean females. Appetite 2021;164:105281.