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DIABETES & CARDIOVASCULAR DISEASE

TAS2R38 taste receptor gene and metabolically unhealthy obesity


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Background:

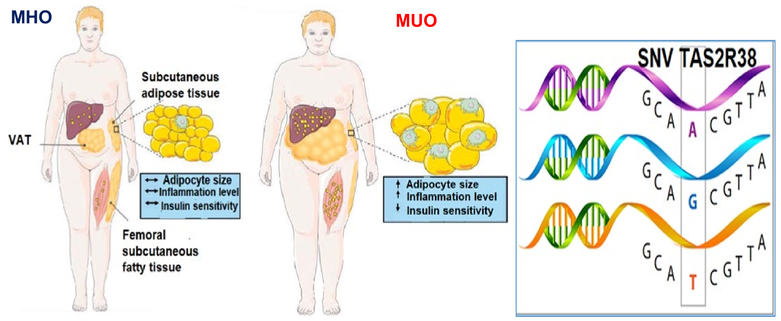
The spread of obesity has become pandemic, and it is expected that during 2021 the number of obese children and adolescents (5 to 19 years) will be 158 million [World Obesity Federation, 2020]. There is an alarming trend towards an increase in the incidence of metabolically unhealthy obesity (MUO), especially among children [Williamson K. et al., 2020].

Genetically determined violation of taste preferences leads to an inversion of the perception of tastes and overeating, distorting the homeostatic feedback of the peripheral energy status with hedonic centers, causing obesity.

In our work, the importance of genetic variants of the taste 2 receptor member 38 (*TAS2R38*) is presented as the most significant predictor of metabolically unhealthy obesity among genes responsible for taste formation, according to GWAS data.

Objective:

to study the role of SNV gene *TAS2R38* in the formation of MUO in children 6-18 years old.



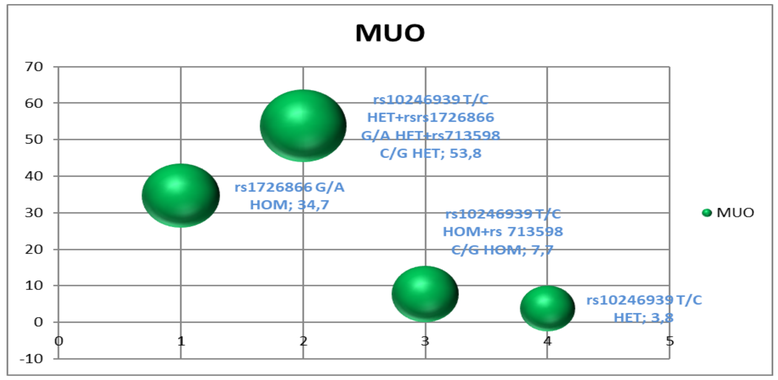


Fig. 1. Genetic variants of SNV TAS2R38 in the MUO phenotype.

Materials and methods

90 obese children aged 6-18 years were examined. The main group (n = 52) was represented by children according to the criteria of the consensus of the International Diabetes Federation (IDF) with MUO. The control group (n = 38) was formed by patients with MHO. To identify the prevailing modalities of taste preferences in the 5 most important categories (sweet, sour, fatty / umami, salty and bitter), a survey was conducted using an adapted version of the approved and used in the study IDEFICS (Identification and prevention of Dietary and lifestyle-induced health EFfects In Children and infantS Study) of the Food and Beverage Preference Questionnaire (FBPQ) and an analysis of food diaries. To determine the SNV of the TAS2R38 gene in the formation of metabolically unhealthy obesity, we used the method of complete genomic sequencing on the Illumina platform in a certified laboratory CeGat (Tübingen, Germany), followed by bioinformation analysis.

For statistical processing of the obtained results the variational analysis with definition of the criterion of reliability of Student, the relation of chances, the correlation analysis of Spearman, calculation of the prognostic factor is used.

Table 1. SNVs of the TAS2R38 gene (missense mutation) and CADD

TAS2R31	CCDS5374	missense	c.213T>G	p.F71L	ttTaat/ttG	0.4329863	NFE		rs78562467	
TAS2R31	CCDS5374	synonymo	c.183A>G	p.=	gtAtta/gtG	0.2925938	NFE			
TAS2R31	CCDS5374	missense	c.103C>T	p.R35W	Cgggtc/Tg	0.5319188	NFE	0.3355000	rs10845295	
TAS2R38	CCDS3476	missense	c.886A>G	p.I296V	Atcctg/Gtc	0.6777343	EAS	0.5206000	rs10246939	9,46
TAS2R38	CCDS3476	missense	c.785C>T	p.A262V	gCtgcc/gTt	0.6360230	SAS	0.4255000	rs1726866	12,51
TAS2R38	CCDS3476	missense	c.145G>C	p.A49P	Gcactg/Cc	0.6768837	EAS	0.5048000	rs713598	13,24
TAS2R42	CCDS3174	downstream_gene				0.2306648	AMR		rs1817104	
TAS2R42	CCDS3174	missense	c.931G>C	p.A311P	Gcttta/Cct	0.9640562	EAS		rs1650017	

Results

The level of the average value of preference for bitter food in the main group was 2.75 ± 0.15 points, while in the control group 3.24 ± 0.14 points and the Student's test in the compared populations was 2.39, with p <0.02 . There were no statistically significant differences in preferences for sour, salty and fatty / umami flavors in the comparison groups, p> 0.05. Analysis of food diaries in children showed a positive correlation between daily non-consumption of fresh vegetables and the formation of MUO (r = -0.32) with a prognostic factor of 2.7; p <0.05.

SNVs of the *TAS2R38* gene (missense mutation) were diagnosed by complete genomic sequencing (Table 1). The probability of detecting a gerozygotic variant of the C/G genotype rs713598 of the *TAS2R38* gene in the main group was 1.75 times higher than in the control group of obese children, p <0.05 (Table 2, Fig. 1).

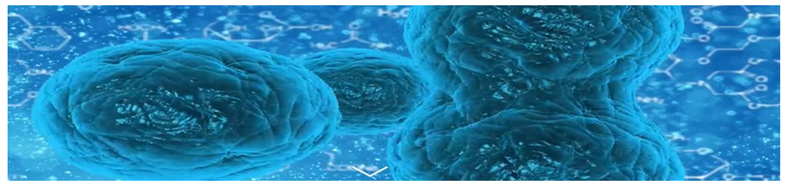
Table 2. SNV of the TAS2R38 gene in the MUO phenotype

Genetic variant SNV *TAS2R38*	Probability of detection in MUO-phenotype
10246939 T/C, HOM	OR 1.167; 95%DI 0.098-14.06
10246939 T/C, HET	OR 1.193; 95%DI 0.33-4.28
1726866 G/A, HOM	OR 0.79; 95%DI 0.21-2.94
1726866 G/A, HET	OR 1.33; 95%DI 0.37-4.76
713598 C/G, HOM	OR 1.167; 95%DI 0.098-14.06
713598 C/G, HET	OR 1.75; 95%DI 1.1-6.35

Conclusion

Decreased taste preferences for bitter foods increase the risk of developing MUO in children.

The C/G genotype rs713598 has the greatest association among the SNV of the TAS2R38 gene detected by us with the formation of metabolically unhealthy obesity.



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Authors' contributions

AA was responsible for the idea and study design, looked over the articles, extracted the data, and interpreted bioinformatics analysis data. DN provided the collection of biological material using dried blood spot shipping kit, AN analyzed the data and interpreted it. Both authors reviewed the paper and approved the final manuscript.

Conflict of Interest: The authors declare that they have no conflict of interest.

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