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Genes and personality characteristics: Possible association of the genetic background with intelligence and decision making in 830 Caucasian Greek subjects

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ABSTRACT

It is well known that intelligence consists of a variety of interactional and cognitive skills and abilities (e.g. tradecraft; critical and divergent thinking; perception of foreign information). Decision making is defined as the conscious choice between given options, relating to a problem. Both genetic background and environment comprise key elements for personality characteristics of the human being. The aim of this study is to determine the frequency distribution of rs324420, rs1800497, rs363050, rs6265, rs1328674 polymorphisms known to be involved in individual personality characteristics, in 830 Greek Subjects. The study is independent from direct clinical measurements (e.g. IQ measurements; physiological tests). The population of the volunteers is described, based on genotype, sex, with the respective gene frequencies, including the Minor Allele Frequency (MAF). A potential influence of the volunteer gender with the above characteristics (based on genotypes and alleles) is examined and finally, volunteers are classified as follows: A volunteer receives +1, for each genotype/allele, which enhances his intelligence or his decision-making. In contrast, he receives −1, for each genotype/allele, which relegates the individual characteristic. No statistically significant gender-characteristics correlation is observed. According to their genetic profile, a rate of 92.5%, of the volunteers may be characterized by prudence and temperance of thought, with

Abbreviations: MAF, Minor Allele Frequency; IQ, Intelligence Quotient; EQ, Emotional Quotient; *FAAH1*, Fatty-Acid Amide Hydrolase 1; *ANKK1*, Ankyrin Repeat and Kinase Associated Containing 1; *SNAP-25*, Synaptosomal-Associated Protein, 25 kDa; *BDNF*, Brain-Derived Neurotrophic Factor; *5-HT2A*, 5-Hydroxytryptamine Receptor 2A; SNAREs, Soluble N-ethylmaleimide-sensitive Factor Attachment Protein REceptors; GPCR, G Protein-Coupled Receptors; EMA, European Medicines Agency.

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only a small proportion of them (7.5%) may be classified as genetically spontaneous and adventurous. Regarding intelligence, the study population may lay around average and a little above it, at a rate of 96.3%, while the edges of the scale suggest only a 0.5% of the volunteers, who, although the "smartest", somehow seem to lack prudence. In conclusion, individuals with low cognitive ability may be more prudent than others and vice versa, while the "smartest" ones tend to be more risky, in decision-making. Therefore, intelligence and decision-making may, after all, be less linked to each other than expected.

Introduction

"Intelligence" is a systematically studied human characteristic. By the viewpoint of Psychology, intelligence consists of a series of interactional and cognitive skills and abilities, such as reasoning, critical and divergent thinking, planning, solving problems, comprehending complex ideas and learning, whether it is quick or experiential. Also intelligence is associated with the ability to observe, collect, and discern meaning from foreign actions; actors and activities.Such parameters determine the degree and structure of intelligence (Gottfredson, 1997) (Greene Sands and Haines, 2013). Today, we are able to estimate certain intellectual human abilities, as the reasonable thought (Intelligence Quotient—IQ) and the sentimental thought (Emotional Quotient-EQ) (Dulewicz and Higgs, 2000).

"Decision-making", is defined as a conscious choice (selection) between given options related to a problem. These can be either initially given or can be the results of cogitative processes, in which intelligence, as well as other characteristics (e.g. spontaneity) are involved. It is comprehensible that both logic and sentiment, along with other individual particularities, determine the pathway of any decision (Kondylis, 1982) (Tryfonas, 2008) (Kreek et al., 2005).

Objective of the present study is to describe the relation between the genetic profile (polymorphisms) and characteristics of personality. The approach of the genetic effect has to be under the prism of an individual, who, as an entity, interacts with his/her environment. Every person has a bidirectional relation with his/her environment, a fact that proposes there be also bidirectional influences. A similar interaction may take place between the gene and an individual. As a result, we assume that the environment might interact with the gene via the individual and vice versa.

A total of 5 polymorphic genes were investigated, including *FAAH1* (fatty-acid amide hydrolase 1), (UniProt: O00519), *ANKK1* (ankyrin repeat and kinase domain containing 1), (GeneCards: GC11P113258), *SNAP-25* (synaptosomal-associated protein, 25 kDa), (UniProt: P60880), *BDNF* (brain-derived neurotrophic factor), (NCBI: 627) and *5-HT2A* (5-hydroxytryptamine receptor 2A), (UniProt: P28223). All these genes are associated with several abilities. SNPs may be responsible and/or may lead to different intelligence and/or decision making.

FAAH1 (fatty-acid amide hydrolase 1)

The *FAAH1* gene encodes an enzyme-hydrolase that degrades a number of bioactive fatty-acid amides, among which are anandamide, oleamide and the endogenous cannabinoid, to their corresponding acids (UniProt: O00519). One of the *FAAH1* gene polymorphisms, registered as rs324420 and known as Pro129Thr, consists in the substitution of a Cytosine (C) (wild type allele), to an Adenine (A) (mutant Allele) (NCBI-dbSNP: 324420). The A allele is associated with an increase of memory (intelligence) (Mazzola et al., 2009) and simultaneously, addiction to substances (Flanagan et al., 2006). The latter is suspected to be a result of spontaneity and risky tendencies (decision-making) (Verdejo-García et al., 2008).

ANKK1 (ankyrin repeat and kinase domain containing 1)

The *ANKK1* gene encodes a protein that belongs to the Serotonin/Threonine protein kinase family, involved in signal transduction pathways. The studied polymorphism is located in exon 8 of *ANKK1* gene and is closely

linked to *DRD2* gene. (GeneCards: GC11P113258). This polymorphism is registered as rs1800497 and known also as Taq1A. The wild type allele, noted as A2, carries a Cytosine (C) nucleotide and the mutant allele, noted as A1, a Thymine (T) one (Lawford et al., 2013). Regarding intelligence, the existence of the mutant allele suggests reduced learning ability (i.e. probabilistic-reversal) (Wong et al., 2012). The mutant type T-allele is also associated with appearance of spontaneous behavior and addiction to substances and alcohol (decision-making) (Esposito-Smythers et al., 2009). Perhaps these phenomena are also result of the close linkage of our gene with its neighboring *DRD2* gene and of the possible interaction between them (McAllister et al., 2008). Specifically, Mc Alister et al. have shown that the T allele is associated with reduced expression of dopaminergic binding sites in the striatum of the brain.

SNAP-25 (synaptosomal-associated protein, 25 kDa)

The *SNAP-25* gene encodes the homonymous SNAP protein that belongs to a family of protein-receptors, known as SNAREs (**S**oluble **N**-ethylmaleimide-sensitive Factor **A**ttachment Protein **RE**ceptors) and has been specifically regarded as member of the t-SNAREs, with major role in the molecular regulation of neurotransmitter release. It may also play an important role in the synaptic function of specific neuronal systems, while it associates with other proteins involved in vesicle docking and membrane fusion (UniProt: P60880). The *SNAP-25* polymorphism studied is registered as rs363050 and has as wild type Guanine (G) allele, or a mutant Adenine (A) one (NCBI-dbSNP: 363050). This particular mutation suggests a slight increase of IQ (intelligence) (Gosso et al., 2006).

BDNF (brain-derived neurotrophic factor)

The *BDNF* gene encodes a protein that is a member of the nerve growth factor family (neurotrophic factors) and an essential factor for the survival of striatal neurons in the brain (NCBI: 627). One of the *BDNF* gene polymorphisms is rs6265, also known as Val66Met. The *BDNF* wild type allele carries a Guanine (G) and the mutant, an Adenine (A) allele (NCBI-dbSNP: 6265). The A allele is linked to a reduction of cerebral operations, regarding cognitive ability, such as learning (intelligence) (McHughen et al., 2010; Savitz et al., 2006) while it is associated with increased introversion (Terracciano et al., 2010), addiction (Su et al., 2011) and suicidal tendencies (decision-making) (Sarchiapone et al., 2008).

5-HT2A (5-hydroxytryptamine receptor 2A)

The *5-HT2A* gene encodes one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, as a hormone, and as a mitogen. The 2A receptors of serotonin belong to the GPCR (G Protein-Coupled Receptors) family (UniProt: P28223). The polymorphism studied, registered as rs1328674, has either a Guanine (G) wild type allele or an Adenine (A) mutant allele (NCBI-dbSNP, 1328674). The A-allele suggests spontaneity behavior in “go/no-go” situations (Nomura et al., 2006), while it is described to be associated with the appearance of psychopathological problems (e.g. nervous bulimia) (decision-making) (Erritzoe et al., 2009).

Materials and methods

A total of 830 individuals volunteered to be included in the study. All volunteers were of Greek origin and reside within Greece. The recruitment of the study subjects was random and only gender and age were documented. During the recruitment period of 6 months 420 men (median age 35 years, range 1–95 years) and 410 women (median age 38 years, range 1–91 years) were included. The latter were calculated in the year of 2013. All volunteers have consented to the use of their genetic information after anonymization, following the EMA (European Medicines Agency) guidelines (EMEA/CPMP/3070/01).

Collection of buccal epithelial cells from the oral cavity of all volunteers by buccal swabs was followed by *DNA* isolation using a commercial *DNA* extraction kit (Promega). Then, the genotype of each individual was identified, for genes *FAAH1*, *ANKK1*, *SNAP-25*, *BDNF* and *5-HT2A* and their respective polymorphisms rs324420, rs1800497, rs363050, rs6265 and rs1328674, with Real Time PCR, by using the LightCycler480 platform (Roche-Diagnostics).

The frequencies of genotypes, as well as alleles, for each polymorphism, were calculated. Those alleles that present more often, according to the literature, were considered as "dominant alleles". This assumption is based on the Minor Allele Frequency (MAF), an index that represents the frequency of the second most-occurring allele for each polymorphism (NCBI-dbSNP, MAF): Accordingly, for *FAAH1* gene the A allele (NCBI-dbSNP: 324420), for *ANKK1* gene the T allele (GeneCards: GC11P113258), for *SNAP-25* gene the A allele (NCBI-dbSNP: 363050), for *BDNF* gene the A allele (NCBI-dbSNP: 6265), and for *5-HT2A* gene the A allele (GeneCards: GC13M047407), represent the recessive alleles.

The MAF for each polymorphism was calculated by using a statistical equation, also presented by Professor Phillip McClean (North Dakota State University) (NDSU). The formula writes as follows:

$$MAF = \frac{Minor\ \ Allele\ \ Count}{Total\ \ Allele\ \ Count}$$

Which, in the case of *FAAH1*, is transmuted in the below form:

$$MAF = \frac{2 \times A:A + C:A}{2 \times (A:A + C:A + C:C)} (\times 100)$$

Contingency 2×2 tables (1 degree of freedom) were constructed (Gender vs. Polymorphisms) and odds ratios — as well as their respective confidence intervals (CI) — were calculated, by using computer software. The statistical control was held at level of significance a = 0.05 (p-value) (Sullivan KM).

In addition, participating volunteers were studied in groups, depending on the combined genotypes/alleles they carry. For this purpose, a "+1" score was given to a volunteer, for each genotype/allele, which, theoretically, enhances his intelligence or his decision-making and a "−1" score was given for each genotype/allele, which relegates the individual characteristic. A polymorphism can have a positive effect for both intelligence and decision making (+1,+1), a negative effect for both intelligence and decision making (−1,−1), a positive effect for intelligence and negative effect for decision making (+1,−1), or, finally, a negative effect for intelligence and positive effect for decision making (−1,+1). As presented in the introduction, intelligence is associated with the polymorphisms of genes *FAAH1*, *ANKK1*, *BDNF* and *SNAP-25*, while decision making is associated with those of genes *FAAH1*, *ANKK1*, *BDNF* and *5-HT2A*. Hence, such a classification of the 830 subjects takes place.

Results

Initially, a general statistical evaluation of the volunteers was held, from which the percentage of occurrence of each homozygous mutant, homozygous wild-type and heterozygous genotype was determined, for each polymorphism separately. Subsequently, the individual frequencies for each gender separately were evaluated. Finally, the MAFs, for each polymorphism, were calculated.

The wild type allele distribution of *FAAH1*, *ANKK1* and *5-HT2A* genes seem to be overrepresented in male subjects. The wild type allele distribution of *BDNF* gene seem to be overrepresented in female subjects, while no difference of the wild type allele frequencies between male and female was observed for the *SNAP-25* gene. The results are presented in tabular form, where the respective calculated MAFs from the literature are also listed (Table 1).

The differences between the two genders are documented in Table 2. Although, concerning genotypes, the odds ratios of male versus female vary between 0.51 and 2.54, the odds ratios of all alleles is around 1.00 (0.88–1.08). The single gene evaluation showed no significant allelic distribution differences between male and female subjects (Table 2).

Meanwhile, scores were calculated for all the volunteers based on the combination of genotypic profiles, for all polymorphisms, according to the criteria mentioned above. The results are compiled in Table 3 for intelligence and in Table 4 for decision making. Most of the 794 volunteers evaluated for the genes involved with intelligence (*FAAH1*, *ANKK1*, *BDNF* and *SNAP-25*) showed a zero score (62.6%). A score of +2 was calculated in 33.7% of the studied population and only 0.5% and 3.2% had scores of +4 and −2, respectively (Table 3). Interestingly, 95.5% of the 796 volunteers evaluated for the genes involved with decision making

Table 1
Description of population, concerning polymorphism, gender, presenting the corresponding percentages, including MAF. [1](NCBI-dbSNP: 324420) [2](GeneCards: GC11P113258) [3](NCBI-dbSNP: 363050) [4](NCBI-dbSNP: 6265) [5](GeneCards: GC13M047407).

Gene/ SNP	Volunteers	Genotype/ Percentage		Genotype/ Percentage		Genotype/ Percentage		Observed MAF Vs. Bibl.
***FAAH1* rs324420**	**all (n = 806)**	**A:A**	2.36%	**C:A**	31.51%	**C:C**	66.13%	18.12%
	male (n = 406)		2.96%		31.77%		65.27%	Vs. 24.8%[1]
	female (n = 400)		1.75%		31.25%		67.00%	
***ANKK1* rs1800497**	**all (n = 822)**	**T:T**	2.19%	**C:T**	27.37%	**C:C**	70.44%	15.88%
	male (n = 420)		3.10%		27.14%		69.76%	Vs. 30%[2]
	female (n = 402)		1.24%		27.61%		71.14%	
***SNAP-25* rs363050**	**all (n = 804)**	**A:A**	34.20%	**G:A**	47.01%	**G:G**	18.78%	57.71%
	male (n = 404)		32.43%		45.79%		21.78%	Vs. 47.3%[3]
	female (n = 400)		36.00%		48.25%		15.75%	
***BDNF* rs6265**	**all (n = 826)**	**A:A**	2.42%	**G:A**	31.84%	**G:G**	65.74%	18.34%
	male (n = 419)		1.67%		34.13%		64.20%	Vs. 22.9%[4]
	female (n = 407)		3.19%		29.48%		67.32%	
***5-HT2A* rs1328674**	**all (n = 828)**	**A:A**	0.85%	**G:A**	11.59%	**G:G**	87.56%	6.65%
	male (n = 420)		1.19%		10.71%		88.10%	Vs. 6%[5]
	female (n = 408)		0.49%		12.50%		87.01%	

(*FAAH1*, *ANKK1*, *BDNF* and *5-HT2A*) showed a +4 score, 7% showed a +2 score and only 0.5% showed a 0 score. No volunteer was found with a negative score for the decision making associated genes (Table 4).

These results were confirmed by calculating the allele combinations. The vast majority of the 2540 intelligence associated alleles (82.2%) show scores between 0 and +4 and only 17.8% fall below 0 (Table 5).

Table 2
Correlation of genes and volunteers gender — odds ratios, confidence intervals and statistical significance (CI, p-value) calculation. Genotypes and alleles are used.

Gene	Frequency	Male	Female	Odd ratio	95% CI	p
***FAAH1* (rs324420)**	***Genotypes* (n = 806)**	**(n = 406)**	**(n = 400)**			
	AA (n = 19)	12	7	1.71	0.67–4.39	0.37
	CC + CA (n = 787)	394	393	0.58	0.23–1.50	
	***Alleles* (n = 1060)**	**(n = 535)**	**(n = 525)**			
	A (n = 273)	141	132	1.07	0.81–1.40	0.70
	C (n = 787)	394	393	0.94	0.71–1.24	
***ANKK1* (rs1800497)**	***Genotypes* (n = 822)**	**Male (n = 420)**	**Female (n = 402)**			
	TT (n = 18)	13	5	2.54	0.90–7.18	0.11
	CC + CT (n = 804)	407	397	0.39	0.14–1.12	
	***Alleles* (n = 1047)**	**Male (n = 534)**	**Female (n = 513)**			
	T (n = 243)	127	116	1.07	0.80–1.42	0.71
	C (n = 804)	407	397	0.94	0.70–1.25	
***SNAP-25*(rs363050)**	***Genotypes* (n = 804)**	**Male (n = 404)**	**Female (n = 400)**			
	AA (n = 275)	131	144	0.85	0.64–1.14	0.32
	GG + GA (n = 529)	273	256	1.17	0.88–1.57	
	***Alleles* (n = 1182)**	**Male (n = 589)**	**Female (n = 593)**			
	A (n = 653)	316	337	0.88	0.70–1.11	0.30
	G (n = 529)	273	256	1.14	0.90–1.43	
***BDNF* (rs6265)**	***Genotype* (n = 826)**	**Male (n = 419)**	**Female (n = 407)**			
	AA (n = 20)	7	13	0.51	0.20–1.30	0.23
	GG + GA (n = 806)	412	394	1.94	0.77–4.92	
	***Alleles* (n = 1089)**	**Male (n = 562)**	**Female (n = 527)**			
	A (n = 283)	150	133	1.08	0.82–1.41	0.63
	G (n = 806)	412	394	0.93	0.71–1.22	
***5-HT2A* (rs1328674)**	***Genotype* (n = 828)**	**Male (n = 420)**	**Female (n = 408)**			
	AA (n = 7)	5	2	2.45	0.47–12.6	0.48
	GG + GA (n = 821)	415	406	0.41	0.08–2.12	
	***Alleles* (n = 924)**	**Male (n = 465)**	**Female (n = 459)**			
	A (n = 103)	50	53	0.92	0.61–1.39	0.78
	G (n = 821)	415	406	1.08	0.72–1.63	

Table 3
Volunteers grouped, according to their score in intelligence. The corresponding percentages are presented. Method of genotypes.

Grades	−4	−2	0	2	4	Total
Population	0	25	497	268	4	794
%	0.0%	3.2%	62.6%	33.7%	0.5%	100.0%

Similarly, allele scoring for the decision making associated alleles (n = 1979) range above 0 (96.5%), as demonstrated in Table 6.

Finally, volunteers were classified for both characteristics, simultaneously. In particular, account taken of all the above, we exported scoreboards, in which the number of volunteers, as well as their score, concerning intelligence and decision-making, are presented lengthwise. The results are compiled in Table 7 for the genotypes and in Table 8 for the alleles. According to the first the majority of the volunteers (60.2%) have scored 0 for intelligence and +4 for decision-making, while many (32.3%) seem to be a little above the average, concerning intelligence and have also scored the maximum for decision-making. All the rest of the candidates (7.5%) have a score of 0 to +2 for decision-making with their intelligence ranging between −2 and +4. Here only a very small portion of the sample (0.5%) seems to be of high intelligence (+4), with their decision-making capability lacking a bit (+2). The second table shows a larger variety of score combinations, as expected, due to the use of alleles and the consequential growth of the sample. However, still most of the volunteers (79.8%) are around +2 to +4, concerning decision-making, with their intelligence varying a bit more, from −2 to +4. The rest (21.2%) are lower on the decision-making scale (−4 to 0) and they also have their intelligence varying, this time from −4 to +4.

Discussion

This study was designed to evaluate the frequency distribution of specific SNPs, known to be involved in decision making and intelligence. The purpose was to develop a quick and accurate test to reveal individual personality characteristics based only on the genotype of gene combinations. Clinical measurements, which would describe intelligence and decision making, were not performed. Accordingly, no confounding factors, such as environmental, socioeconomic, educational or other acquired characteristics were taken into consideration. Also the age of the volunteers is an independent variable and does not interfere with the results.

The results of polymorphism *FAAH1*/rs324420 indicated that 33.87% (Table 1: A:A + C:A) of all volunteers achieve, probably, increased memory (Mazzola et al., 2009), but they also have an elevated tendency in addiction to substances (Flanagan et al., 2006), increase of spontaneity and higher likelihood to show reckless behavior (Verdejo-García et al., 2008). Concerning the *ANKK1*/rs1800497, which appears in 29.56% (Table 1: T:T + C:T) of our Greek volunteers, this polymorphism suggests impaired learning (Wong et al., 2012) as well as spontaneous behavior and an increased likelihood to addiction (Esposito-Smythers et al., 2009). The *SNAP-25*/rs363050 polymorphism, observed in 81.21% (Table 1: A:A + G:A) of all volunteers, is reported to be connected to increased intelligence (Gosso et al., 2006, nd). The *BDNF*/rs6265 polymorphism, measured in 34.26% (Table 1: A:A + G:A) of all volunteers, defines a reduced cognitive ability (McHughen et al., 2010), increased introversion (Terracciano et al., 2010) and addiction (Su et al., 2011), as well as suicidal tendencies (Sarchiapone et al., 2008). Finally, the *5-HT2A*/rs1328674 polymorphism, was found in 12.44% (Table 1: A:A + G:A) of the present study volunteers and is linked to an increase of spontaneity (Nomura et al., 2006). The allele frequencies of all studied polymorphisms in this random Greek population are similar to those of the literature, in regard to MAF and gene distribution. (NCBI-dbSNP: 324420) (GeneCards: GC11P113258) (NCBI-dbSNP: 363050) (NCBI-dbSNP: 6265) (GeneCards: GC13M047407).

Table 4
Volunteers grouped, according to their score in decision making. The corresponding percentages are presented. Method of genotypes.

Grades	−4	−2	0	2	4	Total
Population	0	0	4	56	736	796
%	0.0%	0.0%	0.5%	7.0%	92.5%	100.0%

Table 5
Volunteers grouped, according to their score of intelligence. The corresponding percentages are presented. Method of alleles.

Grades	−4	−2	0	2	4	Total
Population	49	406	1020	891	194	2560
%	1.9%	15.9%	39.8%	34.8%	7.6%	100.0%

In addition, the statistical analysis reveals that most polymorphisms follow a fixed pattern, in which one allele occurs quite more frequently than the other. The only exception is the rs363050 polymorphism of *SNAP-25*, where both alleles are almost equally distributed.

Based on Darwin's "Natural Selection Theory" and the subsequent resulting "Hardy-Weinberg" equilibrium, which follows the Mendelian Inheritance (NFSTC), rare alleles, possibly responsible for nervous system disorders (not addressed in this study) may occasionally increase human morbidity or even mortality and, especially when homozygous gradually lead to allele extinction. This would explain the allele frequencies of the rs363050 polymorphism, which is probably less pathogen and thus, both wild-type and mutated allele appear equally frequent.

The results obtained regarding the possible association between the polymorphisms and the gender of our volunteers, are statistically insignificant, however, practically very important. It should not be ignored, that the two genders clearly differ in many biological systems (e.g. hormones) and they also differ in the way and extent they interact with their environment (Wood and Eagly, 2012) (Becker and Hu, 2008).

In the present study numerous other factors may, however, be involved that affect the outcome. It has to be considered that all genes evaluated in this study are located on autosomal chromosomes and not on the sex chromosomes. At the same time, a larger sample of volunteers needs to be studied, possibly by evaluating their whole genome in order to elucidate possible interactions between other gene polymorphisms, not included in this study. In parallel with other clinical data (e.g. psychometric), expression and epigenetic studies should be conducted to verify genetic results.

A number of publications do not find any differences between the two genders regarding "intelligence" but many others agree that women seem to have better artistic and verbal reasoning skills, while men excel at abstract thinking and problem solving (Sánchez and Vilain, 2010). Similarly, the cause of addictive behavior is not attributed, by scientists, to gender, but rather to individual genes (Perkins et al., 2008). These data are in agreement to the results, of this study showing, no overall but very specific differences between male and female volunteers.

In contrast, regarding "decision making", the opinion of the scientific community is divergent. Taking in account a simple example of decisions making such as the choice between short-term and long-term gain in gambling, some scientists do find differences between the two genders and some others do not. There are also some scientists who believe that differences, if any, may be due to different strategies that male and female follow (Brabec et al., 2012) (Buelow and Suhrb, 2013) (Weller et al., 2010) (Van den Bos et al., 2013). The list of speculation is long indicating that ultimately the issue of decision-making is not easy to study. The results differ, depending on the specific approach or strategy of each scientist to the matter.

In the present study, 62.6% (for genotypes) and 39.8% (for the alleles) of the population score at the zero/neutral point on the intelligence scale, which constitutes the baseline of intelligence. Beyond this baseline, the population intelligence scores rank between −4 and +4 (−4, −2, 0, +2, +4). There are some subjects with scores, just a little above or below the average but very few achieve very high or very low scores. Nevertheless, the population of this study revealed more individuals with high to very high scores than individuals with low to very low scores (genotypes: 34.2% high vs. 3.2% low, alleles: 42.4% high vs. 17.8% low).

Regarding the decision making genetic profile, the majority of the study population volunteers (genotypes: 99.5%, alleles: 79.3%) was rated as "wise", while only a very small number of individuals, were rated

Table 6
Volunteers grouped, according to their score in decision making. The corresponding percentages are presented. Method of alleles.

Grades	−4	−2	0	2	4	Total
Population	6	63	340	834	736	1979
%	0.3%	3.2%	17.2%	42.1%	37.2%	100.0%

Table 7
Volunteers grouped according to their combined scores for intelligence and decision making by the genotype method.

Population	%	Grades: intelligence	Grades: decision making
1	0.1%	2	0
3	0.4%	0	0
4	0.5%	4	2
11	1.4%	2	2
16	2.0%	0	2
25	3.2%	−2	2
256	32.3%	2	4
477	60.2%	0	4

as "spontaneous and daring" (genotype: 0.1%, alleles: 3.5%), placing the study population among those individuals that, in general, prefer more cautious or conservative decisions.

Generally, we observe that the majority of the study volunteers (genotypes: 95.9%, 62.1% alleles) lies around an average level of intelligence and is characterized by sobriety in making decisions. Spontaneity and riskiness coexists rather with the low intelligence (genotype: 3.2%, alleles: 17.6%), while a minority of volunteers (genotype: 0.5%, alleles: 7.8%), were evaluated as the smartest and were lacking in prudence. This fact can be attributed, according to the present study, to the dual nature of polymorphism rs324420/*FAAH1*, as the A allele leads to an increased memory and simultaneously to an increased riskiness, spontaneity and addiction to addictive substances. This associated with the endogenous cannabinoids (e.g. anantamide) (UniProt: O00519) (Mazzola et al., 2009) gene has been proven to increase nerve function, in case of sub functioning or inhibition.

In any case, high intelligence involves multifactorial thinking, which does not necessary include rational or risky decisions, providing usually beneficial decisions. Spontaneity and riskiness involved in the thinking process should not be confused with the decision outcome. Consequently, most people (genotypes: 95.9%, alleles: 62.1%) think logically, but their "average" intelligence often prevents them from choosing the most useful option. A small proportion of the volunteers (genotypes: 3.2%, alleles: 17.6%) is characterized as irrational and their lower to moderate intelligence supports a less considerate decision making. On the other hand, a few individuals, representing highly intelligent people (genotype: 0.5%, alleles: 7.8%), tend to be somehow risky, complicating their beneficial decision making. Probably, although they can fully appreciate the dangers of a risky decision, their high intelligence leads them to attempt novel trails.

Table 8
Volunteers grouped according to their combined scores for intelligence and decision making by the allele method.

Population	%	Grades: Intelligence	Grades: Decision Making
1	0.0%	−2	−4
5	0.2%	0	−4
6	0.2%	−4	−2
20	0.7%	2	−2
28	1.0%	−2	−2
30	1.1%	0	−2
30	1.1%	4	0
48	1.7%	−4	0
106	3.7%	−2	0
142	5.0%	2	0
161	5.6%	0	0
191	6.7%	4	2
241	8.4%	2	2
313	11.0%	−2	2
463	16.2%	0	2
477	16.7%	0	4
595	20.8%	2	4

Further studies, which combine genetic and psychometric tests, could be conducted in order to include factors affecting both intelligence and decision making, such as social, economical, environmental, educational and other ones.

Conclusion

Intelligence and decision making, alongside with many other personality characteristics have been recently associated with the genetic background and all the relevant studies are highly controversial. However, in a society of abundance and bliss, where material and intellectual goods are lavishly supplied, the knowledge of the genetic basis for intelligence and decision-making may be important. Even more important seems to be in societies lacking these benefits, because the expression of these characteristics is often not evident.

Our data agrees with the literature suggesting that intelligence and decision making are not so closely linked to each other. We observed people with low intelligence (cognitive ability) to be more prudent than others and vice versa. In fact, the theoretically "smartest" people in this study tend to be genetically more risky, in decision-making. This paradox is attributed to the *FAAH1* polymorphism's dual nature. So, while high intelligence leads a person's way of thinking to be more logical, yet also complex, there are those who have a genetic tendency to be more impulsive and risky, regardless of their cognitive ability.

Genetic testing may predict a persons' genetic predisposition to be intelligent or to have the ability to take decisions without being aware of any other possible confounding environmental, cultural, socioeconomic or educational factors. This may present an additional diagnostic tool for clinicians in order to better evaluate or interpret their patients' behavior.

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