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Data Article

Frequencies of alleles, genotypes and haplotypes of two polymorphisms in the clusterin gene in the Russian elderly population categorized by cognitive performance

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ABSTRACT

This article contains data on the frequencies of alleles, genotypes and haplotypes of the single nucleotide polymorphisms (SNPs) rs2279590 and rs1532278 in the CLU gene in a cohort of normal elderly from the Russian population. The SNPs have been reported to be associated with Alzheimer's disease and cognitive functions in genome-wide and candidate genes association studies. Cognitive performance in sample set was estimated by the Montreal Cognitive Assessment (MoCA). The frequencies of alleles, genotypes and haplotypes of two SNPs were calculated in 3 groups: total sample set, sample set with MoCA score less than 21 (the first quartile) and group with MoCA score more than 24 (the fourth quartile).

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Specifications Table

Subject area	Human Genetics
More specific subject area	Genetics of cognitive functions
Type of data	Table and figure
How data was acquired	MALDI/TOF mass spectrometry using Sequenom MassARRAY 4.0 platform (Agena Bioscience™)
Data format	Analyzed
Experimental factors	Genomic DNA was extracted from whole blood samples using phenol–chloroform extraction.
Experimental features	Genotyping of two SNPs was carried out using Sequenom iPLEX Assay following the recommended protocol by the manufacturer (Agena Bioscience™).
Data source location	Tomsk, Russian Federation
Data accessibility	The data is available within this article

Value of the data

- The variation in CLU gene may play a role in genetics of cognition and normal ageing.
- The data on the allele, genotype and haplotype frequencies are an important resource for understanding genetic structure of different populations.
- The frequencies of alleles, genotypes and haplotypes for rs2279590 and rs1532278 in the CLU gene in the Russian population were not previously known.
- The data can be used for comparative genetic studies of neurodegenerative diseases such as Alzheimer's disease, as well as cognitive performance in various populations.

1. Data

The data represent the frequencies of alleles, genotypes and haplotypes for single nucleotide polymorphisms (SNPs) rs2279590 and rs1532278 in human clusterin gene (CLU) associated to Alzheimer's diseases in previously published genome-wide and candidate genes association studies [1–5]. Russian sample set was classified into three groups according to their MoCA scores: all samples, the first quartile (total MoCA ≤ 20), the fourth quartile (total MoCA ≥ 25). The frequencies of alleles and genotypes are presented in Table 1. The description of haplotype and its frequencies are listed in Table 2. The structure of linkage disequilibrium of rs2279590 and rs1532278 in clusterin gene (CLU) is demonstrated in Fig. 1.

2. Experimental design, materials and methods

2.1. Subjects

The study protocol was approved by the Ethics Committee of the Research Institute of Medical Genetics, Tomsk, Russian Federation. Sample of 700 elderly individuals without dementia and neurological diseases (age range 59–89 years, mean age 70.8 years) of Russian descent was randomly selected from a population-based cohort study on primary prevention of Alzheimer's disease in Tomsk, Russia [6,7]. All of the studied individuals were Caucasians from the same ethnic (Russian) and geographical origin, living in the Tomsk region of Russian Federation. Cognitive performance was assessed using the Montreal Cognitive Assessment (MoCA) [8]. MoCA scores ranged between 0–30 points, and higher scores indicate better cognitive function. The data included 3 groups: total sample

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