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Data Article

Data to genetic risk assessment on high-density cholesterol level associated polymorphisms in Hungarian general and Roma populations



Péter Pikó^{a,b}, Szilvia Fiatal^{b,c}, Zsigmond Kósa^d,
János Sándor^{b,c}, Róza Ádány^{a,b,c,*}

^a MTA-DE Public Health Research Group of the Hungarian Academy of Sciences, Faculty of Public Health, University of Debrecen, Debrecen 4028, Hungary

^b Department of Preventive Medicine, Faculty of Public Health, University of Debrecen, Debrecen 4028, Hungary

^c WHO Collaborating Centre on Vulnerability and Health, Department of Preventive Medicine, Faculty of Public Health, University of Debrecen, Debrecen 4028, Hungary

^d Department of Health Visitor Methodology and Public Health, Faculty of Health, University of Debrecen, Nyíregyháza 4400, Hungary

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ABSTRACT

Data obtained by genotyping single nucleotide polymorphisms (SNPs) related to high-density lipoprotein cholesterol (HDL-C) levels were utilized in Genetic Risk Score [unweighted (GRS) and weighted (wGRS)] computation on Hungarian general and Roma populations. The selection process of the SNPs as well as the results obtained are published in our research article (Piko et al., 2017) [1]. Linkage analyses were performed by study groups. Study populations were stratified by quintiles of weighted Genetic Risk Score. Multivariate linear regression analyses were performed using Genetic Risk Scores and HDL-C levels as dependent variables; and ethnicity, sex and age as independent variables. The study subjects were categorized into quintiles according their wGRS values. Associations of Genetic Risk Scores with plasma HDL-C levels (as a continuous variable) were observed in both populations. Finally, the two populations were merged and analyzed together by multivariate logistic regression where reduced

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* Correspondence to: Kassai út 26., Debrecen 4028, Hungary. Fax: +36 52 512 769.

E-mail address: adany.roza@sph.unideb.hu (R. Ádány).

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plasma HDL-C level was the dependent variable; while ethnicity, age and sex were the independent ones.

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Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Molecular genetics, Public health genomics</i>
Type of data	<i>Figure, Table</i>
How data was acquired	<i>Survey, Blood sample collection, MassARRAY platform (Sequenom Inc., San Diego, CA, USA) with iPLEX Gold chemistry</i>
Data format	<i>Analyzed</i>
Experimental factors	<i>Genomic DNA from peripheral blood was isolated</i>
Experimental features	<i>Genotyping method of SNPs was based on MALDI-TOF (Matrix Assisted Laser Desorption-Ionisation-Time Of Flight) analysis, performed on MassARRAY Platform.</i>
Data source location	<i>Debrecen, Hungary, Latitude: 47.544062, 21° 38' 25'' E & Longitude: 21.64283, 47° 32' 33'' N</i>
Data accessibility	<i>Data are presented in this article; DNA sample and raw data are available for further analyses in collaborative studies</i>

Value of the data

- Several studies describe the health status of the Roma, which constitutes the largest ethnic minority in Europe however studies focusing on their genetic predisposition to common chronic diseases are scarce.
- Genetic background of atherosclerosis among Roma as well as the general Hungarian population can be studied separately or in international cohort.
- Genetic risk score assessment can be further utilized to compare susceptibility to reduced HDL-C level among different population groups.

1. Data

Distribution of SNPs related to HDL-C level were analysed in the Hungarian Roma and general populations and weighted Genetic Risk Scores were defined and used to categorize the population into quintiles.

2. Experimental design, materials and methods

2.1. Subjects

Study involved subjects of samples investigated during recent cross sectional surveys [2,3]. The Roma sample is representative to the Roma population living settlements in North-East Hungary in terms of age and sex and includes 646 individuals (Roma). The “General” sample consisting of 1542

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