

Effects of genetic disclosure on SNPs *rs1761667*, *rs8065080*, and *rs662799* on the limitation of salt and fat intake

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Abstract

Excess salt and fat intake in our food leads to a higher risk of obesity and hypertension. One of the factors that affect our preference is genetics, where a person's preference is related to single nucleotide polymorphisms (SNPs) in taste receptors can also influence food choices. Currently, several program to limit salt and fat intake are often unsuccessful because of lack of individual motivation. Therefore, this study aimed to examine the effect of genetic disclosure on salt limitation and fat intake. The study recruited forty-one adult participants aged 20-50 years who underwent a 14-day healthy transformation Nutricare program organized by PT. Nutrifood Indonesia. Participants were divided into two groups, the first group (n = 20) as the control group and the second group (n = 21) as the genetic disclosure group. The genetic disclosure was performed with *rs8065080* on the TRPV1 gene (related to salty taste sensitivity), *rs1761667* in the CD36 gene (related to fatty taste sensitivity), and *rs662799* in the APOA5 gene (related to the hyperlipidemia risk). Overall, 90% of genetic disclosure group participants showed a significant reduction in salt (7.02 ± 2.25 g/day vs. 4.42 ± 1.98 g/day, $p = 0.002$) and fat (70.84 ± 18.45 g/day vs 48.54 ± 12.25 g/day, $p = 0.000$) intake. Results comparison between groups also showed that the group with genetic information resulted in a greater decrease in the intake of salt (-1.95 ± 2.28 vs. 2.60 ± 3.05 , $p = 0.397$) and fat (-11.43 ± 22.01 vs -22.31 ± 21.46 , $p = 0.1$). Therefore, genetic disclosure could help individuals live healthier by motivating the participants to reduce salt and fat intake.

1. Introduction

Rapid technological developments such as mobile applications help us get everything we need in this modern era, including food. However, this situation leads us to have a sedentary lifestyle (less active lifestyle) that will cause various health problems, such as obesity, high blood pressure and lipid disorders. Besides lifestyle factors, another factor contributing to health problems is excess salt and fat intake in daily food (Buja *et al.*, 2020). The government had issued recommendations for the maximum sugar, salt, and fat intake (sugar 5 g/day, salt 5 g/day and fat 67 g/day). Unfortunately, it is known that 30% of the Indonesian population (equivalent to 77 million people) is accustomed to consuming salt and fat that exceeds the

daily recommendation. According to Kementrian Kesehatan RI (2019), it's known that 72.7% of the Indonesian population aged 3 years old are used to consuming high-salt foods and 86.7% are used to consuming high-fat foods (Kementrian Kesehatan RI, 2019). Thus, increasing the risk of imbalance in body composition, obesity, and other diseases (Atmarita *et al.*, 2019).

Food choices are related to some factors such as behavior, culture, environment, socio-economic status and genetics. One of the essential factors that influence our food choices is genetics, where a person's preference will be related to single nucleotide polymorphisms (SNPs) on taste receptors. SNPs on

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the taste receptors of an individual will determine the sensitivity they have. If an individual has low sensitivity, they will tend to consume high levels of related flavor substances. A person's sensitivity to salty taste was significantly affected by *rs8065080* in the TRPV1 gene. Sensitivity to fatty taste was associated with *rs1761667* in the CD36 gene. Meanwhile, a person's risk of hyperlipidemia is influenced by *rs662799* in the APOA5 gene (Chamoun et al., 2017; Chamoun et al., 2018; Pilic et al., 2020).

Currently, several attempts are available to limit salt and fat intake, such as health assistance prog and healthy catering. However, these measures are ineffective due to the lack of awareness from the individual. In improving individual awareness, one of the methods is genetic information disclosure. Based on precedent studies, genetic information disclosure affects individual food intake in such groups, and the transformation is greater than in the group without genetic information disclosure (Nielsen and El-Sohemy, 2014). Besides, a predecessor study concerning the effect of genetic information disclosure associated with Alzheimer's risk also positively correlated with food intake transformation (Vernarelli et al., 2010). Therefore, this study aimed to acquire data regarding the effect of genetic information disclosure based on SNP for salt and fat sensitivity and the risk tendency of hyperlipidemia. SNPs and genes employed for salt, fat, and hyperlipidemia were SNP *rs8065080* in the TRPV1 gene, SNP *rs1761667* in the CD36 gene, and SNP *rs662799* in the APOA5 gene, respectively. The study result is expected to be an alternative to facilitate the limitation of salt and fat intake.

2. Materials and methods

2.1 Eligibility criteria

The study was conducted on random basis with a total of forty-one adults participants aged 20-50 years old who underwent a 14-days healthy transformation program, Nutricare organized by PT. Nutrifood Indonesia. In the beginning of the program, participants are required to fill the form of informed consent. Participants were divided into two groups, the first group (n = 20) referred to the control group and the second group (n = 21) referred to the genetic disclosure group (GD Group). There were four major steps for both groups (control and GD): body composition measurements, food recall-24 hours, health education, and statistical analysis. In addition, there were four additional steps for the GD group: DNA sampling and extraction, SNPs identification,

and Genetic Disclosure. The study was conducted after getting approval 0004A/III/LPPPM-PM.10.05/01/2021 from the Atma Jaya Catholic University of Indonesia Institutional Life Review Committee for exemption of review

2.2 Body composition measurements

Body composition measurements comprised weight, body mass index (BMI), and waist size. The measurements were performed in the morning three times: at the beginning (day 1), middle (day 7) and end of the program (day 14).

2.3 DNA sampling

Participants were provided a buffer solution in a tube to directly collect saliva (whole saliva method) and a saliva sampling guideline card. Before sampling the saliva, participants were asked to fast (only drink water) for 30 mins. Also, participants were asked to gargle with water minutes before sampling. It aimed to eliminate other substances in the mouth. Subsequently, participants were instructed to swab their inner mouth area using their tongue for 30-60 s to augment DNA yield from the saliva.

2.4 Data extraction

The extraction process was conducted by adding SDS 10% and proteinase-K into the saliva and buffer mixture tube. Genomic DNA was extracted using the SDS-PK method based on the procedure by Duardiaková et al. (2012). Lysis was initiated by incubating the mixture in a water bath shaker BS-21 at 56°C for 30 mins. After that, the mixture was added with a PCI mixture (phenol-chloroform-isoamyl alcohol). The mixture was centrifuged to separate DNA from proteins and lipids. The process was followed with further precipitation on DNA by adding ethanol 96%, incubating at 4°C, and centrifuging at 12000 rpm for 2 mins. The pellets from centrifugation were collected and re-washed using ethanol 70% to eliminate residues and increase DNA purity. The supernatant was disposed of, and the tube was dried by air-dry for 20-30 mins. The pellets were resuspended using double distillation water or buffer TE and quantified using Nanodrop 2000 (Thermo Scientific) with a blank of distilled water or buffer TE.

2.5 SNPs identification

SNPs identification performed to observe the polymorphism from DNA extraction results was using the PCR-RFLP method. DNA from the extraction result was amplified using ProFlex PCR with a specific primer to obtain the desired gene. The gene of interest amplified by 12.5 µL GoTaq 2X Green Master Mix, primer (1 µL

for *rs1761667* and *rs662799*, and 0.75 μ L for *rs8065080*, and 2 μ L (500 ng) of DNA were mixed, and the volume adjusted to 25 μ L with NFW. The primer for lipid gene amplification (*rs1761667* on the CD36 gene) was acquired from Momeni-Moghaddam *et al.* (2019). The primer for salt gene amplification (*rs8065080* on the TRPV1 gene) was obtained from Wang *et al.* (2018). Meanwhile, the primer for the amplification of hyperlipidemia risk-related gene (*rs662799* on APOA5 gene) was obtained from Mahrooz *et al.* (2016). The results of PCR condition optimization are shown in Table 1.

Amplified genes were analyzed by electrophoresis using a 2% agarose gel. After obtaining appropriate fragments, a cut is performed using the restriction enzyme. PCR products (150 ng/ μ L) were digested with the suitable enzyme (*HhaI*; *rs1761167*; *Hpy991*; *rs8065080*; and *MseI*; *rs662799*). According to the digestion patterns, three genotypes were determined: *rs1761667* GG (161 and 264 bp), GA (161, 245, and 425 bp), CD36 and AA (425 bp); *rs8065080* CC (294 and 191 bp), TC (485, 294, and 191 bp), TT (485 bp); and; *rs662799* CC (167 and 20 bp), TC (187, 167, and 20 bp), and TT (187 bp). The fragment results were then analyzed using electrophoresis with a 4% agarose gel and visualized using a UV-transilluminator.

2.6 Food recall-24 hours

Participants asked to conduct food recall-24 hours via online video conference twice, i.e., at the beginning (day 1) and end (day 14) of the program. Participants were asked to recall food and beverages consumed in the last 24 hours on three different days (two weekdays and one weekend) during the food recall process. Food recall data was collected by dietician to determine the salt and fat substance intake size using the NutriBase 19 Pro program.

2.7 Genetic disclosure

After acquiring data concerning the genetic information of each participant in the genetic disclosure group, individual data regarding sensitivity to salt and fat and the risk tendency of hyperlipidemia was informed to each participant in a personal report. Participants explained the effect of each gene concerning the tendency of salt and fat intake and the hyperlipidemia risk level.

2.8 Health education

During the Nutricare program, participants were provided with various health education, including infographics about healthy lifestyles, healthy lifestyle challenges, limitations of sugar, salt, and fat, and shared classes and exercises. Challenges related to a healthy lifestyle are given daily to support participants on the limitation of salt and fat intake (Ex: no junk-food day). Participants are also given healthy snacks and cooking essentials from PT. Nutrifood Indonesia at the beginning of the program to support them along the journey of Nutricare. Classes were held virtually via online video conference concerning healthy lifestyle tips and tricks and shared exercises performed each weekend during the program. Besides that, participants also provided a supportive circle created by the Chat Group to share their personal experiences.

2.9 Statistical analysis

Body composition measurement and participant intake data were analyzed using Microsoft Excel and IBM SPSS software to discover the average body composition and the number of consumed salt and fat in three days (g/day). The analysis carried out among and between groups (control and GD groups). The statistical analyses were performed using the Sapphiro-Wilk test (normality test), Kruskal Wallis (Body measurement data), Wilcoxon (intake data), and Mann-Whitney tests (between GD and control groups). The data was determined to be significantly different if the p-values were less than 0.05.

3. Results

3.1 Statistical analysis of the control group

Data on weight transformation, BMI, waist size, and intake were presented in Table 2. Participants in the control group had an average age of 35.6 \pm 6.4. Weight transformation, BMI, and waist size data were processed using Kruskal Wallis ($P < 0.05$), and intake data was processed using Wilcoxon ($P < 0.05$). It shows that salt intake (6.56 \pm 1.39 g/day vs. 4.47 \pm 2.06g /day, $p = 0.001$) and fat intake (70.10 \pm 18.04 g/day vs. 57.33 \pm 21.93 g/day, $p = 0.021$) data were significantly affected after the program. In the protein and fiber intake, data show a slight intake reduction of average protein (70.90 \pm 28.79 g/day vs. 61.01 \pm 23.60 g/day, $p = 0.085$) and fiber (10.30 \pm 4.45 g/day vs. 10.14 \pm 4.86 g/day), although it was

Table 1. PCR condition (optimization result).

SNPs	PCR Condition					
	Initial Denaturation	Denaturation	Annealing	Extension	Final Extension	Cycles
<i>rs1761667</i>	95°C; 5 mins	95°C; 30s	65°C; 30s	72°C; 30s	72°C; 5 mins	35 \times
<i>rs8065080</i>	94°C; 3 mins	94°C; 30s	63°C; 30s	72°C; 1 min	72°C; 5 mins	35 \times
<i>rs662799</i>	96°C; 4 mins	93°C; 40s	58°C; 40s	72°C; 40s	72°C; 5 mins	35 \times

Table 2. Statistical comparison of body parameters and intake in control and GD groups.

Parameter	Mean±SD			p-value	
	Before (day 1)	Middle (day 7)	After (day 14)		
Control Group	Weight (kg)	70.42±20.58	69.03±20.47	69.25±18.84	0.885
	BMI (kg/m ²)	27.05±6.13	26.56±6.08	26.60±5.87	0.813
	Waist (cm)	88.81±14.49	87.20±14.32	86.62±13.39	0.866
	Salt Intake (gr)	6.56±1.39	-	4.47±2.06	0.001**
	Fat Intake (gr)	70.10±18.04	-	57.33±21.93	0.021*
	Protein Intake (gr)	70.90±28.79	-	61.01±23.60	0.085
	Fiber Intake (gr)	10.30±4.45	-	10.14±4.86	0.862
GD Group	Weight (kg)	62.35±10.33	61.72±9.94	61.63±9.66	0.968
	Body Mass Index (kg/m ²)	24.40±3.97	24.16±3.86	24.13±3.78	0.779
	Waist (cm)	80.84±10.89	80.45±9.89	78.73±10.03	0.97
	Salt Intake (gr)	7.02±2.25	-	4.42±1.98	0.002**
	Fat Intake (gr)	70.84±18.45	-	48.54±12.25	0.000**
	Protein Intake (gr)	79.28±17.18	-	53.38±19.56	0.000**
	Fiber Intake (gr)	11.14±9.18	-	11.03±4.47	0.289

*Significant difference at $\alpha = 5\%$, **Significant difference at $\alpha = 1\%$

insignificant. Meanwhile, the table's weight measurement, BMI, and waist size data show an insignificant reduction indicated by a p-value > 0.05 . However, from the observation of the measurement results at the beginning, middle, and end of these three parameters, a constant declining trend was present in each parameter. This analysis result data was then utilized for comparison with the genetic disclosure group.

3.2 Profiling result of the genetic disclosure group

Participant data of the genetic disclosure group were present in Table 3. The genotype distribution shows that most participants had low sensitivity genes regarding salt and fat intake. The distribution percentages of salt and low-fat sensitivities were 57.14% and 90.48%, respectively. It indicates a higher salt and fat intake tendency. This higher intake tendency also demonstrates a high possibility that participants with low-sensitivity genes to experience hyperlipidemia. In addition, the distribution of participants with a higher risk of hyperlipidemia was 66.67%, while the remaining 33.33% had a lower risk. It also shows that people with a high risk are often discovered. Therefore, it is vital to maintain food intake and a healthy lifestyle.

3.3 Statistical analysis of the genetic disclosure group

From Table 4, participants in the GD group had an

Table 3. Profiling result of the GD group.

SNPs	Genotype	Result	Percentage
<i>rs1761667</i> CD36 gene	GG (High Sensitivity)	2	9.52%
	AA + GA (Low Sensitivity)	19	90.48%
<i>rs8065080</i> TRPV1 gene	TT (High Sensitivity)	9	42.86%
	CC + CT (Low Sensitivity)	12	57.14%
<i>rs662799</i> APOA5 gene	TT (Lower risk of cholesterol disease)	7	33.33%
	CC + CT (Higher risk of cholesterol disease)	14	66.67%

average age of 30.00±8.15. Statistical analysis result data of the genetic disclosure group demonstrate significant salt (7.02±2.25 g/day vs. 4.42±1.98 g/day) and fat (70.84±18.45 g/day vs. 48.54±12.25 g/day) intake reduction with p-values of 0.02 and 0.000, respectively. It showed a major significance, indicating a high salt and fat intake in all participants. The protein (79.28±17.18 g/day vs. 53.38±19.56 g/day) and fiber (11.14±9.18 g/day vs. 11.03±4.47 g/day) intake data also experienced a reduction. The average intake reduction in protein was relatively high, indicated by a significant reduction by a p-value of 0.000. Meanwhile, the fiber intake reduction was insignificant. Body parameter measurement results, i.e., weight, BMI, and waist size, demonstrate insignificant differences. Nevertheless, the results show a constant declining trend in the weight (62.35±10.33 kg vs. 61.63±9.66 kg), BMI (24.40±3.97 kg/m² vs. 24.13±3.78 kg/m²), and waist size (80.84±10.89 cm vs. 78.73±10.03 cm) measurements.

Data of body parameter measurement and participant intake results in the genetic disclosure group in Table 4 were then analyzed following the gene profile result. The result shows a constant and significant salt and fat intake reduction in participants with high sensitivity to salt and fat and a higher risk of hyperlipidemia. The statistical analysis showed a very significant (p-value < 0.01) result in reducing salt and fat intake.

Table 4. Statistical comparison of body parameter and intake in GD group.

Parameter	Mean±SD			p-value
	Before (day-1)	Middle (day-7)	After (day-14)	
Weight (kg)	62.35±10.33	61.72±9.94	61.63±9.66	0.968
Body Mass Index (kg/m ²)	24.40±3.97	24.16±3.86	24.13±3.78	0.779
Waist (cm)	80.84±10.89	80.45±9.89	78.73±10.03	0.97
Salt Intake (g)	7.02±2.25	-	4.42±1.98	0.002**
Fat Intake (g)	70.84±18.45	-	48.54±12.25	0.000**
Protein Intake (g)	79.28±17.18	-	53.38±19.56	0.000**
Fiber Intake (g)	11.14±9.18	-	11.03±4.47	0.289

**Significant difference at $\alpha = 1\%$

The statistical analysis also demonstrated that participants with higher hyperlipidemia risk and low salt and fat profile sensitivity had a higher average reduction than those with high sensitivity and a lower risk of hyperlipidemia. The decrease of consumption in higher risk and low sensitivity group also showed a very significant reduction based on statistical analysis ($P < 0.01$). Meanwhile, the decrease in consumption in lower risk and higher-sensitivity groups is not statistically significant. The consumption is significantly reduced in the low-sensitivity group because they tend to have a higher intake. Thus, when they're being educated and exposed to Genetic Disclosure, it resulted in a higher decrease in consumption.

3.4 Statistical analysis between group

The results in control and genetic disclosure groups were compared to observed differences between treatments. Table 5 shows that the fat intake reduction percentage in the genetic disclosure group (90%) is far higher than those in the control group (65%). Meanwhile, the salt intake reduction percentages in batches 1 and 2 were similar between the control and genetic disclosure groups, resulting in 85% and 80%.

The statistical comparison was also performed using a Mann-Whitney statistical analysis based on the delta of control genetic disclosure groups. Based on the statistical

analysis result in Table 6, salt (-1.95 ± 2.28 vs. -2.60 ± 3.05 , $p = 0.397$) and fat (-11.43 ± 22.01 vs. -22.31 ± 21.46 , $p = 0.1$) decrease intake in the genetic disclosure group generated a higher reduction than the control group. However, the reduction difference between groups was insignificant. Unfortunately, in the control and genetic disclosure group, protein and fiber intake also showed a reduction.

Table 6. Percentage of decrease in salt and fat intake between groups

	Control Group	GD Group
% Decrease in Salt Intake	85.00	80.95
% Decrease in Fat Intake	65.00	90.00

4. Discussion

The present study aimed to evaluate the effects of DNA-based genetic disclosure on salt and fat intake. Previous studies concerning genetic disclosure showed that genetic information disclosure might help participants to have healthy lifestyles with intake pattern transformation (Vernarelli *et al.*, 2010; Nielsen and El-Sohemy, 2014). The current study integrated DNA-based genetic disclosure with 14-health transformation challenges, i.e., Nutricare, organized by PT. Nutrifood Indonesia. Data were collected based on seven parameters, comprising three body measurement parameters (weight, BMI, and waist size) and four intake

Table 5. Statistical analysis of intake in GD group based on genetic profile.

			Mean±SD		Sig
			Before (g)	After (g)	
CD36 Gene (Fat Sensitivity)	High Sensitivity (n = 2)	Salt Intake	6.45±0.63	3.06±1.07	0.180
		Fat Intake	69.96±9.23	39.77±12.25	0.180
	Low Sensitivity (n = 19)	Salt Intake	7.08±2.36	4.57±2.01	0.005**
		Fat Intake	70.94±19.32	49.46±12.20	0.001**
TRPV1 Gene (Salt Sensitivity)	High Sensitivity (n = 9)	Salt Intake	6.94±2.37	4.87±2.19	0.110
		Fat Intake	78.18±1.34	50.23±9.95	0.021*
	Low Sensitivity (n = 12)	Salt Intake	7.08±2.26	4.09±1.82	0.013*
		Fat Intake	65.34±12.29	47.27±14.03	0.010*
APOA5 (Hyperlipidemia Risk)	High Risk (n = 10)	Salt Intake	6.38±2.36	3.49±0.59	0.007**
		Fat Intake	69.38±18.13	43.51±13.27	0.007**
	Low Risk (n = 11)	Salt Intake	7.60±2.08	5.18±2.48	0.068
		Fat Intake	72.18±10.51	53.11±9.67	0.021*

*Significant difference at $\alpha = 5\%$, **Significant difference at $\alpha = 1\%$

parameters (salt, fat, protein, and fiber). Body measurement data were analyzed using the Kruskal-Wallis test ($P < 0.05$), intake data were analyzed using the Wilcoxon test ($P < 0.05$), and data between group analyzed using the Mann-Whitney test ($P < 0.05$).

Statistical analyses in the control group demonstrated that the program designed by Nutricare facilitated participants in limiting salt and fat intake to follow daily recommendations. Significant reduction was observed in the average salt (6.56 ± 1.39 vs. 4.47 ± 2.06 , $p = 0.001$) and fat (70.10 ± 18.04 vs. 57.33 ± 21.93 , $p = 0.021$) intake. Average salt and fat intake reduction also affected the average body parameter measurements. Data of body parameter measurements, i.e., weight (70.42 ± 20.58 vs. 69.25 ± 18.84 , $p = 0.885$), BMI (27.05 ± 6.13 vs. 27.05 ± 6.13 , $p = 0.813$), and waist size (88.81 ± 14.49 vs. 86.62 ± 13.39 , $p = 0.866$), acquired at the beginning, middle, and end of the program demonstrated positive results with a constant declining trend in each measurement. The declining finding in body parameters was insignificant since it took a long time to observe a significant body parameter reduction. Approximately after week three of consistent changes to healthy lifestyle and intake, the changes in body parameters could be observed. It will become more significant after week four of consistent changes (Feig and Lowe, 2017). Both declining trends in the average salt and fat intake and body parameter measurements show that the program helped salt and fat limitation.

In the genetic disclosure group, the results reveal that the Nutricare program integrated with genetic disclosure also had a positive result, with a significant reduction of salt (7.02 ± 2.25 g/day vs. 4.42 ± 1.98 g/day, $p = 0.002$) and fat (70.84 ± 18.45 g/day vs. 48.54 ± 12.25 g/day, $p = 0.000$) intake. The result shows that the genetic information given to the participant plays a psychological role in motivating them during the program. This salt and fat intake transformation also affected body parameter measurements. Measurement results of weight, BMI, and waist size displayed a declining trend in each measurement, although insignificant. After comparing the salt and fat intake reduction in the control and GD groups, it is discovered that the genetic disclosure applied in the GD group increased the number of participants experiencing fat intake reduction to meet the daily recommendation from 65% to 90%. Meanwhile, no significant effects were found in salt intake. Genetic information disclosure facilitated fat intake reduction due to the APOA5 gene *rs662799* addition in genetic disclosure associated with fat. APOA5 gene *rs662799* codes the hyperlipidemia risk, increasing the information and participant emergence to have healthy lifestyles by limiting salt and fat intake. This positive result could

happen regarding adding the APOA5 gene into the genetic disclosure comparable to the previous study of Sparks *et al.* (2017) where disclosure of RA risk personalized with genotype results increased motivation to improve Rheumatoid Arthritis-risk related behaviors. It is also comparable to the previous study, which showed that receiving genetic susceptibility testing, Alzheimer's disease was positively associated with dietary supplement use after risk disclosure (Vernarelli *et al.*, 2010).

Interestingly, data between the control and GD groups shows that the average salt and fat intake reduction in the GD group was higher than in the control group. The average salt and fat intake reduction in control and GD groups were as follow: salt (-1.95 ± 2.28 vs. -2.60 ± 3.05 , $p = 0.397$) and fat (-11.43 ± 22.01 vs. -22.31 ± 21.46 , $p = 0.1$) intake data, although the difference was insignificant. A higher declining trend of average salt and fat intake in the GD group demonstrates that genetic disclosure may increase participant motivation to live healthy, particularly by limiting salt and fat intake. The result follows feedback from participants, both in control and genetic disclosure groups. This success is due to DNA-based genetic disclosure integrated with the Nutricare program that provides information in daily infographics, challenges, and supporting activities such as shared seminars and exercises, and the support system among participants.

In the genetic disclosure group, gene profiling was performed concerning the hyperlipidemia risk, salt sensitivity, and creamy/fatty taste sensitivity. The genotype distribution collected from participants ($n = 21$) was as follows: CD36 gene *rs1761667* concerning fatty/creamy taste sensitivity demonstrated that 90.48% of participants had the AA+GA gene profile causing low fatty taste sensitivity in individuals. In comparison, 9.52% of participants had a GG gene profile with high fatty taste sensitivity. This genotype distribution was comparable to the distribution in Mexican, African-American, Egyptian, Chinese, and Moroccan populations (Bayoumy *et al.*, 2012; Keller *et al.*, 2012; Lopez *et al.*, 2015; Zhang *et al.*, 2015; Bajit *et al.*, 2020). On TRPV1 gene *rs8065080*, the genotype distribution showed that 57.14% of participants had the CC+CT gene causing low salt sensitivity, while 42.86% of participants had the TT genotype causing high salt sensitivity. This genotype distribution was comparable to the Australian population (Ferraris *et al.*, 2020). It was comparable to the previous study results held by Tapanee *et al.* (2021) on 129 participants from Caucasians, African-Americans, Asians, and Latino Hispanics.

Meanwhile, the genotype distribution from SNP

rs662799 on the APOA5 gene revealed that the CC+CT gene percentage coding a higher hyperlipidemia risk occurred in 66.67% of participants. It indicates that two of three participants have a higher risk of catching hyperlipidemia. Therefore, it is crucial to limit salt and fat to have a healthy lifestyle and avoid various health disorders.

Furthermore, salt and fat intake data were analyzed further based on the participant's gene profile. The results show that participants with low salt and fat sensitivity displayed a higher average of salt and fat intake reduction than in the control group. Thus, it also showed that participants with low sensitivity have statistically significant intake reduction in both salt and fat, while those with high sensitivity were not. However, there was a limitation in the statistical comparison between the reduction of salt and fat intake based on fat-sensitivity genetic profile because the number of participants with high sensitivity is very low compared to the low sensitivity. The statistical analysis also showed that participants with low salt sensitivity had a statistically significant intake reduction in salt, while those with high sensitivity did not. It also occurred in the analysis result of participants with high hyperlipidemia risk. The participant with a higher risk of hyperlipidemia has a very significant reduction of salt and fat intake ($P < 0.01$); meanwhile, the participant with lower risk were not. That probably occurred considering a participant with lower risk is less worried than a participant with higher risk. But with the comprehensive package education (personal report and explanation, infographics) that was given along the program, there was still a chance, especially in fat intake, which showed a significant reduction also ($P < 0.05$). The differences in reduction also showed in salt intake where the participant with higher risk showed a significant reduction of salt intake, while the participant with low risk was not. Considering many of the high-fat foods around us is also contain high salt (ex: fried chicken, burgers) when they tried to limit their fat intake, it would also affect their salt intake. It was also constant, participants with these three gene profiles demonstrated a significant reduction pre and post-program. This evidence reinforces that the DNA-based genetic disclosure facilitates participant motivation marked by a positive transformation of salt and fat intake reduction. Moreover, it will impact more in the participant with low sensitivity and high-risk gene profiles. Genetic information disclosures reinforce particular emergence and motivation, primarily on participants with riskier gene profiles and high salt and fat intake to have a lifestyle and salt and fat intake following daily recommendations to avoid plausible health problems.

In addition, the study also examined the intake of protein and fiber. Results show that the average protein intake reduction followed both groups' average salt and fat intake reduction. This average protein and fiber intake reduction show that implementing a healthy lifestyle by reducing salt and fat intake may induce misunderstanding regarding other intakes, such as protein and fiber, to remain following daily recommendations. Limiting salt and fat intake is recommended to replace the food with healthier options, e.g., low-salt and low-fat food, rather than eliminating them, substituting fried food with grilled food.

4. Conclusion

The study concludes that genetic disclosure plays a role in increasing participant motivation to limit salt and fat intake to follow daily recommendations. The Nutricare 14-day health transformation program helps participants reduce their salt and fat intake, especially when the program integrated with genetic disclosure showed a higher reduction. Better observation of the effect of genetic disclosure integrated with a healthy lifestyle program in body parameter measurements (weight, BMI and waist size) requires a prolonged period and a bigger sample size than the current study.

Conflict of interest

The authors declare no conflict of interest.

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