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Alcohol consumption behaviour of the Hungarian general and Roma populations and the effect of taste preference-related gene polymorphisms on alcohol consumption patterns

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INTRODUCTION

Harmful alcohol intake has been documented as a principal risk factor for illness, disability, and mortality at global level. Though previous research suggests that moderate consumption of alcohol may be beneficial to health via decreasing cardiovascular diseases' risk and overall mortality, excessive intake of alcohol may lead to the development of several diseases. Over 200 illnesses and/or health-related conditions are directly or indirectly linked to alcohol consumption among which alcohol dependence, liver cirrhosis, cancers and injuries are the predominant ones. It was also revealed that during the first year of COVID-19 pandemic, the intake of alcohol as well as associated harms increased.

Countries of the WHO European Region can be characterized by the highest levels of per capita intake of alcohol. Though the substantial differences in alcohol consumption among the countries of this region, the average alcohol intake decreased from 12.3 litres in 2005 to 9.8 litres in 2016. In Hungary, pure alcohol consumption changed from 12.1litres in 2010 to 11.4 litres in 2016, and the average alcohol consumption varied from 19.1 litres for males to 4.5 litres for females. Although there has been a decreasing trend of alcohol consumption in Hungary, the consumption level was still higher compared to the Organisation for Economic Co-operation and Development (OECD) average and this country was among those which reported yearly per capita pure alcohol consumption of more than 11 litres. Additionally, the reported prevalence of heavy episodic drinking among Hungarian citizens aged over 15 years was 33.5% which is much higher than the global prevalence of 18.2%. Furthermore, Hungary had a significantly higher prevalence of alcohol use disorders (21.2% in Hungary versus 8.8% in Europe) and alcohol dependence (9.4% in Hungary, while 3.7% in Europe) compared to the average of the WHO European Region's. Moreover, standardized mortality rates related to alcohol intake were the highest in Hungary among European countries.

Health behaviour together with alcohol consumption patterns may vary not only across populations but also between different races and ethnicities. Findings of earlier studies demonstrated that prevalence rates of overweight, poor diet and physical inactivity were higher among black women compared to white women, while among black and white men differences were less both in magnitude and consistency. Alcohol consumption levels may not only show regional differences but may also differ between ethnic minority groups. For instance, in one study among individuals above or equal to 12 years of age, American whites demonstrated higher (57.4%) alcohol consumption than other ethnic/racial groups. Furthermore, the results of another study elucidated that the persistence of alcohol dependence was greater among blacks and Hispanics than non-Hispanic whites.

Roma is acknowledged as the largest and most widely distributed ethnic minority population in the European Union. Linguistic, cultural, anthropological, and genetic evidence suggested that Roma individuals came from the Indian subcontinent and entered Eastern Europe around 1000 years ago. Later, they spread all over Europe by the end of the fifteenth century. Though, due to inadequate documentation, worry about stigmatization as well as disinclination to self-identification, the exact number of Roma remains unspecified . It is estimated that about 10-12 million Roma are inhabited in the European Region, where the majority of them are concentrated in Central and Eastern Europe. In most Central, Eastern, and Southern European countries representation of Roma individuals exceeds 5% of the total population. Among the countries with the highest representation of Roma, in Romania, this minority group accounted for 1.2–2.5 million (8.3% of the population), while in Bulgaria Roma represented 10.3% (700,000–800,000) of all individuals living in the country. Hungarian Roma represents 8.9% of the country's population with an estimation of 876,000 inhabitants and the number is rising continuously. All over Europe, compared to mainstream populations, Roma individuals faced generations of discrimination and oppression which is manifested in racism, marginalisation in the formal labour market, poor education as well as inadequate access to healthcare services. Besides, several studies comparing Roma to the general majority populations revealed that along with worse health and well-being, the majority of Roma suffered from increased rates of communicable and non-communicable diseases, and higher mortality rates compared to non-Roma.

In Europe, numerous studies were conducted to compare patterns of alcohol consumption behaviour between Roma and the majority populations. Among them, a study conducted by Zelko et al. on the Roma and non-Roma populations of Slovenia is the only study where an

AUDIT questionnaire was applied to evaluate drinking patterns. Results of the study demonstrated that for abstainers (Roma: 39.0%; non-Roma: 16.0%) and non-hazardous drinkers (Roma: 38.0 %; non-Roma: 64.0 %), there were significant differences between participants of Roma and non-Roma. One of the Slovak studies did not find any difference in overall alcohol consumption among males of Roma and non-Roma but in the case of binge drinking the rate was higher among Roma females than non-Roma. Additionally, a study on Roma and non-Roma mothers in Slovakia revealed that during pregnancy, Roma mothers had a greater risk of alcohol intake. The odds of alcohol drinking were 11.7 times higher for non–Roma mothers ($p<0.001$). Though results from another study in Slovakia indicated that Roma adolescents drank less frequently than non-Roma. Findings of a study in Moldova represented that compared to non-Roma, Roma families spent more (116% of the non-Roma) on alcohol and tobacco, where the expenditure for essential goods among Roma was significantly lower than among non-Roma. In comparison with non-Roma, a higher proportion of Roma children in Lithuania and Latvia were daily alcohol users, though the differences were not statistically significant. Results of a study conducted on the Roma social workers in the Czech Republic showed that substance use including regular excessive alcohol intake was 2–6 times higher among Roma than that of the general population. Similar findings were also obtained from another study conducted in Spain stating that Roma women had significantly higher levels of alcohol consumption compared to non-Roma women. Gender-specific results were obtained from another study in Spain, it illustrated that young Roma men were more likely to drink alcohol compared to other young men, but among women, the frequency of alcohol consumption was lower among Roma than in the general population. Both daily alcohol consumption and drunkenness were more common among Roma adolescents in Hungary. Another study conducted among Hungarian Roma and non-Roma adolescents revealed that Roma ethnicity was significantly associated with the lifetime prevalence of alcohol intoxication. Besides poorer socioeconomic conditions, higher consumption of sweets and soft drinks, children living in Roma settlements in Hungary could also be characterized by earlier initiation of alcohol consumption and at the age of 11 years and trying alcohol was also more prevalent among Roma boys than non-Roma ones. Another Hungarian study described that between 2003 to 2014 there were negative changes regarding alcohol intake among Roma individuals and in comparison, with the general population, the gap was widened for alcohol consumption. From this study, it was articulated that during the surveys of 2014/2015 for both men and women and all age groups between 18 and 64 years, the percentage of heavy drinking was higher among Hungarian Roma than that of the general population. On the other hand, Kosa et al revealed that the prevalence of abstainers was significantly higher among Roma compared to the Hungarian general adult population.

Both patterns and the amount of alcohol consumed are accountable for the adverse health outcomes of alcohol intake. Numerous factors comprising both genetic variations and non-genetic variables influence the quantity and patterns of alcohol consumption. Nongenetic factors include gender, age , duration of involuntary unemployment, extent of poverty and relevant lifestyle factors like smoking and inadequate physical activity. Several genes, particularly those coding for enzymes involved in alcohol metabolism have a substantial influence on alcohol consumption. Alcohol dehydrogenase (ADH) and aldehyde dehydrogenase (ALDH) are the two important enzymes responsible for the degradation of alcohol in the oxidative pathway. ADH is responsible for the oxidation of ethanol to acetaldehyde, which is further oxidized to acetate by aldehyde dehydrogenase ALDH. This toxic by-product of hepatic oxidation is responsible for the unpleasant effects of alcohol consumption. Furthermore, numerous genes related to neurotransmitter pathways involved in the mediation of positive reinforcing effects of alcohol were also found to be associated with certain alcohol consumption-related phenotypes.

Besides alcohol metabolizing and neurotransmitter genes, taste preference-related genetic variants may also influence drinking behaviours. Perceived taste is one of the sensory components assumed to influence alcohol intake. Alcohol consumption was found to be negatively influenced by the degree of responsiveness towards bitter component 6-*n*-propylthiouracil (PROP), while sweet taste sensitivity is assumed to increase preference for alcoholic beverages. Individuals with higher bitter taste perception are supposed to consume fewer alcoholic beverages compared to those with a lower perception of bitter taste. Numerous known genes are responsible for mediating bitter taste perception and many of them belong to the superfamily of G protein-coupled receptors of the TAS2R family. The TAS2R family in humans is capable of interacting with several substances belonging to various taste qualities. Bitter-tasting compounds are linked to 25 different bitter taste receptors functioning as monomers of the TAS2R gene family among which TAS2R38 is the most studied one. Different variants of the TAS2R38 gene are linked to variation in responsiveness towards two bitter-tasting compounds called phenylthiocarbamide (PTC) and PROP and are associated with preferences for numerous foods such as brassica vegetables, other bitter-tasting foods, sweets, spicy foods and different alcoholic beverages. Three common variants such rs713598, rs1726866 and rs10246939 of TAS2R38 involved in changes of amino acids sequences and thus, results in two haplotypes, called AVI (alanine-valine-isoleucine) and PAV (proline-alanine-valine) which are liable for variation in human bitter taste sensitivity. Carriers of AVI homozygous are mainly non tasters while heterozygous and PAV homozygous carriers tend to be tasters. Additionally, the bitter taste modality is also affected by other genes like TAS2R19 (Taste 2 Receptor Member 19), TAS2R31 (Taste 2 Receptor Member 31), TAS2R4 (Taste 2 Receptor Member 4), TAS2R5 (Taste 2 Receptor Member 5), TAS2R9 (Taste 2 Receptor Member 9) and CA6 (Carbonic Anhydrase 6) (gustin). In humans, receptor proteins of the TAS1R family functioning as heterodimers are vital for the perception of sweet and umami taste modalities Sweet taste perception is mostly mediated by the activation of TAS1R2 (taste receptor type 1, member 2) and TAS1R3 (taste receptor type 1, member 3) heterodimers and umami are mainly linked to TAS1R1/TAS1R3 heteromers.

Alcohol use disorder is a multifactorial disorder that can be influenced by a wide variety of genetic determinants and social, cultural and personal factors such as more permissive attitudes towards heavy drinking, physical and financial availability of alcohol), poor family support parental drinking and individual expectations of alcohol effects may also contribute to AUD. ADH1B and ALDH2, two important genes responsible for coding for alcohol-metabolizing enzymes were found to exhibit associations with different levels of alcohol consumption and with potential intermediate phenotypes of alcohol use disorder (AUD). Findings from genetic association studies represented that GABRA2 and other GABA-A receptor genes *were* significantly linked with alcohol dependence. Dopamine has been considered to be involved in the development of alcoholism through the reward system since the mesolimbic dopamine system plays a crucial role in the rewarding effects of alcohol. Alcohol consumption leads to the release of neurotransmitters in the limbic system via stimulating dopamine neurons in the mesolimbic system and thus mediates positive reinforcement and reward. Dysfunction in the dopaminergic transmission is linked with a craving for ethanol and appears to impact withdrawal symptoms. Serotonin (5-hydroxytryptamine; 5-HT) is also believed to be involved in the mediation of alcohol intake. Moreover, 11 SNPs of cholinergic receptor muscarinic 2 (CHRM2) showed statistically significant associations with alcoholism.

Genetic association studies regarding alcohol drinking behaviours of the Hungarian general and Hungarian and other Roma populations are scarce. One Hungarian study illustrated that variations in alcohol consumption patterns among Hungarian general and Roma participants were not linked to the genetic constitution, but rather exposure to different environmental factors and respective cultural values that may have a prominent influence on alcohol intake. Another study of Hungarian men exhibited that ADH1B rs1229984 had a significant association with lower odds of drinking frequency and in the case of Hungarian males ADH1C rs1693482/ rs698 alleles enhanced the risk of excessive and problematic drinking, respectively. Findings from another study illustrated that the allele frequency of ADH1B rs1229984 did not differ significantly between participants of Roma and Czech populations. At the same time, the effect of taste preference genetic variants on different dimensions of alcohol consumption among Roma individuals and in the Hungarian general population has not been investigated yet.

AIM OF THE STUDY

Our study aimed to identify the factors that may influence alcohol consumption behaviours of the Hungarian general and Roma populations of North-East Hungary. The specific objectives were to:

1. Describe and compare alcohol consumption behaviours of the Hungarian general (HG) and Roma (HR) populations.
2. Evaluate the potential effect of taste preference-related gene polymorphisms on alcohol consumption behaviours among participants of HG and HR populations.
3. Synthesize the evidence on the effect of taste preference-related genetic variants on various aspects of drinking behaviours.

MATERIALS AND METHODS

3.1 Study design and sampling

The current research used data derived from a cross-sectional study conducted in 2018 from 17 May to 29 August. Within the framework of this three pillar (questionnaire survey, physical examinations, and laboratory analysis) complex comparative health survey, representatives of the HG and HR populations segregated settlements of two counties of North-East Hungary named Borsod-Abaúj-Zemplén and Szabolcs-Szatmár-Bereg, where most of Roma populations are inhabited. In the beginning, it was intended to comprise 500 participants from each of the two study groups. The inclusion of study subjects was aided by the pre-determined principle that if somebody was not available to reach, it was acceptable to add another individual, but when anyone denied to participate in the study, it was unacceptable to include another subject for the one who refused to participate. To collect data from study participants of HG and HR groups, questionnaires were administered by practice nurses and Roma field workers, respectively. For genetic analysis, blood samples were collected at General Practitioners' (GPs) practices. This study was approved by the Ethical Committee of the Hungarian Scientific Council on Health (61327-2017/EKU). By following the Helsinki Declaration written consent was taken from the study respondents of both groups.

3.2 Sample representative of the Hungarian general population living in Northeast Hungary

Participants for the HG population sample were derived from a population-based disease registry called the General Practitioners' Morbidity Sentinel Stations Programme (GPMSSP). This registry was set up to observe the incidence and prevalence of various chronic non-communicable diseases (diabetes, hypertension, ischaemic heart disease, liver cirrhosis, acute myocardial infarction, stroke, malignancies of the respiratory tract, colon and rectum, breast, cervix, and prostate). The reference HG population sample for the present study was randomly recruited from the GPMSSP registry. The sample comprised individuals of 20–64 years residing in private houses in two selected counties of Northeast Hungary (Borsod-Abaúj-Zemplén and Szabolcs-Szatmár-Bereg) and registered by GPs involved in the GPMSSP. GPs documented the medical history, conducted physical examinations, and collected blood samples for routine examinations and DNA extraction. At the beginning, it was intended to recruit 25 respondents from each of twenty previously nominated GPs, which ultimately would have accounted for 500 subjects of the general population. Two GPs refused to take part; thus, the final sample size comprised 450 respondents from eighteen GPs. Health-related information was collected at the time of the participants' visits at the GP's practices and practice nurses administered questionnaires in a face-to-face mode.

3.3 Sample representative of the Hungarian Roma population living in segregated colonies in Northeast Hungary

A stratified multistep sampling technique was applied to enrol representative subjects of the Hungarian Roma population from the same two counties (Borsod-Abaúj-Zemplén and Szabolcs-Szatmár-Bereg), where most of the Roma populations are inhabited. Earlier, an environmental survey was conducted in all settlements of Hungary, where Roma field workers were engaged to detect and characterize segregated Roma settlements of no less than, 100 residents and the ethnicity of the individuals of these segregated colonies was authenticated by self-statement. Followed by the required validation of this registry, twenty colonies were selected randomly for the present study and 25 households were chosen randomly from each of these selected colonies. Afterward, from each selected household all individuals within the age range of 20–64 years were identified and one person of this age group from every house was nominated by using a random table for subsequent face-to-face interviews. To avoid probable adversities and mistrust of Roma participants regarding interviewers, skilled Roma university students were engaged to collect information related to health behaviours.

3.4 Sociodemographic and economic variables

Several sociodemographic and economic variables (gender, ethnicity, sex, marital status, highest education level, economic activity, and self-perceived financial status) were used in this study, as predictor variables for different alcohol consumption phenotypes. During this study, different age categories (20-34, 35-49, and 50+ years) were used for describing study participants. The highest educational level was classified as primary or less, secondary, high school, and tertiary school. Based on their marital status the respondents were categorized as married, single, and widow, or divorced, while economic activity was illustrated by categories such as worker, unemployed, and pensioner/other allowance/student. A five-point Likert scale varying from very bad to very good was applied to gather information on participants' self-perceived financial status, and the responses were subsequently converted to three different options: good, satisfactory, and bad.

3.5 Assessment of alcohol consumption patterns

Patterns of alcohol intake were evaluated by utilization of the 10-item Alcohol Use Disorders Identification Test (AUDIT-10) tool, where the total AUDIT score varies between 0 to 40 and total scores of 20 or greater indicate possible alcohol dependence. This tool comprises questions on three important domains of alcohol consumption such as hazardous alcohol use related to the frequency and quantity of drinking, dependence symptoms, and harmful alcohol use describing problems due to alcohol consumption. AUDIT questions 1- 8 have five response options to be chosen, while each response category has a corresponding score varying from 0 to 4. Questions 9 and 10 are scored on either of the three available options such as 0 (no), 2 (yes, but not in the last year), or 4 (yes, during the last year). In our study, the Hungarian version of the AUDIT was applied. The first question of the AUDIT questionnaire provides information on drinking frequency, while questions 2 and 3 gather data on the typical quantity of alcohol consumed and frequency of heavy drinking, respectively. Additionally, a score of more than 0 on questions 4 to 6 indicates the presence of alcohol dependence while points on questions 7 to 10 infer the possibility of alcohol-related harm being experienced. Total scores ≥ 8 out of 40 are generally suggested as an indication of hazardous as well as harmful alcohol use and the possibility of alcohol dependence. However, in certain cases improvements (obtaining optimal sensitivity and specificity of assessment) have been done by lowering the cut-off score, depending on the population investigated. Results from several other research on AUDIT indicated that for optimal revealing of hazardous and harmful alcohol use among women, lower than the originally suggested cut-off score of 8 is recommended by some researchers. Findings from another similar type of study revealed that among females, optimal sensitivity and specificity of the assessment of different alcohol consumption behaviours were obtained at AUDIT score cut-off point ≥5. During the current study, several alcohol consumption phenotypes, i.e., problematic drinking, hazardous level of alcohol use, alcohol dependence, alcohol-related harm, and past alcohol problems were evaluated as primary outcome variables. To evaluate problematic drinking the following thresholds of total AUDIT score were considered: ≥ 8 points for men and ≥5 points for women. Additionally, a score of ≥ 1 on questions 2 or 3 specified a hazardous consumption level, while a score above 0 on questions 4 to 6 indicated alcohol dependence. Furthermore, score on questions 7-10 pointed towards alcohol-related harms being experienced. Finally, the last two questions provided evidence of past problems. These domains were also considered separately in our research to gain more insight into several aspects of alcohol-related phenotypes of our two study samples, which might point out ethnic-specific problems and the need for more tailored interventions. Moreover, for genetic association analysis the first three questions of the AUDIT questionnaire were used as potential outcome variables. The first question ("How often do you have a drink containing alcohol?") and the second question ("How many standard drinks containing alcohol do you have on a typical day when drinking?") of the AUDIT questionnaire measure the frequency of drinking and the typical quantity consumed respectively, while the third question ("How often do you have six or more drinks on one occasion?") indicates the frequency of heavy drinking.

3.6 Selection of genetic polymorphisms

A systematic literature review was conducted to identify single nucleotide polymorphisms linked to different taste preference genes, which are assumed to be associated with various alcohol consumption behaviours. Based on the literature search, SNPs, whose effects regarding bitter and sweet taste preference and/or perception were investigated comprehensively and likely to be related to diverse alcohol intake phenotypes were included in the present study. Four SNPs, TAS1R3 (taste 1 receptor member 3) rs307355, TAS2R38 (taste 2 receptor member 38) rs713598, TAS2R19 (taste 2 receptor member 19) rs10772420 and CA6 (carbonic anhydrase 6) rs2274333 were selected for further analysis.

3.7 DNA preparation

DNA extraction was conducted from previously collected ethylenediaminetetraacetic acid (EDTA)-anticoagulated blood samples. To isolate DNA from 500-µl aliquots of blood, the "MagNA Pure LC DNA Isolation Kit – Large Volume" made by Roche Diagnostics of Germany was used.

3.8 Genotyping

Genotyping of the selected 4 SNPs was conducted by the Mutation Analysis Core Facility (MAF) of the Clinical Research Center of Karolinska University Hospital of Stockholm, Sweden. Genotype assessment was conducted on the Sequenom Mass Array platform using the iPLEX Gold Chemistry. During the process, initially, a locus-specific polymerase chain reaction (PCR) reaction is carried out, and then a locus-specific primer extension reaction is accomplished, where oligonucleotide primers anneal to the polymorphic site of interest. In the iPLEX assay, both primers and amplified target DNA are incubated with mass-modified dideoxynucleoside terminators. Extended primer mass can be determined by matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, when the mass of primer specifies the sequence, thus alleles existing at the specific polymorphic site (205). Furthermore, validation, quality control as well as concordance analysis was carried out by MAF. The success rate of genotyping was over 98%.

3.9 Statistical analysis

Data were analysed by utilizing the statistical software STATA 10 version (Stata Corporation, College Station, Texas). The normality of the age distribution of HG and HR respondents was checked by the Shapiro-Wilk test, while a comparison of mean age and gender distribution of HG and HR respondents was made by execution of the Mann-Whitney U and chi-square (χ2) tests, respectively. To compare the distribution of different sociodemographic variables between the study populations (HR versus HG) χ^2 and Fisher's exact tests were executed. Furthermore, both crude and gender-stratified distributions of different alcohol consumptions behaviours (problematic drinking, alcohol intake at hazardous levels, dependence syndrome of alcohol, harms associated with alcohol intake, and evidence of past problems related to alcohol consumption) between the two groups were calculated by χ^2 and Fisher's exact tests. To investigate the association between above mentioned sociodemographic variables and different alcohol consumption behaviours included in this study, multiple Poisson, as well as, logistic regression analyses were applied, where outputs of the association analyses were presented as respective odds ratios with corresponding 95% confidence intervals.

To assess the deviation from the Hardy-Weinberg equilibrium (HWE) and to calculate allele frequencies of the included SNPs the STATA commands “hwsnp” and “genhw” were executed, respectively. The $\chi2$ test was used to depict the differences in genotype frequencies between HG and HR populations. Additionally, an association of included genetic variants with different alcohol intake behaviours among HG and HR participants were evaluated by applying “qtlsnp” command in STATA. During all association analyses, adjusments were made for potential covariates (age, gender and marital status), and dominant and recessive models were considered (based on corresponding minor alleles). In the case of HWE p-value of <0.001 was applied as a significance threshold, while in every other case of analysis p<0.05 indicated statistical significance. Additionally, Bonferroni corrected p-values were presented for multiple testing analyses.

3.10 Systematic literature search to identify taste preference genetic variants related to alcohol consumption behaviours

To identify articles investigating associations of taste preference-related genetic variants with various aspects of drinking behaviours, a systematic literature search was conducted using three search engines PubMed, Web of Science and, ProQuest Central. Principles of the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) statement were followed throughout the search process. During the literature search the following keywords were applied to ascertain desired articles: (“taste preference” OR “taste perception” OR “taste sensitivity” OR “sweet taste preference” OR “sweet taste perception” OR “sweet taste sensitivity” OR “bitter taste preference” OR “bitter taste perception” OR “bitter taste sensitivity” OR “fat taste preference” OR “fat taste perception” OR “fat taste sensitivity” “salty taste preference” OR “salty taste perception” OR “salty taste sensitivity” OR “sour taste preference” OR “sour taste perception” OR “sour taste sensitivity” OR “umami taste preference” OR “umami taste perception” OR “umami taste sensitivity” OR “taste threshold” OR “sweet taste threshold” OR “fat taste threshold” OR “salty taste threshold” OR “sour taste threshold” OR “umami taste threshold”) AND (“genes”) AND (“alcohol consumption”) NOT (“animal”). From the findings of the literature search articles meeting the desired criteria such as focusing on human samples, written in English, published in peer-reviewed journals, and existing in a full-text format were included for subsequent analysis. The validated 11-item quality assessment tool of genetic association studies called the Q-Genie tool was used to assess the quality of the included articles, where a 7-point Likert scale varying from 1 (poor) to 7 (excellent) was applied to evaluate included studies regarding certain quality aspects defined by each item. After the removal of duplicated studies, abstracts of the remaining publications were screened to identify eligible articles for further analysis.

RESULTS

4.1 Characteristics of the Study populations:

The study comprised altogether 797 respondents from both HG and HR populations: 410 HG and 387 HR subjects, respectively. The mean age of HG respondents did not differ significantly from that of HR participants (HG: 44.3 ± 12.3 years, HR: 42.8 ± 12.1 years, $p=0.075$). Additionally, the output of $\chi 2$ test analysis postulated that the proportion of male respondents was significantly lower in the HR (0.26 vs 0.44, $p<0.001$) than in the HG sample. Except for marital status and age categories, all other socioeconomic variables included in the study such as education, economic activity, financial status, and gender differed significantly ($p<0.001$) between the two study groups. Among HR, the majority of the individuals (84.5%) could be characterized by primary educational level or less while for HG, most of the study individuals (33.66%) completed high school. Additionally, 18.29% of HG participants were tertiary-level educated, while for HR this percentage was less than 1%. It is also articulated that the rate of unemployment was almost three times higher (HG: 7.80%; HR: 21.45%) among HR compared to HG. Furthermore, 30.98% and 14.99% of the HG and HR participants, respectively, were in good financial status, while for bad financial status, the percentage was almost three times higher (HG: 11.71%; HR:30.23%) among participants of HR than HG. Moreover, the percentage of female participants was significantly higher among HR (73.9%) compared to HG (56.1%).

4.2 Alcohol consumption patterns of the Hungarian general and Roma populations

4.2.1 Drinking frequency of the study participants:

There is a statistically significant ($p<0.001$) difference in the frequency of having alcoholic drinks between HG and HR. In comparison with HG, a lower proportion of HR participants had alcoholic drinks “2-4 times a month” (HG: 12.01%; HR: 4.17%) and “2-3 times a week or more” (HG: 12.75%; HR: 5.47%). Meanwhile, a higher percentage of HR individuals (37.76%) had alcoholic drinks “monthly or less” compared to HG participants (28.43%). Additionally, after stratification by gender, the frequency of alcohol intake remained statistically significant between HG and HR males (p=0.007) and between HG and HR females (p<0.001).

Number of standard drinks consumed on a typical day and how often 6 or more alcoholic drinks per occasion were consumed by study participants were also analysed. It is observed that the number of standard drinks consumed did not differ significantly between the participants of HG and HR. After stratification by gender, consumption of standard alcoholic drinks varied significantly (p=0.011) between HG and HR females. From the table, it is observed that 7.0% and 12.1 % of the HG females and HR females, respectively, consumed 3 to 4 standard alcoholic drinks, while in the case of 5 or more drinks it was 0.4% for HG females and 4.3% for HR females. Additionally, it was also observed that in the case of 6 or more alcoholic drinks, there was no significant (p>0.05) difference between participants of both study groups and even after stratification by gender.

4.2.2 Alcohol consumption behaviours of the study respondents

Mean AUDIT-C (HG: 1.38 ± 1.86; HR: 1.13 ± 1.89; p=0.063) and AUDIT-10 (HG: 1.60 ± 2.35; HR: 1.65 ± 3.64; p=0.766) scores did not show any significant difference (p>0.05) between respondents of two study groups even after stratification by gender.

Among the listed five, only two alcohol consumption behaviours such as “alcohol-related harm” and “past problems” differed significantly between participants of the two study groups. Among Roma participants, the frequency of alcohol-related harm was significantly higher (13.33%) than in the HG sample (6.20%). After stratification by gender, the frequency of alcohol-related harm also varied significantly between males of HG and HR (p<0.001) females (p=0.001). Among Roma males experience of alcohol-related harm was more than 2 times higher than among HG males (HG: 12.92%, HR: 30.69%), while for females the experience of harm was nearly 7 times higher among HR compared to HG (HG: 0.89%; HR: 6.93%).

Additionally, past problems related to alcohol consumption differed significantly between respondents of the two study populations. It was observed to be 1.71% and 4.95% among respondents of HG and HR, respectively. The study also represents that after stratification, differences in evidence of past problems remained significant between males of HG and HR ($p<0.007$) and females ($p=0.035$) as well. Around 13% of the Roma males reported alcohol-related past problems, while 2.12% of Roma females reported such problems. Furthermore, though none of the HG females experienced past alcohol problems, 2.12% of HR females reported having evidence of past problems. The table also demonstrates that the three listed alcohol consumption behaviours such as problematic alcohol drinking, alcohol intake at hazardous levels and alcohol dependence showed no statistically significant ($p>0.05$) differences between the two study groups (HG versus HR).

Additional descriptive analysis using a cut-off score of AUDIT ≥8 for both men and women as an indicator of hazardous and harmful alcohol intake demonstrated that there was no significant difference (HG: 3.5%; HR: 5.18%; $p>0.05$) in hazardous and harmful alcohol intake between participants of both study groups when AUDIT ≥8 was used as a threshold. Even after stratification by gender, the difference remained insignificant among males and females of HG and HR. The binary logistic regression analysis has also been conducted to elucidate the association between different socioeconomic factors and hazardous and harmful alcohol intake using the AUDIT ≥8 cut-offs for both sexes and the outcome of the analysis exhibited that though gender and the oldest age category showed significant associations with hazardous and harmful alcohol intake, ethnicity and other factors included in the study did not depict any significant associations.

4.2.3 Association of listed socioeconomic variables with various alcohol consumption phenotypes:

Outcomes of univariate and multivariate logistic regression analyses between various listed socioeconomic variables and different alcohol consumption behaviours are illustrated in our study. The study depicts the associations of listed socioeconomic variables (ethnicity, educational level, economic activity, marital status, financial status, age categories, and gender) with different alcohol consumption behaviours (total AUDIT score, problematic drinking, hazardous alcohol intake, alcohol dependence, harms related to alcohol intake and evidence of past problems associated with alcohol consumption). Among different predictor variables, ethnicity showed a statistically significant ($p<0.05$) association with alcohol-related harms and evidence of past problems. The odds of having alcohol-related harms were 3.47 times higher (OR: 3.47; 95% CI:1.61-7.49) among respondents of Hungarian Roma compared to Hungarian general. Similarly, the odds of having evidence of past alcohol problems were 4.09 times higher (OR: 4.09; 95% CI:1.02-16.46) among HR participants than those of HG. Additionally, the marital status of the respondents also postulated a significant association with alcohol intake at the hazardous level. In comparison with married respondents, the odds of having hazardous alcohol intake were 1.57 times higher (OR: 1.57; 95% CI:1.00-2.48) among the individuals who were single. Like marital status, the age of the study population was also significantly associated with alcohol consumption at a hazardous level. It was observed that respondents of the oldest age category (≥50 years of age) had lower odds (OR: 0.55; 95% CI:0.32-0.93) of having alcohol intake at the hazardous level compared to the youngest category. Gender was also significantly associated with all the alcohol consumption behaviours analysed in the study. The odds were lower among females compared to male participants for total AUDIT score (OR: 0.27; 95% CI:0.22-0.33), problematic drinking (OR:0.30; 95% CI:0.16-0.60), hazardous alcohol intake (OR:0.18; 95% CI:0.12-0.26), alcohol dependence (OR:0.11; 95% CI:0.04-0.26), alcohol-related harms (OR:0.14; 95% CI:0.08-0.25) and evidence of past alcohol problems (OR:0.12; 95% CI:0.04-0.32).

4.2.4 Decomposition analysis

The predicted ethnic-specific differences in alcohol-related harms were decomposed by using Blinder Oaxaca decomposition methods for non-linear models. The outcomes of this decomposition analysis demonstrated that the single marital status and gender explained -7.90% and -59.86% of the alcohol-related harm frequency gap, respectively, between HG and HR respondents. These findings indicate that equalization of differences explained by gender and marital status may be expected to reduce the gap of alcohol-related harms between the two study groups by about 8% and 60%, respectively. And the effect of endowment coefficient for marital status was statistically significant ($p<0.05$), while for gender the coefficient effect was highly significant ($p<0.01$). For other socioeconomic variables (education, economic activity, financial status, and age category) the coefficient's effect was not statistically significant ($p>0.05$), which implies that the protective or risk effect of these studied variables is as strong for HG as for HR subjects. Additionally, Roma ethnicity had a significant positive effect (13.32%) on alcohol-related harm frequency. In other words, if there was no ethnicity-specific effect, the outcome gap would be 89.24% lower.

The decomposition analysis could not be done for evidence of past alcohol problems due to low stratum-specific numbers (only 7 respondents identified as having past alcohol problems among HG participants).

4.3 Effect of selected taste preference genetic variants on alcohol intake:

4.3.1 Genotype and allele frequencies of the selected polymorphisms

None of the included SNPs deviated significantly ($p<0.001$) from HWE in either of the two study groups (HG and HR). Genotype and allele frequencies did not differ significantly ($p<0.05$) between HG and HR subjects.

4.3.2 Association analysis of selected genetic polymorphisms with alcohol consumption Phenotypes:

Associations of included genetic polymorphisms with different alcohol consumption phenotypes in study populations are analysed. To evaluate alcohol consumption phenotypes, the first three questions (AUDIT 1, AUDIT 2, and AUDIT 3) of the AUDIT questionnaire were used, where AUDIT 1 and AUDIT 3 provide information about the frequency of drinking and frequency of heavy drinking, respectively. AUDIT 2 assesses the number of standard alcoholic drinks on a typical day. During the association analysis dominant and recessive models were used, where models were defined based on the minor allele frequency of the respective SNPs. Adjustments were made for the potential covariates such as age, gender, and marital status.

It is articulated that except TAS2R38 rs713598, no other selected SNPs showed significant association with any of the alcohol consumption phenotypes of interest in both study groups. Among HG respondents TAS2R38 rs713598 showed a statistically significant association (p=0.028) with AUDIT 2, while in the case of HR participants this variant was significantly (p=0.048) associated with AUDIT 3. The study also reveals that none of the included SNPs depicted a significant association with AUDIT 1 in either of the study groups. Furthermore, from the recessive model analysis, it is observed that TAS2R38 rs713598 (CC or GC vs GG) was significantly associated with AUDIT 2 (Coef: -0.136; p=0.028) and AUDIT 3 (Coef: -0.170; p=0.049) among HG and HR respondents, respectively.

4.4 Relationship of taste preference genetic variants with different drinking behaviours

4.4.1 Findings of literature search

Overall, 293 publications were identified in our search, among them 18 and 125 articles were derived from PubMed and Web of Science, respectively, while the rest (150) were obtained from ProQuest Central. Initially, 26 duplicated publications were removed, and then 229 articles that were unable to meet the inclusion criteria were excluded. The remaining 38 articles were preliminary selected for full-text assessment. After initial assessment 21 articles were eliminated, which led to the availability of the final 17 publications for extensive analysis.

4.4.2 Quality assessment of the included genetic association studies

Among the 17 studies selected for the systematic review, 5 (29.4%) articles were of good quality and the rest 12 (70.6%) were rated as moderate quality.

4.4.3 Effect of taste preference genetic variants on drinking behaviours

The systematic review focused on 43 single nucleotide polymorphisms (SNPs) of 27 different taste preference-related genes. The relationships between different dimensions of alcohol consumption behaviour and TAS2R38 rs713598 (n=10), rs1726866 (n=9), rs10246939 (n=8) followed by TAS2R16 rs846672 (n=4); TAS2R16 rs1308724 (n=3); TAS2R50 rs1376251 (n=3); TAS2R16 rs846664 (n=3); TAS2R19 rs10772420 (n=3); TAS2R20 rs12226920 (n=2); TAS2R8 rs1548803 (n=2); and CA6 (Carbonic Anhydrase 6) rs2274333 (n=2) were analysed by multiple studies. The effects of other included polymorphisms on alcohol intake patterns were examined only by single studies.

DISCUSSION

Globally, harmful alcohol intake is considered a major public health problem. Besides individuals and their families, alcohol addiction also affects the whole community altogether. Harmful use of alcohol is linked to the reduction of production, increase in accidents, violence, and injuries, which ultimately distress the health, social and economic conditions of the community as a whole. Globally, the WHO European Region is recognised as the area of the highest alcohol intake together with highest percentage of poor health and premature death attributable to alcohol intake. In Hungary, consumption of alcohol has declined in recent years, and it was estimated to decline in the future as well in the pre-pandemic era. Though the pre-pandemic decrease in alcohol consumption levels, the prevalence of alcohol use disorders and dependence in Hungary was one of the highest in the world and among the countries of OECD areas, which presumably will be influenced by the COVID-19 pandemic influence on alcohol consumption levels.

The findings of our study demonstrated that 4.25% and 25% of HG participants had problematic drinking (total AUDIT score ≥8 for men and ≥5 for women) and hazardous drinking, respectively, and the percentage was higher among males compared to females for both drinking patterns. A study using a similar methodology was conducted in Australia by O’Brien to examine hazardous alcohol intake among respondents of 14 years or above, where the AUDIT questionnaire was used to assess drinking at hazardous levels (total AUDIT score ≥8). Results of the study indicated that in 2016 around 29.60% of the respondents, irrespective of age and gender had drinking patterns at hazardous levels, while for men it was 14.99%. In our study, only 7.39% of HG males had problematic drinking (total AUDIT score ≥8). In addition, the latest available data regarding alcohol intake exhibited that among the population of 15 years and above recorded alcohol intake was higher in Hungary than in Australia. This lower percentage of HG men with problematic drinking may have resulted from underreporting of drinking behaviours, as unhealthy alcohol drinking is a sensitive issue and in our study information on problematic drinking was collected by the practice nurses. The study of Australia also demonstrated that a higher percentage of males were identified as positive for hazardous drinking compared to females, which is consistent with our study findings depicting that male respondent had higher odds of having alcohol intake at hazardous levels. Another study was conducted in Sweden to compare alcohol consumption between 1997 and 2018, where the AUDIT questionnaire was applied to evaluate harmful alcohol habits and alcohol-related problems. The results of this research illustrated that males were rather characterized by higher drinking than females.

The present study also represented that 81% of HG participants never reported consuming 6 or more alcoholic drinks on one occasion, while 13.90% of them had 6 or more alcoholic drinks on one occasion less than monthly. Similar Hungarian research called “Population National Survey on Addiction Problems in Hungary (NSAPH 2015)” provided comparable information with our study regarding various aspects of alcohol intake of the HG population. Research findings indicated that around 79% of participants never experienced ≥ 6 alcoholic drinks on one occasion, and 14.6% respondents consumed alcohol less than monthly, which is consistent with our study findings. Among HG participants of our study, higher abstinence rates may be due to higher health awareness of the study participants. During the study, data of HG respondents was collected in the GP’s offices, thus, for collection of data an additional visit was required to GPs, which may have indicated high levels of consciousness, compliance, and understanding of various health-related issues. The contrary to NSAPH, our study questionnaire was administered by practice nurses in a face-to-face way, therefore we should note that certain aspects of alcohol intake could have been considered as a potentially sensitive issue by patients attending the GPs’ offices. Furthermore, the present study was conducted in two counties of Northeast Hungary, which counties are a part of the Northern Great Plain, where abstinent rates were the highest in the country. Furthermore, NSAPH gathered information nationwide on alcohol consumption for three years before our research was conducted. Another European study was conducted within the framework of the GENACIS project among nine countries such as Switzerland, Spain, the U.K. Sweden, Finland, the Netherlands, the Czech Republic, Iceland, and Hungary applying the AUDIT tool for describing various aspects of alcohol intake. The study results showed that monthly or more often consumption of ≥ 6 drinks among men and women of Hungary were 35.2% and 9.2%, respectively, which were higher compared to or present study (HG men: 10.56%; HG women: 0.87%).

It was also observed from our study that 12.75% of HG participants had 2 to 3 times alcoholic drinks in a week or more, while for HG men and HG women, it was 24.58% and 3.49%, respectively. Findings of the European study conducted in nine European countries illustrated that consuming 2 or more drinks a week was highest among males (79.4%) and females (55.6%) in Switzerland, while among Hungarian males and females, the percentages were 43.2% and 11.2%, respectively, which are much higher than the findings of the current study. The results of this study were hard to compare with our study findings as age category, time and process of interviews as well as analysis of alcohol-related harms were different between the studies. During this European study data collection was carried out more than one and half decades ago (between 2000-2001) when alcohol intake was higher in Hungary and continued to remain at higher levels till 2006. After 2006 a decreasing trend in alcohol intake was observed among the Hungarian population.

The current study also aimed to compare the alcohol consumption patterns of HG and HR participants. From the study findings, it is observed that there was a significant difference in the frequency of having alcoholic drinks between the respondents of HG and HR, even when analysing the two sexes separately. In comparison with HG, a lower proportion of HR participants had alcoholic drinks 2 to 4 times a month and 2 to 3 times a week or more, while a higher percentage of HR individuals had alcoholic drinks monthly or less compared to HG participants. Additionally, a higher percentage of HR males had alcoholic drinks monthly or less than HG males. On the contrary, compared to HR females, a higher proportion of HG females drank alcohol monthly 2-4 times. Findings obtained from one study of Slovakia revealed Roma women were identified to report less frequent recent drinking than non-Roma women. Additionally, Sudzinová et al. stated that Roma patients of coronary angiography consume alcohol less frequently than non-Roma patients undergoing the same procedure, though after adjustment for several covariates such as educational level, gender and age these differences became statistically insignificant.

The present study also depicted that the number of standard alcoholic drinks consumed varied significantly between females of HG and HR, where 7.0% and 12.1 % of the HG females and HR females consumed 3 to 4 standard alcoholic drinks, respectively. Furthermore, in the case of 5 or more drinks, it was 0.4% for HG females and 4.3% for HR females. Similar findings were obtained from another study in Slovakia stating that there was no significant difference in alcohol drinking (the previous day of data collection) of ≥1 drink and ≥6 drinks ever or once a month between Roma and non-Roma men. While Roma women were identified to report less frequent recent drinking as well as binge alcohol drinking of 6 or more drinks on a single occasion compared to females of the mainstream population.

Our study also demonstrated that ethnicity had a statistically significant association with the experience of alcohol-related harms and evidence of past problems related to alcohol drinking. The odds of having both harms and past problems were higher for Roma respondents. Results from another study demonstrated that among different U.S. ethnic groups, whites and Asians had lower alcohol-related harm than Native Americans, Hispanics, and blacks. It is also observed from another study that in comparison with white, African American, and Hispanic drinkers reported significantly higher social consequences attributable to drinking and the racial gap in alcohol-related problems was the highest among drinkers with little or no heavy drinking. The study also presented that these ethnic-specific differences in alcohol- related problems may be due to racial or ethnic stigma. Additionally, another European study also demonstrated that alcohol-related problems varied differentially with different socioeconomic statuses, where higher harms existed among individuals of low socioeconomic status even though accompanied by lower alcohol consumption.

It is also articulated from the present study that gender had a significant association with all the alcohol consumption behaviours considered during this study. The odds were lower among females compared to male participants for total AUDIT score, problematic drinking, hazardous alcohol intake, alcohol dependence, alcohol-related harms, and evidence of past alcohol problems. One explanation for these lower alcohol intake and subsequent alcohol problems by females may be gender-specific differences in alcohol metabolism. Besides, women from different ethnic communities have to follow specific cultural norms and practices which may have an influence on their drinking habits. Results of the study conducted in 16 European countries revealed that males had significantly higher alcohol intake at hazardous levels compared to females which is in line with our study findings. Another study in the United States also showed that in comparison with women, men drank alcohol more often and more heavily. Our study also illustrated that marital status showed a significant association with alcohol intake at hazardous level. The odds of having hazardous alcohol intake were 1.57 times (OR: 1.57; 95% CI:1.00-2.48) and 1.16 times (OR: 1.16; 95% CI:0.67-2.03) higher among single individuals compared to those who were married and widow, divorced, respectively. Furthermore, Power et.al. demonstrated that divorced and married respondents had the highest and the lowest levels of heavy drinking (women: >20 units/week; men: >35 units/week; 1 unit equals 8 grams of alcohol), respectively, while single participants could be characterized by intermediate heavy drinking. These diverse associations of alcohol consumption patterns may be due to the quality of the marriage/relationship life. Living in a well-functioning relationship contributes to more favourable mental and physical health and happiness, which situation changes negatively if losing the partner. On the other hand, alcohol consumption could be a certain “coping strategy” for some individuals living in problematic relationships, and in these cases, alcohol consumption levels may decrease after divorce.

The present study also demonstrated that age category had a statistically significant association with hazardous level alcohol intake, where the odds of having hazardous alcohol intake was lower among the respondents of the oldest age group. Similar findings were obtained from another two studies, where higher age groups had a lower risk of hazardous alcohol consumption and lower age group respondents scored higher in the AUDIT test. Life experience, prevalence of long-term illness, and overall health condition may be the most important factors for lower hazardous alcohol consumption among the oldest age group respondents of our study. Additionally, an increase in social responsibility with increasing age and a decrease in the ability to metabolize alcohol may also contribute to lower intake at hazardous levels. One study illustrated that among Hungarian respondents of both males and females alcohol intake is influenced by chronic disease conditions. Our study finding is also justified by some earlier European studies presenting that among individuals, heavy drinking declines with increasing age and social responsibilities.

The decomposition analysis of the present study also demonstrated that in the case of alcohol-related harms gender and differences in marital status acted more intensively among respondents of Roma compared to Hungarian general participants. Single marital status and female gender were associated with differences in alcohol-related harm. After equalization of these differences, the alcohol-related harm frequency gaps could be expected to be reduced by 8% and 60% for HG and HR participants, respectively. These gaps in alcohol-related harms may be due to the cultural factors of Roma respondents because in Roma communities single status and being a female are considered as inferior status.

Additionally, taste receptor proteins mediating the oral sensation of taste may also mediate alcohol intake. Differences in receptor function for bitter, sweet, salty, sour, umami, and fat tastes could be the basis for inter-individual variations in taste perception. Changes in the functional properties of these receptor proteins can result from alterations in their genomic sequences, which consequently leads to differences in responsiveness and preference for a specific taste. Thus, genetic variability in the taste perception mechanism might contribute to differences in alcohol consumption. People with increased sensitivity towards bitter-tasting compounds like PTC and PROP have been found to drink less alcohol compared to those with less sensitivity. Individuals with intense responsiveness (supertaster) towards PROP, also experience more irritation and higher bitterness from ethanol compared to less sensitive persons (supertaster) which ultimately decreases alcohol consumption among supertasters. There is a positive association between PROP bitterness and a number of fungiform papillae where non-tasters have fewer taste papillae on the anterior tongue compared to supertasters and thus experience less bitterness and more sweetness sensations from alcohol. Supertasters of sweet drink more alcohol as sweetness elicited by ethanol was found to stimulate neural fibres sensitive to sweetness in gustatory nerves. Furthermore, central mechanisms like opioidergic, serotonergic, and dopaminergic systems activated by ethanol and sweet solutions, potentially contribute to the reward linked to alcohol intake consistent with that of sugar intake.

Results of our study presented that TAS1R3 rs307355, TAS2R19 rs10772420, and CA6 rs2274333 depicted no statistically significant relationships with any phenotypes of our interest. The T alleles of TAS1R3 rs307355 were previously found to decrease sucrose taste sensitivity. This polymorphism may introduce variation in the perception of sweet and alcohol via alteration of gene transcription through a substitution of cytosine to thymine. Though this finding is in line with our study results, since no other research demonstrated associations with alcohol intake. TAS2R19 rs10772420, which was intensively investigated by the literature in relation to bitter taste phenotypes, exhibited no association with alcohol intake and heavy drinker status in previous research. The A allele of TAS2R19 rs10772420 was found to be linked to the more intense perception of quinine and grapefruit juice, which may be resulted from strong linkage disequilibrium (LD) between two polymorphisms such as TAS2R19 and TAS2R31. In our study, we also did not find any association between TAS2R19 rs10772420 and the first three questions of the AUDIT questionnaire. Moreover, results of other studies postulated that individuals with A alleles of CA6 rs2274333 were linked to PROP super tasting. The CA6 rs2274333 was not linked to frequency of alcohol intake and daily intake of alcohol in other studies which corresponds with our findings.

It is articulated from our study that TAS2R38 rs713598 showed a significant association with AUDIT 2 (typical quantity of alcohol drinking) and AUDIT 3 (frequency of heavy drinking) among respondents of HG and HR, respectively. In the haplotypes of TAS2R38 (defined by rs713598, rs1726866, rs10246939) rs713598 (P/A) is placed in the first location, while rs1726866 (A/V) and rs1024693 (V/I) are located in second and third positions, respectively. The dominant haplotype of these three SNPs (PAV; proline–alanine–valine) indicates the taster phenotype and AVI (alanine-valine-isoleucine) homozygotes characterize the non-taster phenotype, while heterozygotes are entitled by intermediary responsiveness towards PROP and

PTC. For signal transduction of bitter taste modality, rs713598 and rs1726866 retain the highest and the weakest effects, respectively, while rs10246939 depicted no quantifiable impact. Contradictory results were derived from other relevant studies. Some research established that carriers of taster genotypes drank less alcohol, though these studies varied extensively in study participants and way of phenotype evaluation, while numerous studies were unable to report the relationship between these SNPs and alcohol consumption behaviours. On the contrary, another study, where the first three AUDIT questions were used to assess alcohol intake demonstrated that the major "C" allele was linked to decreased alcohol intake among head and neck cancer participants. The minor allele-based recessive model analysis in our study indicated that the non-taster GG genotype was negatively correlated with number of standard drinks consumed and the frequency of having six or more drinks per occasion among HG and HR participants, respectively. Similar to our findings, another study presented that taster consumed more alcohol. This study also proposed that other factors may be involved in stimulating alcohol intake among individuals with increased responsiveness to bitterness sensitivity, such as the consumption of wine, which may be linked to an enhanced perception of PROP bitterness. Analogous factors may explain the findings of the present study.

The abovementioned results exhibited ethnicity-specific differences in alcohol intake in some respects. TAS2R38 rs713598 was significantly associated with the number of standard drinks consumed and having six or more drinks on one occasion among HG and HR participants, respectively. This difference in alcohol consumption behaviours between the two study groups could be due to differences in the influence of taste perception and preference on alcohol consumption. Additionally, the taste profile of consumed alcohol may vary among participants of two study populations. Furthermore, ethnic-specific findings were also found in some genetic association studies, even when comprising taste preference genetic variants, which may be resulted from variations in ethnic-specific LD. Thus, the impact of investigated genetic polymorphisms might be weakened or masked by other not yet studied genes being responsible for the occurrence of phenotypes of interest. It may also be assumed that certain alleles act differently in certain populations and research findings also suggest that various alcohol consumption-related phenotypes (frequency and quantity measures, AUD) encompass different genetic backgrounds.

Several limitations need to be considered during the interpretation of the study results. There is a high possibility of underreporting alcohol intake, which is demonstrated by other studies even with the standard structured AUDIT questionnaire. Moreover, the effectiveness of the AUDIT screening tool may vary between ethnic groups and minorities. Results of other studies indicated that compared to mainstream populations, Roma respondents may tend to please the field investigators, which may affect the quality of collected information. Additionally, during our study, AUDIT questions were interviewed in a face-to-face manner and Roma participants are already subject to negative stereotypes, which may manipulate their responses on alcohol in a way that will not be considered negatively by others. Furthermore, the AUDIT questionnaire provides no information on lifelong alcohol use and associated problems, as well as fundamental causes of abstinence. During the present study the Roma population was recruited only from two counties of North-East Hungary, where the majority of Roma individuals inhabit, thus included Roma participants did not represent the whole country's Roma population. Besides, some Roma individuals, who were integrated into the Hungarian population may not be willing to declare themselves as Roma; consequently, the Hungarian reference sample may have also comprised some Roma individuals. It is also important to mention that the proportion of female participants was higher among HR compared to HG which is in line with the previous survey and study conducted on segregated Roma settlements in Hungary and in Slovakia, respectively. The potential reason for the higher proportion of HR female participants is that in our study data was collected during the daytime when the majority of the households' women were at home and males travelled for public work. From 2010 to 2015 the Hungarian government expanded the budget for public works in all municipalities. These works were particularly pertinent for the villages, where the majority of the Roma communities are settled and most of the workers involved in the program are males from Roma communities. Furthermore, the present study did not comprise individuals aged ≥ 65 years as from previous Roma studies it was suggested that people ≥ 65 years of age represent only 3–4% of the total population, which is low to derive reliable inference for this stratum of the population.

To our knowledge, this is the first study that analysed factors potentially influencing several aspects of alcohol consumption behaviours of HG and HR populations applying the AUDIT questionnaire. Although the systematic review on taste preference genetic polymorphisms influencing alcohol drinking behaviours indicated that TAS2R38 rs10246939, rs1726866, rs713598 were mostly investigated, additional research is still recommended to elucidate susceptible and protective genetic factors for alcohol consumption-related phenotypes due to inconclusive findings. Understanding the ethnic-specific differences of genetic and other factors expected to impact alcohol consumption behaviours may facilitate the development of efficient policy and related interventions to address harmful alcohol use.

NEW FINDINGS

1. Though ethnicity did not have an effect on problematic drinking based on total AUDIT scores, alcohol related harm and past problems differed significantly between participants of HG and HR populations. Among Roma, the frequency of alcohol-related harm and experience of past problems were significantly higher compared to the HG sample.
2. For alcohol-related harms, gender and differences in marital status acted more intensively among Roma compared to the Hungarian general population. After equalization of these differences, the alcohol-related harm frequency gaps could be expected to be reduced by 8% and 60% for HG and HR participants, respectively.
3. TAS2R38 rs713598 showed a significant association with AUDIT 2- number of standard drinks on a typical day (Coef: -0.136; p=0.028) and AUDIT 3- frequency of having six or more drinks per occasion (Coef: -0.170; p=0.049) among HG and HR populations, respectively.
4. TAS1R3 rs307355, TAS2R19 rs10772420 and CA6 rs2274333 showed no statistically significant associations in our study populations with any of the alcohol consumption phenotypes investigated.
5. Although the systematic review on taste preference genetic polymorphisms influencing alcohol drinking behaviours indicated that TAS2R38 rs10246939, rs1726866, rs713598 were mostly investigated, additional research is still recommended to elucidate susceptible and protective genetic factors for alcohol consumption-related phenotypes due to inconclusive findings.

SUMMARY

Background: Unhealthy alcohol use is considered a significant public health problem globally, and the burden of mortality and disability related to alcohol intake varies disproportionately among certain populations and ethnic minority groups. Alcohol consumption is a complex human trait, which is influenced by a wide variety of environmental factors and numerous genetic variants including taste preference genetic polymorphisms.

Objective: The present study aimed to characterize and compare alcohol consumption behaviours of Hungarian general (HG) and Hungarian Roma (HR) study participants and to evaluate the effect of potential influencing factors on various alcohol consumption patterns. We also aimed to synthetize evidence of the effect of taste preference-related genetic variants on various drinking behaviours.

Methods: 410 HG and 387 HR respondents of 20-64 years of age were included in our study and the AUDIT questionnaire was used to assess alcohol consumption patterns. Univariate and multivariate logistic regression analyses were performed to elucidate the associations between various socioeconomic variables and different alcohol consumption phenotypes. To identify the taste preference-related genetic polymorphisms associated with various alcohol consumption behaviours, a systematic review was prepared. Based on this review, four single nucleotide polymorphisms (SNPs), TAS1R3 rs307355, TAS2R38 rs713598, TAS2R19 rs10772420 and CA6 rs2274333 linked to bitter and sweet taste preferences, were selected for further analysis.

Results: Compared to HG, Roma participants experienced more alcohol related harms and evidence of past problems related to alcohol intake. When alcohol-related harms were considered, impacts of differences in gender and marital status are much higher among Roma compared to non-Roma. Additionally, TAS2R38 rs713598 had a significant association with AUDIT 2 and AUDIT 3 questions among HG and HR participants, respectively.

Conclusion: Roma ethnicity was demonstrated to influence having experience of alcohol-related harm as well as evidence of past problems. After equalization of differences in gender and marital status among Roma, the alcohol-related harm frequency gaps could be expected to be reduced. We may also presume that genetics influencing bitter taste phenotypes may have an effect on alcohol consumption patterns in our study samples, though it is suggested to interpret the findings with caution.

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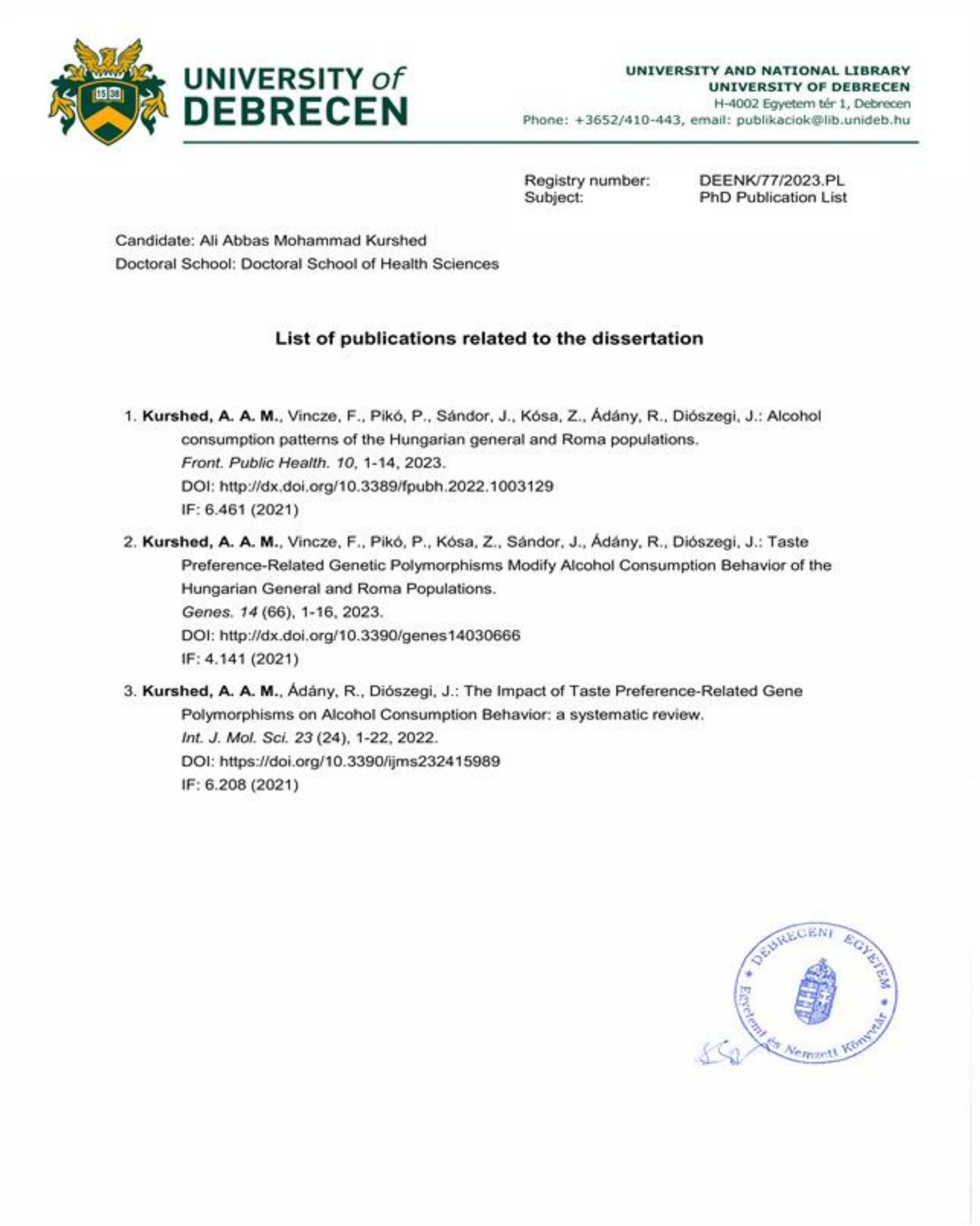
List of Publications



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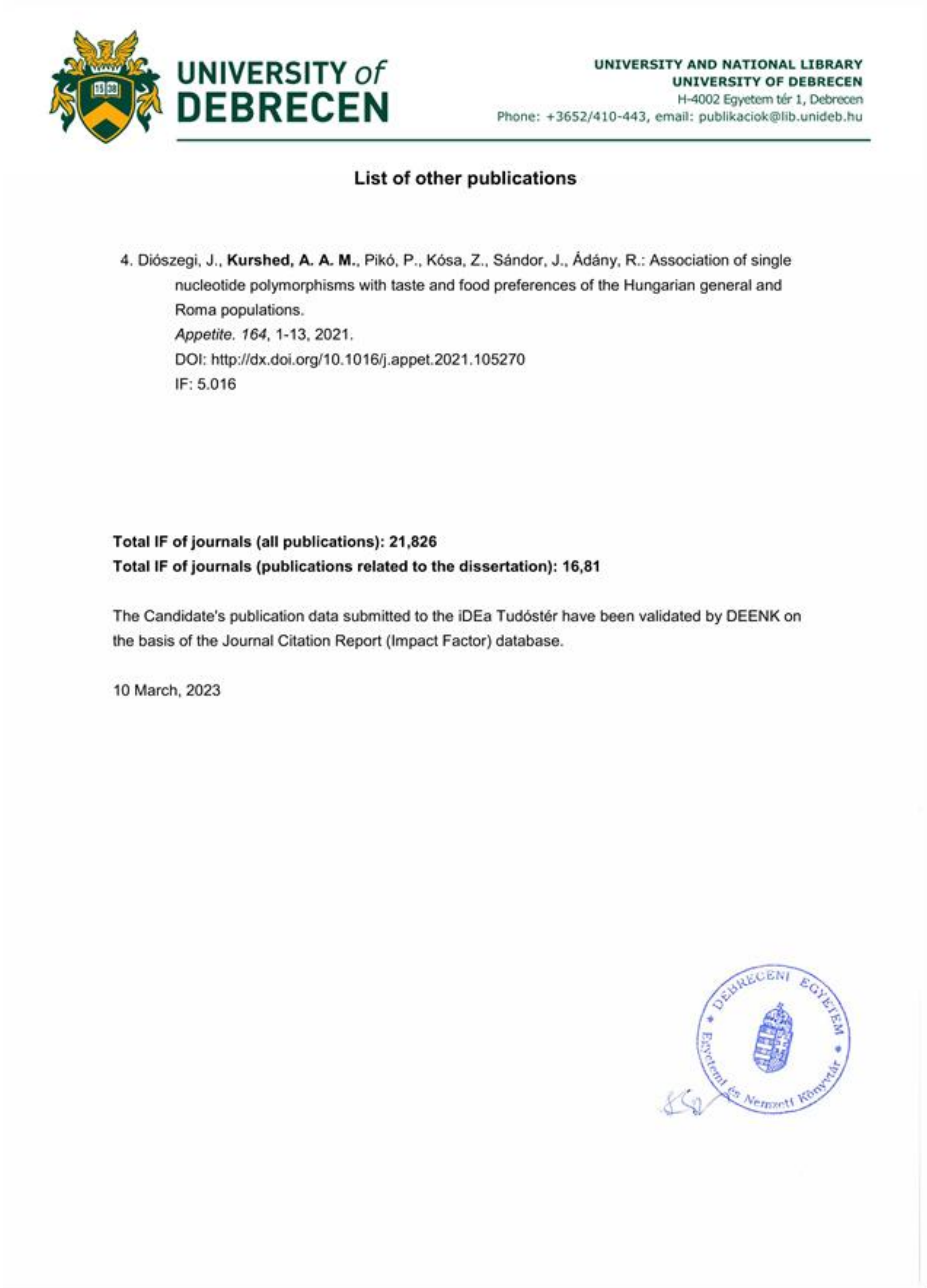
Subject: PhD Publication List

Candidate: Ali Abbas Mohammad Kurshed
Doctoral School: Doctoral School of Health Sciences

List of publications related to the dissertation

1. **Kurshed, A. A. M.**, Vincze, F., Pikó, P., Sándor, J., Kósa, Z., Ádány, R., Diószegi, J.: Alcohol consumption patterns of the Hungarian general and Roma populations.
   Front. Public Health. 10, 1-14, 2023.
   DOI: http://dx.doi.org/10.3389/fpubh.2022.1003129
   IF: 6.461 (2021)
2. **Kurshed, A. A. M.**, Vincze, F., Pikó, P., Kósa, Z., Sándor, J., Ádány, R., Diószegi, J.: Taste Preference-Related Genetic Polymorphisms Modify Alcohol Consumption Behavior of the Hungarian General and Roma Populations.
   Genes. 14 (66), 1-16, 2023.
   DOI: http://dx.doi.org/10.3390/genes14030666
   IF: 4.141 (2021)
3. **Kurshed, A. A. M.**, Ádány, R., Diószegi, J.: The Impact of Taste Preference-Related Gene Polymorphisms on Alcohol Consumption Behavior: a systematic review.
   Int. J. Mol. Sci. 23 (24), 1-22, 2022.
   DOI: https://doi.org/10.3390/ijms232415989
   IF: 6.208 (2021)



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List of other publications

4. Diószegi, J., **Kurshed, A. A. M.**, Pikó, P., Kósa, Z., Sándor, J., Ádány, R.: Association of single nucleotide polymorphisms with taste and food preferences of the Hungarian general and Roma populations.
Appetite. 164, 1-13, 2021.
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Total IF of journals (all publications): 21,826
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The Candidate's publication data submitted to the iDEa Tudóstér have been validated by DEENK on the basis of the Journal Citation Report (Impact Factor) database.

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