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TAS2R38 PAV Haplotype Predicts Vegetable Consumption in Community-Dwelling Caucasian Adults at Risk for Cardiovascular Disease

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Abstract

Introduction: A heart-healthy diet might reduce cardiovascular disease (CVD) risk. Genetic variants that affect taste are associated with food choices. This study aims to investigate the associations of the *TAS2R38* haplotype with consumption of sodium, sugar, saturated fats, and vegetables. **Hypothesis:** We hypothesized that, compared to people who are alanine-valine-isoleucine (AVI) homozygous for the *TAS2R38* gene, those who are heterozygous or homozygous for the proline-alanine-valine (PAV) haplotype would have (a) a higher intake of sodium, sugar, and saturated fat, and (b) a lower vegetable intake. **Methods:** DNA from participants at risk for CVD was genotyped, and participants were assigned to groups by haplotype. Intake for sodium, sugar, saturated fat, and vegetables was assessed using the Viocare Food Frequency Questionnaire. Intake was categorized as higher versus lower consumption, divided at the median, and examined by logistic regressions. All models controlled for age, sex, smoking status, body mass index, education level, and financial status. **Results:** The 175 participants had a mean age of 52 $\pm$ 13 years, 72.6% were female, 100% were Caucasian, 89.1% were overweight or obese, and 82.9% were nonsmokers. Participants with one or two PAVs were grouped together, as PAV is the dominant gene, and comprised a majority of the sample (80.6%). Haplotype did not predict intake of sodium, sugar, or saturated fats. Compared to AVI homozygotes, participants with PAV homozygous or heterozygous haplotype had lower odds of being in the higher vegetable intake group (95% CI [0.17, 0.92], $p = .032$). **Conclusions:** PAV haplotype predicted lower consumption of vegetables. Variants of taste-related genes appear to play a role in food choices.

Keywords

TAS2R38, genotype, cardiovascular disease, eating patterns

Cardiovascular disease (CVD) is the underlying cause of one in three deaths in the United States, and direct and indirect costs to the health care system are estimated to be more than USD$329 billion annually (Benjamin et al., 2018). The most effective way to decrease CVD rates is through prevention that targets risk factors such as unhealthy diet (American Heart Association's Diet and Lifestyle Recommendation, 2015). The association of diet with CVD risk is well known. For example, consumption of sodium, sugar, and saturated fat is positively associated with CVD risk, while vegetable consumption is negatively associated with this risk (D'Elia et al., 2017; Strazzullo et al., 2009; Yang et al., 2014).

The diets of most people in the United States do not meet recommendations for CVD prevention. The average sodium consumption for American adults is double the American Heart Association's recommendation of no more than 2,400 mg per day (American Heart Association's Diet and Lifestyle Recommendations, 2015; Centers for Disease Control and Prevention, 2016). According to U.S. Department of Agriculture (USDA) guidelines, less than 10% of daily calories should come from sugars or saturated fats. Yet sugar comprises 13% of the average adult's daily calories and saturated fats 11% (Chung et al., 2015; Ervin & Ogden, 2013; U.S. Department

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of Agriculture, 2016). Vegetable intake follows a similar pattern, with 90% of the U.S. adult population failing to meet the recommended daily vegetable intake (Centers for Disease Control and Prevention, 2018; Lee-Kwan et al., 2017).

A large number of studies have been conducted to better understand dietary choices, including studies in which the influences of socioeconomic status (Darmon & Drewnowski, 2015), access to healthy food choices (Dubowitz et al., 2015), food preparation time, knowledge (Monsivais et al., 2014), and culture (Mariani-Costantini, 2000) have been examined. Likewise, the role of the taste of foods, which can affect food choices and eating patterns, has been explored in both developmental choices in children and obesity. Among these studies, patterns have emerged that support the importance of taste in dietary choices. In experiments in which participants rated the importance of food taste when considering items for purchase, 77% rated taste as very important (Aggarwal et al., 2016). In children, studies have investigated the effects of taste on food selection, particularly in sweet and bitter foods, as well as how those taste preferences develop as the child grows (Mennella, 2014; Mennella et al., 2005). In the obesity literature, researchers have investigated taste's role in food choices in relation to both heritability and lipid taste preference (Besnard, 2016; Reed et al., 1997). In their review of the role of smell and taste in eating behavior, Boesveldt and de Graaf (2017) found that there was enough evidence to suggest that the role of these two senses was different and distinct in dietary choices, with taste being more closely related to ingestion behavior and satiety. Finally, study participants have frequently identified healthier food choices as being less desirable due to poor taste. For example, adherence to a low-sodium diet is difficult for many patients with heart failure due to the perceived poor taste of low-sodium foods (Bennett et al., 2005; Bentley et al., 2005; Heo et al., 2009).

Taste is a unique sense that varies greatly among individuals (Garcia-Bailo et al., 2009). Taste preferences are based on learned patterns, social and cultural influences, and genetic variations in taste receptors. Taste is related to many physical factors as well. Taste thresholds, the level of the substance needed to taste it, can be affected by physical state. Age is one factor that can raise thresholds, making it more difficult to taste (Ng et al., 2004). Preferences for modalities such as salty taste can change through development and across the life span, as children show a greater preference for salt than adults (Bobowski, 2015; Mennella et al., 2010). Physical conditions such as obesity can alter thresholds of substances such as lipids (Besnard, 2016). Sex can also be a factor that affects the perception of taste through hormonal shifts in women leading to a greater liking for salt (Frye & Demolar, 1994) and differences in brain wave activity between the two sexes, with women showing more high-frequency channels than men (Gemousakakis et al., 2011).

The science of genetics in taste perception and sensation holds promise for elucidating the basis of the wide variation in taste preferences among individuals. Scientists have been studying genetic underpinnings of taste for heritability and the locations of genes that result in taste alterations for decades (Mennella et al., 2005; Reed et al., 1997, 1999, 2006). Differences in genotype can produce variation in proteins that determine the structure and function of taste receptors in the tongue (Bufe et al., 2005; Tepper et al., 2008, 2009). Taste receptors, in turn, have a central role in the detection and processing of flavors in foods and are ultimately responsible for variations in the five taste modalities: salty, sweet, bitter, sour, and umami, or savory. Genetic variations in these taste-related genes thus influence how flavors are perceived (Reed et al., 2006).

Table 1. *TAS2R38* SNPs and Their Haplotype Locations.

SNP	Haplotype Location
rs713598	First location: P or A
rs1726866	Second location: A or V
rs1024693	Third location: V or I

Note. All 175 participants were genotyped for *rs713598* and *rs1726866*, and none were genotyped for *rs1024693*. SNPs = single-nucleotide polymorphisms.

One of the most well-studied genetic variations that influences taste is located in the *TAS2R38* gene. This gene codes for a bitter taste receptor, and individuals with well-characterized *TAS2R38* haplotypes show significant variation in sensitivity to bitter taste. The names of these haplotypes are dictated by the different proteins that are produced, which depends on the inherited genetic variation. The two most common variants of this gene are proline-alanine-valine (PAV) and alanine-valine-isoleucine (AVI). These changes occur at three different single-nucleotide polymorphisms (SNPs): *rs713598* is the first location (P or A of the haplotype), *rs1726866* is the second location (A or V of the haplotype), and *rs1024693* is the third location (V or I of the haplotype [Table 1]). The dominant PAV haplotype, but not the recessive AVI haplotype, is associated with an enhanced sensitivity to bitter taste, as demonstrated with glucosinolates in food and 6-n-propylthiouracil (PROP) in testing (Hayes et al., 2008; Kim et al., 2003; Tepper et al., 2009). Approximately 70% of people have at least one copy of the PAV haplotype and are able to taste bitter properties of foods and chemicals (referred to as the taster phenotype), whereas 30% are homozygous for the AVI haplotype and are unable to taste these properties (referred to as the nontaster phenotype; Hayes et al., 2008; Tepper et al., 2009). Other haplotypes are possible, such as alanine-alanine-isoleucine, alanine-alanine-valine, and proline-alanine-isoleucine, which all denote some sensitivity to PROP when inherited, and proline-valine-isoleucine, which is extremely rare and has been less studied for its effect. These variants have rarely been observed because these SNPs are in strong linkage disequilibrium (Boxer & Garneau, 2015).

People with the PAV haplotype are less likely to consume cruciferous vegetables than those who are homozygous AVI, likely due to the bitter properties of these foods (Duffy et al., 2010). In an earlier study, Hayes and colleagues (2010) found that people with the taster phenotype that corresponds to the

PAV haplotype tasted sodium more intensely and needed less sodium in concentration to detect changes in sodium flavor, but they did not test this for *TAS2R38* haplotype associations. These results correspond to the salty taste modality. Mennella and colleagues (2005) have found that children with the PAV haplotype have a greater preference for sweet foods compared to those with the AVI haplotype, corresponding to the sweet taste modality. Finally, Loper and colleagues (2015) found that PROP tasters had a higher average consumption of fat and calories when compared to their nontaster counterparts. However, researchers have not examined this association for the *TAS2R38* haplotype directly; rather, the higher consumption of fat and calories corresponds to the currently suspected fat taste modality (Besnard, 2016). Similarly, the association between *TAS2R38* haplotype and vegetable consumption in general has not been well investigated. There has been some research on the impact of *TAS2R38* haplotype on sodium, sugar, and fat consumption because of known associations with taste intensity of the taste modalities of sour, salty, and sweet (Fischer et al., 2015). In their study, Fischer and colleagues found that people with the PAV haplotype had heightened taste intensity across all other taste modalities, specifically salt, sweet, and sour. Research has also found this association to be true for phenotype as well; that is, those who have strong intensity of taste for PROP also have a strong intensity of salty taste (Bartoshuk et al., 1998).

Many of these prior studies took place in the laboratory setting, with participants visiting the lab to sample solutions of the related tastants or samples of food items for rating (Fischer et al., 2015; Hayes et al., 2010). Studies of this nature do not fully represent the behavior of participants who make their own dietary choices in the community. Therefore, studies that examine the role of the *TAS2R38* haplotype and other taste-related genes in a community setting in which participants make their own dietary choices are particularly important. Studies of this nature could increase our understanding of how these choices are made and allow nurses and other care providers to create better dietary interventions from the perspective of the community-dwelling adult.

We conducted the present study to better understand the potential role of the PAV and AVI haplotypes of the *TAS2R38* gene in dietary patterns in a community setting. The purpose of this study was to examine associations of the *TAS2R38* haplotype with daily intakes of sodium, sugar, saturated fat, and vegetables in community-dwelling Caucasian adults with two or more CVD risk factors. We hypothesized that, compared to people who are AVI homozygous, those who are heterozygous or homozygous for the PAV haplotype would (a) be more likely to have a higher consumption of sodium, sugar, and saturated fat, as earlier studies have shown that people with either this haplotype or its associated phenotype have consumed more of these nutrients (Hayes et al., 2010; Loper et al., 2015; Mennella et al., 2005), and (b) have lower vegetable intake, as demonstrated in the early study by Duffy and colleagues (2010).

Method

Design, Sample, and Setting

The present study was a secondary analysis of baseline data from the Gene–Environment Interactions Regulating CVD Inflammation and Success of Behavioral Therapies study, which was leveraged on the HeartHealth in a rural Kentucky study. The original study was conducted to examine the effects of genetic variation on responses to a CVD risk reduction intervention in a rural population at increased risk for CVD. Participants were 18 - 85 years of age and community dwelling and had two or more of the following CVD risk factors: (1) unhealthy diet, physical inactivity, overweight or obesity; (2) current smoker; (3) age 45 years or older for males and 55 years or older for females, as women tend to develop CVD later in life than men do (Mosca et al., 2011); (4) family history of heart attack or stroke; (5) diagnosis of hypertension, diabetes, or abnormal lipids; or (6) depression or anxiety. Patients were excluded if they (1) were taking medications that interfered with lipid metabolism; (2) were cognitively impaired; (3) did not speak English; (4) suffered from chronic drug abuse; (5) had end-stage renal, liver, or pulmonary disease; (6) had current, active cancer; (7) had a gastrointestinal disease that required a special diet; (8) had any condition that prohibited physical activity; or (9) had known coronary artery disease or genetic or congenital heart disease. Data analyses were limited to those who self-identified as Caucasian (>92% of participants) to control for population stratification. Researchers recruited participants from rural Eastern Kentucky and did not confirm genetic ancestry, so it is unknown if their ancestries were similar. We compared carriers of the dominant PAV haplotype on the *TAS2R38* gene to non-PAV carriers, that is, AVI homozygotes; participants with rare non-PAV or AVI haplotypes were excluded from analyses. Investigators obtained approval from the University of Kentucky Institutional Review Board prior to initiating the study. All participants gave informed consent before collection of baseline data.

Measures

Sociodemographic, clinical, and behavioral data. Age in years, sex, and education in years were collected by self-report. To measure financial status, participants were asked if they had more than enough to make ends meet, enough to make ends meet, or not enough to make ends meet. The variable was dichotomized as participants with sufficient income (enough or more than enough to make ends meet) and those with insufficient income (not having enough to make ends meet). Smoking was assessed using a single item in which participants self-identified as being current smokers, recent smokers (quit in the past 12 months), past smokers (quit more than 12 months ago), or never smokers. Smoking status was categorized as (1) current or recent smoker or (2) past or never smoker. Weight in kilograms divided by height in meters squared was used to calculate body mass index (BMI). Weight was measured on a

professional digital scale and height on a stadiometer with participants in light clothing and shoes removed.

Dietary intake patterns. Data on dietary intake of sodium, sugar, saturated fats, and vegetables were obtained using a web-based version of the Viocare Food Frequency Questionnaire (FFQ), a well-validated method for estimating dietary intake patterns (Kristal et al., 2014). Participants indicated how often they had consumed foods over the past 90 days, focusing on foods they consumed at least once a month, portion sizes of these foods, and how food was purchased and prepared. Participants could complete the FFQ independently during the baseline data collection period or have questions read aloud by a research nurse. The FFQ was analyzed using the Nutrition Data System for Research (NDSR) software that provides data on the number of vegetable servings consumed daily as well as milligrams of sodium, grams of sugar, and grams of saturated fats consumed daily in each participant. The NDSR relies on a food and nutrient database provided by the Nutrition Coordinating Center at the University of Minnesota. This database includes over 18,000 foods, of which about 7,500 are name-brand products (Nutrition Coordinating Center, 2019). Choice of ingredients and methods of preparation are included to give more than 160,000 food variants. The primary source of nutrient values and nutrient composition is the USDA Nutrient Data Laboratory.

DNA. DNA was obtained from expectorated saliva collected using Oragene-DNA Collection Kits (DNA Genotek Inc., Ottawa, Ontario, Canada). Research has shown that saliva is as accurate as whole blood for DNA isolation and genotyping, yet its collection creates a lower participant burden and provides a high quantity and quality of DNA (Abraham et al., 2012; Matthews et al., 2013; Nunes et al., 2012; Rogers et al., 2007; Rylander-Rudqvist et al., 2006). DNA was quantified by ultraviolet absorbance with a NanoDrop UV-vis spectrometer (Thermo Fisher Scientific, Waltham, MA). Genotyping was performed using TaqMan® with Life Technologies' primers and probes (FAM and VIC labeled) according to manufacturer's instructions (Applied Biosystems, Foster City, CA). Genotypes were determined using an MJR Chromo-4 real-time polymerase chain reaction system (MJ Research, San Diego, CA). Specifically, two SNPs, *rs713598* and *rs1726866*, from the *TAS2R38* gene were genotyped using samples from all participants who consented to DNA analyses. These SNPs are associated with the PAV/AVI haplotype and code for the first and second positions, respectively. Because the third SNP of the haplotype, *rs1024693*, is in perfect linkage disequilibrium with *rs1726866*, it was not genotyped. SNPs and their haplotype locations are presented in Table 1.

Data Analysis

We categorized dietary intake of each of the dietary components of interest as either high or low consumption, with the cutoff at the median, for sodium, sugar, and saturated fat. For vegetable intake, we used number of servings consumed per day, also divided into high and low consumption at the median. We grouped participants by *TAS2R38* genotype as either (a) PAV homozygous or heterozygous or (b) AVI homozygous. To ascertain differences between groups, we conducted independent *t*-tests and χ^2 analyses as appropriate for the level of measurement. To examine whether genotype predicted consumption of sodium, sugar, saturated fat, or vegetables, we conducted logistic regressions. In all models, we controlled for factors that affect taste, including age, gender, smoking status, BMI, education level, and financial status. Prior research has identified these variables as influential in taste perception (age, gender, and smoking status; Bobowski, 2015; Frye & Demolar, 1994; Krut et al., 1961; Mennella et al., 2010; Ng et al., 2004; Redington, 1984) or food choices (BMI, education, and financial status; Darmon & Drewnowski, 2015; Monsivais et al., 2014). We analyzed data using SPSS, version 24. *p* Values reflect nominal *p* values. Because we are looking at a specific SNP type and its association with food consumption behavior instead of looking at multiple SNP types, we did not correct for multiple testing. For all analyses, we used an α level of .05.

An a priori power analysis indicated that, with α level equal to .05 and a sample size of 125 (representing an anticipated 38 participants with at least one PAV-dominant haplotype and 87 heterozygous or homozygous AVI individuals), the power for group comparison of genotypes would be at least 85%. This calculation assumed that the ratio of the standard deviation of the group means to the standard deviation of the observations within the populations was as small as 0.36. This effect size is more modest than that reported previously in a similar study (Essick et al., 2003). Our more conservative approach should ensure that our sample size was sufficient to detect differences.

Results

Sample Characteristics

The mean age of the 175 participants was 52.0 $\pm$ 13.4 years (mean $\pm$ *SD*), and 72.6% were female. The majority were overweight or obese (mean BMI 32.8 $\pm$ 7.4 kg/m^2) and nonsmokers (82.9%). The mean number of years of education was 14.1 $\pm$ 3.2, and 93.1% of participants reported that they had enough money to make ends meet. The majority (80.6%) were homozygous or heterozygous for the PAV haplotype. Only 16.6% of participants consumed less than the daily recommended 2.4 g/day of sodium, 1.1% met the recommended intake of sugar (<10% of total caloric intake), and 25.1% met the recommended intake of saturated fats (<10% of total caloric intake). Mean vegetable consumption was 1.5 $\pm$ 1.4 servings of vegetables per day. As shown in Table 2, there were no significant group differences in characteristics between participants who were homozygous or heterozygous for the PAV haplotype and those who were homozygous for the AVI haplotype.

Table 2. Demographic Characteristics by *TAS2R38* Haplotype.

Characteristic	Total Sample $N = 175$	PAV/PAV or PAV/AVI ($n = 141$)	AVI/AVI ($n = 34$)	p
Age (years), mean ± *SD*	52.0 ± 13.3	51.5 ± 12.7	52.7 ± 15.5	.638
Sex (female), *n* (%)	127 (72.6)	99 (70.2)	28 (82.4)	.200
BMI (kg/m^2), mean ± *SD*	32.8 ± 7.4	33.0 ± 7.6	31.8 ± 6.2	.381
Smoking status (nonsmoker), *n* (%)	145 (82.9)	113 (80.1)	32 (94.1)	.073
Education (years), mean ± *SD*	14.1 ± 3.2	14.1 ± 3.2	14.0 ± 3.3	.857
Financial status (enough dollars to make ends meet), *n* (%)	163 (93.1)	132 (93.6)	31 (91.2)	.423

Note. BMI = body mass index; AVI = alanine-valine-isoleucine; PAV = proline-alanine-valine.

Table 3. Predictors of Vegetable Consumption (Servings/Day).

Variable	Odds Ratio	95% CI	p
Age	1.02	[0.98, 1.05]	.060
Sex	1.28	[0.62, 2.63]	.507
Smoking status	0.78	[0.33, 1.83]	.566
BMI	0.97	[0.93, 1.02]	.237
Years of education	1.16	[1.04, 1.29]	.008
Financial status	0.50	[0.14, 1.88]	.307
PAV haplotype	0.39	[0.17, 0.92]	.032

Note. Total sample size = 175, PAV/PAV or PAV/AVI = 141, AVI/AVI = 34. BMI = body mass index; CI = confidence interval; AVI = alanine-valine-isoleucine; PAV = proline-alanine-valine.

Predictors of Dietary Intake Patterns

Neither the PAV nor the AVI haplotype predicted dietary intake of sodium, sugar, or saturated fats. In the logistic regression models, BMI was the only significant predictor of adherence to dietary sodium recommendations ($p = .001$). *TAS2R38* genotype was a significant predictor of vegetable consumption (Exp[B] = 0.392, CI [0.17, 0.92], $p = .032$; Table 3). Those with at least one PAV haplotype had 2.6 times lower odds of being in the higher consumption group compared to those homozygous for AVI. Years of education was also a significant predictor of vegetable consumption (Exp[B] = 1.155, CI [1.04, 1.23], $p = .008$). People with more education were 1.155 times more likely to be in the higher consumption group.

Discussion

Our results in the present study support the hypothesis that people who are heterozygous or homozygous for the PAV haplotype have lower vegetable consumption than those who are homozygous for the AVI haplotype. Previous research has shown a similar relationship between *TAS2R38* haplotype and consumption of vegetables. Supporting our results, Duffy et al. (2010) found that *TAS2R38* haplotype was associated with vegetable intake in college students, with AVI homozygotes consuming significantly more vegetables than PAV heterozygotes or homozygotes. Feeney and colleagues (2011) found higher intakes of folate and vitamin B_6 (found in green, leafy vegetables) in women who were AVI homozygotes. Likewise, Colares-Bento and colleagues (2012) found higher vegetable consumption in a sample of adults in Brazil who were nontasters of phenylthiocarbamide. Studies have also found that the PAV homozygous haplotype is associated with avoidance of such bitter tasting foods as cabbage, broccoli, coffee, tea, chocolate, and alcoholic beverages (Allen et al., 2014; Duffy et al., 2010).

We found no significant differences between haplotype groups on consumption of sodium, sugar, or saturated fats. This finding is in contrast to other studies that have demonstrated *TAS2R38* haplotype differences in patterns of sodium, sugar, and saturated fat consumption (Hayes et al., 2010; Hoppu et al., 2014; Loper et al., 2015). Results of several studies indicate that PROP supertasters, the phenotype that corresponds to the PAV homozygous haplotype, taste sodium more intensely than people with the phenotype that corresponds to the AVI homozygous haplotype (PROP nontasters; Bajec & Pickering, 2008; Fischer et al., 2015; Hayes et al., 2010). Furthermore, Bartoshuk et al. (1998) found that salt taste intensity is positively correlated with taste intensity of bitter chemicals, which is associated with the PAV haplotype of the *TAS2R38* gene. The researchers who conducted these prior studies, however, performed food taste testing in the laboratory and did not examine sodium consumption in daily life. In the present study, we found no relationship between *TAS2R38* haplotypes and consumption of foods higher in sodium among community-dwelling adults. Our finding suggests that experiencing greater salt intensity may not translate to increased sodium consumption in community settings.

Similarly, the results of other studies have suggested that *TAS2R38* haplotype is associated with patterns of sugar and fat consumption. In a population-based cross-sectional study conducted with children, Hoppu and colleagues (2014) found that children who were homozygous for the PAV haplotype had significantly higher sugar consumption than those heterozygous or homozygous for the AVI haplotype. Furthermore, Loper et al. (2015) reported that PROP supertasters had higher intakes of fat and calories when compared to nontasters, and they found the same difference between PAV homozygotes and AVI homozygotes. Research has also shown that PROP-tasting status interacts with the food environment in children: Nontaster children living in healthy food environments liked more vegetables than did taster children in healthy environments, and taster children living in unhealthy environments had higher BMI (Burd et al., 2013). In the present study, however, among socioeconomic factors like financial status, only education level was associated with dietary patterns. In their study of dietary patterns in Irish children, O'Brien et al. (2013) found that, while bitter taste perception may have influenced some

individual food consumption habits, it did not affect overall dietary patterns.

A limitation of the present study is that our sample comprised only Caucasians of European descent, meaning that our findings are not generalizable to other racial and ethnic groups. Likewise, our sample was primarily female, and thus the results may not be generalizable to males. Thus, while the results of the present study, which was conducted with a large community-based sample, provide important insights into potential genetic influences on dietary patterns, future studies should investigate further among more diverse populations. Another limitation of the present study was the use of the FFQ to determine dietary intake. This instrument relies on participants to remember and estimate what and how much they ate, which can produce some measurement error. Portion sizes may be difficult for participants to communicate; however, the Viocare VioScreen FFQ provides visual references and six different portion sizes from which to select instead of relying on the terms *small*, *medium*, and *large* in order to address this limitation. Nonetheless, participants may overestimate their intake of desirable foods while underestimating their intake of less desirable foods, introducing bias into the measurement.

A strength of the present study was that it was conducted in a community setting where the participants made their own dietary choices. Researchers conducted earlier studies in the laboratory setting and asked participants to rate food items that may or may not have been part of their diets. In the present study, we derived our data from participants' reports of foods they chose to eat, which should create a better representation of the actual diet of the participants and provide information on which we can base dietary interventions that meet the needs of community-dwelling Caucasian adults who are at risk for CVD.

In conclusion, we did not find that the *TAS2R38* haplotype independently predicted consumption of sodium, saturated fats, or sugar, but it did predict consumption of vegetables. While these findings partially support earlier findings in the case of vegetable consumption, they may also indicate that other physiological as well as socioeconomic factors play a stronger role in these dietary behaviors. Future research is needed to elucidate the contributions of *TAS2R38* haplotypes to eating behaviors. Such research should consider a wider array of social and behavioral variables such as taster phenotype and fungiform papillae density. Also, because prior research has shown PROP phenotype to be a strong predictor of food choices, and it is easy to determine using an inexpensive, noninvasive test, researchers may find it more beneficial to examine PROP phenotype in future studies rather than genotype alone.

Author Contributions

Jennifer L. Smith contributed to conception, design, and acquisition; drafted the manuscript; critically revised the manuscript; gave final approval; and agreed to be accountable for all aspects of work ensuring integrity and accuracy. Steven Estus contributed to acquisition, critically revised the manuscript, gave final approval, and agreed to be accountable for all aspects of work ensuring integrity and accuracy. Terry A. Lennie contributed to acquisition and interpretation, critically revised the manuscript, gave final approval, and agreed to be accountable for all aspects of work ensuring integrity and accuracy. Debra K. Moser contributed to acquisition, critically revised the manuscript, gave final approval, and agreed to be accountable for all aspects of work ensuring integrity and accuracy. Misook L. Chung contributed to acquisition, analysis, and interpretation; critically revised the manuscript; gave final approval; and agreed to be accountable for all aspects of work ensuring integrity and accuracy. Gia Mudd-Martin contributed to conception, design, acquisition, analysis, and interpretation; critically revised the manuscript; gave final approval; and agreed to be accountable for all aspects of work ensuring integrity and accuracy.

Declaration of Conflicting Interests

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