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Interleukin-1β (rs1143634) polymorphism and adiposity traits in *Quilombolas*

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ABSTRACT

Background: Recent studies have shown a relationship between adiposity traits and a low-grade inflammation of adipose tissue resulting from chronic activation of the innate immune system as interleukin-1 beta (IL-1β). However, this association remains controversial. Besides, the *Quilombola* communities that have presumed different genetic background and it could change the obesity vulnerability.
Objective: To estimate the association between IL-1β and adiposity traits like obesity or abdominal obesity in *Quilombola* communities. A cross-sectional population-based study was conducted the northern region of Minas Gerais with the representative sample of 756 individuals aged ≥ 18 years. The swab oral was used for DNA extraction and the IL-1β rs1143634 polymorphism was evaluated by RFLP-PCR. The interviewed and measures were done using specific protocols. It was estimated to outcomes: the overweight (body mass index ≥ 25 kg/m^2), abdominal obesity (waist circumference ≥ 88 cm for women and ≥ 102 cm for men), and the high conicity index (≥ 1.18 cm or women e ≥ 1.25 cm for men). Poisson regression multivariate models were constructed considering genotype and the outcomes, adjusted for socioeconomic and lifestyle variables.
Results: The distribution of IL-1β for the TT genotype was (11.9%), CT (25.1%) and CC (63.0%). The women TT carriers showed a higher regular soft drink consumption (p = 0.048). The height was lower in man TT carriers (p = 0.041) and lower weight (p = 0.025). The CT genotype showed higher BMI (p = 0.037). The CT and TT carriers showed less prevalence ratio to abdominal obesity even adjusted to socioeconomic and lifestyle variables, there no associations between genotype and overweight or high conicity index.
Conclusions: In conclusion, after socioeconomic and lifestyle adjustment T variant of rs1143634 is a protection factor for central obesity in *Quilombola* communities.

1. Introduction

Obesity is a public health problem with multifactorial causalities involving genetic, biological, economic, social, cultural and political questions (Farzadfar et al., 2011; Koebnick et al., 2012; Wanderley and Ferreira, 2010). The consequences of obesity depend not only on excess fat but also its body distribution, (Prevention, 2007) in particular with the abdominal fat (Popkin et al., 2012) that is mainly associated with diseases chronic such as hypertension (Kochergin et al., 2014; Oliveira et al., 2014) and diabetes (Soares and Barreto, 2015).

Certain populations are more affected by overweight, including African-American and Hispanic adults and people living marginalized or segregated ethnically more urban communities (Popkin et al., 2012; Prevention, 2007). Brazil is considered one of the countries with the

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largest African-population outside Africa, with about 1500 recognized "*Quilombolas*" communities and 33 of these are located in the northern state of Minas Gerais distributed in 20 small cities (Oliveira et al., 2014).

Regarding ethnic inequalities, the vulnerable condition of the *Quilombolas* it is a historical process of slavery after the abolitionism. Even though this free state by the Federal Constitution since 1988, the *Quilombolas* suffer from a poor health and social conditions (Kochergin et al., 2014).

The genetic and social risk factors to obesity could explain the high frequency of nutritional disorders, with 31.8% of overweight and 10.2% of obesity (Soares and Barreto, 2015). Studies involving genetic and environmental factors are important to elucidate possible associations and metabolic pathways for chronic diseases such as obesity because genetic variations could be responsible for the phenotypic variation found in populations (Speicher and Antonarakis, 2010) and interact with environmental risk factors (Blackett and Sanghera, 2013; de Oliveira et al., 2008; Pilia et al., 2006; Xu et al., 2013). It is important to develop studies in this population because there is rare information about these communities, particularly regarding health (Oliveira et al., 2015) or genetic topics.

The adipose tissue has an endocrine, metabolic role and releases several cytokines such as the interleukin 1 (IL-1) one of the most known as a regulator of the highly synthesized energy homeostasis in adipocytes, are strongly involved in pro response -inflammatory and pro-atherogenic (Girn et al., 2007; Guimaraes et al., 2007; Zeybek et al., 2011).

IL-1 β gene has different polymorphisms that occur in the promoter region of the gene and a transcriptional region. The transcriptional polymorphism is located at nucleotide + 3953 through cytosine substitution of thymine (C → T). This change appears to modify the production of mature IL-1β and thus associated with gastric changes, cardiovascular diseases, and body fat mass (Farshad et al., 2010; Strandberg et al., 2006; Zeybek et al., 2011).

Considering there are not studies about this polymorphism in a *Quilombola* communities for our knowledge and their genetic and environmental vulnerability to obesity, the present study aims to investigate the association between the polymorphic variant of rs1143634 polymorphism Interleukin-1β gene with adiposity traits and estimate the associations between this polymorphism and the distribution of body fat in *Quilombolas* communities in North of Minas Gerais, Brazil.

2. Materials and methods

2.1. Design, sampling, and ethical aspects

A cross-sectional population-based study was conducted the northern region of Minas Gerais. This area is distributed in many cities in which about 40% of the *Quilombolas* population of that state. So, it is considered the Brazilian Southeast region that concentrates more *Quilombolas* rural communities. There are 33 communities spread across 20 different municipalities. The target population was defined as people aged 18 years or older at the time of the survey.

In this sense, the representative sample calculation was conducted using sampling model by conglomerates. The prevalence of the studied event was 50% considering a conservative value, which provides the largest element in the sample number, the confidence level was 95% and the sampling error assumed was 5%. The value was multiplied by a design correction effect (*deff*) 1.5. Thus, the minimum sample size estimated for this study was 756 individuals.

The probability sampling occurred in two stages, initially, communities were selected randomly; wherein each community was elected a reference point so that the households were visited. Each household was randomLy selected a single adult individual to participate in the study, including those that were not being addressed at another time if it were the case. The data were collected during the year 2013, the residence of the respondent. The interviews were conducted by trained professionals.

The local leaders were called to support and mediate the access *Quilombolas* communities. All participants were instructed about the research objectives and signed the free and informed consent. The study was approved by the Ethics Committee of the Universidade Estadual de Montes Claros (UNIMONTES) by protocol CAAE 04337412.8.0000.5146.

2.2. Interviews and measures

The data collection instruments were adapted from the questionnaire proposed by the national survey "Surveillance System for Risk and Protective Factors for Chronic Diseases by Telephone Survey – VIGITEL." (Saúde, 2013). Sociodemographic and economic data was collected such as age, gender, the color of skin self-reported, marital status, education and family income. Other factors were also investigated as smoking, binge drinking and food consumption (Moura Souza et al., 2011; Silva et al., 2014). The regular consumption of red meat with fat and/or chicken with skin was considered when the intake of red meat is always with visible fat or always chicken with skin. The regular soft drink consumption and regular consumption of fruits were taken into consideration when equal or > 3 times a week.

Anthropometric measures were performed according to World Health Organization (WHO, 1995). To weight was used a calibrated portable scale with a precision of 100 g and maximum to 200 kg. The height was measured with a stadiometer with an accuracy of 0.1 cm. The body mass index (BMI) was estimated and the individuals classified with cutoffs of < 18.5 kg/m^2 (underweight), 18.5–24.9 kg/m^2 (normal weight), from 25 to 29.9 kg/m^2 (overweight) and ≥ 30 kg/m^2 (obesity). The excess of weight was considered by the sum of overweight and obesity. Waist circumference (WC) was measured with inextensible tape (accuracy of 1 mm) at the midpoint between the edge of the last rib and the iliac crest with the participant in a standing position. The cutoff for high WC (central obesity) was WC ≥ 102 cm for men, and WC ≥ 88 cm for women The conicity index (CI) was determined using height, weight and waist circumference, considered abdominal obesity when ≥ 1.25 for men and ≥ 1.18 for women (Hoffstedt et al., 2000). All anthropometric measurements followed the classically recommended procedures were performed in duplicate and considered the arithmetic average.

2.3. DNA extraction and genetic analysis

The genetic material was collected from swab oral, and it immersed in sterile 2 mLmicrocentrifuge tubes containing 1.500 mL of Krebs buffer (NaCl 20% KCl 2% $CaCl_2$,2%, 2% H_2O, $MgSO_4$, KH_2PO_4, $C_6H_{12}O_6$). The samples were isolated using silica method (Guimaraes et al., 2006) and stored in Bank of Human Biological Materials of North of Minas Gerais (Institutional Biobank-UNIMONTES/CONEP Registration: B-013).

So, the material was washed to remove impurities and eluted in TE buffer as described in a previous study (Guimaraes et al., 2007). The Single Nucleotide Polymorphism - SNP (T > C; rs1143634) was evaluated by Restriction Fragment Length Polymorphism (PCR-RFLP). The polymerase chain reaction (PCR) for the Interleukin receptor gene – beta-1 was performed on 500 ng genomic DNA, 5 μM of each primer (F: 5′CTCAGGTGTCCTCGAAGAAATCAAA-3′; A: 5′GCTTTTTTGCTGTGAGTCCCG-3′; 194 bp) 2.5 μL dNTP mix (25 mM each; Amersham Biosciences®, Pittsburgh, PA, USA), 2.5 μL of 10 × PCR buffer, 1.25 mL of magnesium chloride (50 mM) and 2.5 U DNA polymerase Taq polymerase (Invitrogen Life Technologies®, Carlsbad, CA, USA).

The amplification conditions were 95 °C for 5′ followed by 35 cycles of 95 °C for 1′, 56 °C for 1′ and 72 °C for 1′, and finally 72 °C for 10′. The PCR product (194 bp) was digested with restriction endonuclease

(TaqI) (Fermentas Life Sciences®, Vilnius, LTU) that recognizes the restriction site (T/C; C/T). Ten microliter of the amplified DNA was digested with 1.0 U of Taq I - Phoneutria® (Pht) for 16 h at 37 °C. The PCR and restriction reactions were performed in a thermocycler (Eppendorf AG®, Hamburg, Germany). PCR products were visualized by gel electrophoresis in 15% acrylamide stained with silver. Positive control was used in each reaction of enzymatic digestion. After that, the DNA fragments were separated using polyacrylamide gel electrophoresis to 6.5%, a gel of 1% agarose and silver staining and photographed. The C allele was cleaved by the enzyme into two fragments, one of 97 bp and 85 bp other (CC). The haplotype CT is composed of three fragments: 182, 97, and 12 bp. The A allele is not cleaved by the enzyme and therefore generated a fragment of 182 bp (TT).

Lastly, the present study was performed with 756 subjects, and we perform the genotyping in 708 that have enough genetic material to DNA analysis. Because this study is a population-based study, the results could be different depending on the type of data.

2.4. Statistical analysis

Descriptive analyses with calculations Of the proportions and prevalence of the socioeconomic, lifestyle, adiposity variables and genotype of rs1143634 polymorphism were performed and the associations estimated by Chi-square test of Pearson or Fisher exact considering p-value < 0.05 with 95% of confidence interval.

The Poisson regression was used to the univariate and multivariate models estimating the prevalence ratio (PR) with robust variance estimator. This regression is suggested because it is a cross-sectional study whose the primary outcome studied is frequent (Barros and Hirakata, 2003).

To perform the models, the overweight by (BMI $\geq 25\ kg/m^2$) and abdominal obesity by high waist circumference and conicity index (WC, CI) were considered dependent variables (WHO, 2003, 1995). The independent variables were: genotype like primary exposure (Carter et al., 2008; Juge-Aubry et al., 2004; Lackland et al., 2014; Strandberg et al., 2006; Suzuki et al., 2009) and covariates skin color, sex, age, marital status, family income, education, smoking, alcohol and food consumption (Barros et al., 2007; Pessoa et al., 2015; Popkin et al., 2012; Kopelman, 2000; Moura Souza et al., 2011; Pessoa et al., 2015; Saúde, 2013). The interactions between the genotype and sociodemographic or lifestyle variables were tested by Mantel-Haenszel test.

3. Results

Initially, the present study included 756 people, mainly female (64.2%), married (65.7%) and aged 30 to 39 years (65.7%). The distribution of IL-1β for the TT genotype was (11.9%,n = 84), CT (25.1%,n = 178) and CC (62.9%,n = 446). The most of the sociodemographic characteristics and lifestyle habits were not associated with genotype categories (Table 1). The CC carries women were more frequently married (p = 0.024) and showed a high regular consumption of soft drink consumption (p = 0.048). The women also showed a higher weight and BMI with the CT genotype. The man TT carries showed lower height (p = 0.041).

When these factors were analysed by obesity traits and sex (Table 2), the income, schooling, and smoking were associated with overweight in man. Besides that, the age and income were associated with high abdominal obesity (WC and IC) in women. Lastly, the marital status was associated with overweight and schooling with waist circumference in women.

In data in Table 3 shows there were not associations the variant rs1143634 polymorphism of interleukin-1β gene and overweight and conicity index. To high conicity index, there were significant interactions between soda consumption and genotype. On the other way, the CT and TT genotype showed 40% and 70% approximately lower prevalence of abdominal obesity even adjusted.

4. Discussion

In the present study was shown that the frequency of the IL1-β (rs11143634) polymorphism was 11.9% TT, 25.1% CT, and 63% CC until then not known in *Quilombolas* communities. Besides this, women T carriers showed a lower frequency of soda consumption and the CC or CT showed a higher weight and body mass index. To understand better the relations among the third variables, the Poisson regression was done, and even after adjustments, the T carriers were a lower prevalence of abdominal when compare with CC carriers.

Obesity has been discussing of various public policies, even because is associated with other chronic diseases, including cardiovascular, diabetes and cancer (Farzadfar et al., 2011; Koebnick et al., 2012). Intense efforts have been made to investigate the relation between genetic and obesity. Adipose tissue is an important endocrine organ that releases several cytokines involved in the etiology of obesity (Yu et al., 2012).

The increase in adipose tissue in obese individuals can be related to the growing production of IL-1 beta (Juge-Aubry et al., 2004). T genotype had a fourfold increase in the IL-1 levels when compare o C allele. (Pociot et al., 1992). This found is inverse with the results in the present study that no observed association with obesity by body mass index. Moreover, the IL-1 is produced by many cells such as macrophages, monocytes, epithelial-endothelial and glial cells (Tocci, 1997). Although the IL-1 could positively modulate the immune systen, this cytokine family is considered pro-inflammatory (Farshad et al., 2010; Zeybek et al., 2011) and these mechanisms are related to obesity (Ruf and Samad, 2015).

Regarding the genotypes, the T allele has a low frequency in populations, been considered the rarer allele (El-Omar et al., 2000; Hulkkonen et al., 2000; Takamatsu et al., 2000). In contrast, the allele C has a high rate in many Caucasian populations (Suzuki et al., 2009). In these studies, the genotypes range from 51.5 to 56.4% CC, 36.8% to 41% CT and 6.8 to 7.5% TT in Polish and Finnish (El-Omar et al., 2000; Hulkkonen et al., 2000). In Asiatic populations (Japanese) the T allele tends to zero (92.2% CC and 7.8% CT) (Takamatsu et al., 2000). CC genotype had a higher prevalence in obese subjects, and the T allele had a low frequency in the Brazilian population (Manica-Cattani et al., 2010). Strandberg et al. (2006) showed that carriers of the T variant (CT and TT) of the 3953 C to T IL-1gene polymorphism had significantly lower total fat mass and also significantly reduced arm, leg, and trunk fat, compared with CC individuals in 1068 young men. On the other hand, the same group in 2008 showed that rs1143634 polymorphism was not associated with a total fat mass in 3014 elderly men (Strandberg et al., 2008, 2006). The variation in the frequency in literature includes the frequencies found in this present study.

In another study with 181 Taemin female subjects, the frequency of IL-1β T allele was apparently decreased in the overweight group compared with the lean group with a BMI $< 25\ kg/m^2$ (P = 0.007, OR = 0.152) (Lee et al., 2008). However, many studies suggest that the rs1143634 polymorphism influences the obesity (Manica-Cattani et al., 2010; Song et al., 2008; Strandberg et al., 2008; Suzuki et al., 2009).

On the other hand, Carter et al. (2008) evaluated 556 subjects with a coronary heart disease population and the TT homozygous at either SNP had larger waist circumference compared with major CC homozygotes (Carter et al., 2008). The findings suggested that IL1-β may be involved with increased central obesity, wherein the genetic influence is more evident in patients with high levels of obesity (Carter et al., 2008).

In this sense, it was observed that high body fat and high BMI in TT carriers then CC genotype (P for trend = 0.037) in men and women, respectively (Suzuki et al., 2009). In the present study was not found an association between the polymorphic variant of rs1143634 of interleukin-1β gene and overweight and high conicity index.

This differences found between the previous studies is probably because of the firstly, the differences in populations, for example, in the

Table 1
Sociodemographic characteristics and lifestyle habits by genotype categories in *Quilombolas* in the north of Minas Gerais. 2013.

Variables	Total (756)	Male % (n)				Female % (n)			
		CC (59%; n = 148)	CT (28.3%; n = 71)	TT (12.7%; n = 32)	p-valor[a]	CC (65.2%; n = 298)	CT (23.4%; n = 107)	TT (11.4%; n = 52)	p-valor[a]
Skin color/ethnicity									
Caucasian. Asiatic. *Pardos*. Indigenous	35.8 (271)	70.3 (26)	21.6 (8)	8.1 (3)	0.308	61 (47)	26 (20)	13 (10)	0.699
African-descendents	64.2 (485)	57 (122)	29.4 (63)	13.6 (29)		66.1 (251)	22.9 (87)	11.1 (42)	
Age group (years)									
18–19	3.4 (26)	72.7 (8)	27.3 (3)	0 (0)	0.651	53.3 (8)	26.7 (4)	20 (3)	0.740
20–29	24.6 (186)	58.9 (33)	30.4 (17)	10.7 (6)		63.2 (72)	25.4 (29)	11.4 (13)	
30–39	29.4 (222)	55.1 (38)	31.9 (22)	13 (9)		65 (93)	22.4 (32)	12.6 (18)	
40–49	24.3 (184)	51.8 (29)	28.6 (16)	19.6 (11)		64.9 (74)	21.9 (25)	13.2 (15)	
50–59	11.1 (84)	72.7 (24)	18.2 (6)	9.1 (3)		75 (36)	20.8 (10)	4.2 (2)	
≥ 60	7.1 (54)	61.5 (16)	26.9 (7)	11.5 (3)		65.2 (15)	30.4 (7)	4.3 (1)	
Marital status									
Single/widower	34.25 (259)	59 (148)	28.3 (71)	12.7 (32)	0.966	69.9 (109)	24.4 (38)	5.8 (9)	0.024
Married/consensual	65.7 (497)	69.9 (109)	24.4 (38)	5.8 (9)		62.8 (189)	22.9 (69)	14.3 (43)	
Schooling (years)									
Illiterate	21.7 (164)	62.5 (40)	32.8 (21)	4.7 (3)	0.330	71.3 (62)	17.2 (15)	11.5 (10)	0.257
1–4	21.4 (162)	53.4 (39)	27.4 (20)	19.2 (14)		66.7 (71.3)	19.2 (17.2)	14.1 (11.5)	
5–8	29.9 (226)	60.3 (44)	26 (19)	13.7 (10)		64.7 (66.7)	22.3 (19.2)	12.9 (14.1)	
≥ 9	27.0 (204)	61 (25)	26.8 (11)	12.2 (5)		61.4 (94)	30.1 (46)	8.5 (13)	
Income (Minimum wage)[b]									
< 0.5	23.3 (176)	68.6 (70)	21.6 (22)	9.8 (10)	0.095	66.9 (81)	20.7 (25)	12.4 (15)	0.928
≥ 0.5–1	44.4 (336)	59 (148)	28.3 (71)	12.7 (32)		65 (134)	23.8 (49)	11.2 (23)	
≥ 1	32.2 (244)	66.9 (81)	20.7 (25)	12.4 (15)		63.8 (83)	25.4 (33)	10.8 (14)	
Smoking									
Never smoke	59.9 (453)	60.8 (62)	26.5 (27)	12.7 (13)	0.811	62.2 (209)	26.2 (88)	11.6 (39)	0.065
Ex-smoker	16.1 (122)	59 (148)	28.3 (71)	12.7 (32)		76.4 (42)	18.2 (10)	5.5 (3)	
Smoker	23.9 (181)	62.2 (209)	26.2 (88)	11.6 (39)		71.2 (47)	13.6 (9)	15.2 (10)	
Alcohol consumption[c]									
Yes	31.6 (239)	58.2 (78)	27.6 (37)	14.2 (19)	0.765	63.3 (241)	23.3 (86)	13.3 (40)	0.804
No	68.4 (517)	59.8 (70)	29.1 (34)	11.1 (13)		65.7 (241)	23.4 (86)	10.9 (40)	
Regular consumption of red meat with fat									
No	57.1 (432)	58.3 (56)	26 (25)	15.6 (15)	0.529	64.1 (95)	24 (29)	11.9 (15)	0.677
Yes	41.8 (316)	58.8 (90)	30.1 (46)	11.1 (17)		68.3 (95)	20.9 (29)	10.8 (15)	
Regular consumption of chicken with skin									
No	55.7 (421)	58.6 (146)	28.5 (71)	12.9 (32)	0.452	67.1 (96)	20.3 (29)	12.6 (18)	0.526
Yes	43.9 (332)	64.2 (201)	24.9 (78)	10.9 (34)		65.1 (297)	23.5 (107)	11.4 (52)	
Regular soft drink consumption									
No	76.5 (578)	57.1 (97)	28.8 (49)	14.1 (24)	0.562	66.2 (247)	24.1 (90)	9.7 (36)	0.048
Yes	23.5 (178)	63 (51)	27.2 (22)	9.9 (8)		60.7 (51)	20.2 (17)	19 (16)	
Regular fruit consumption									
No	33.9 (256)	63.8 (44)	20.3 (14)	15.9 (11)	0.207	65.7 (113)	23.8 (41)	10.5 (18)	0.890
Yes	65.9 (498)	57.2 (103)	31.1 (56)	11.7 (21)		64.9 (185)	23.2 (66)	11.9 (34)	
	Mean (SD)					**Mean (SD)**			
Weight (kg)	66.86 (13.17)	68.87(12.49)	68.86 (13.46)	65.38 (11.98)	0.123	65.20 (13.56)	68.04 (13.52)	65.09 (12.49)	0.025
Height (cm)	162.09 (9.25)	168.89 (8.87)	168.09 (8.14)	165.90 (8.26)	0.041	158.69 (7.72)	158.83 (7.70)	158.79 (7.68)	0.367
Body mass index (kg/m^2)	25.55 (5.14)	24.15 (3.94)	24.46 (4.79)	23.82 (4.48)	0.586	25.94 (5.52)	27.07 (5.63)	26.27 (5.10)	0.037
Waist circumference (cm)	88.80 (12.13)	87.35 (10.66)	88.34(10.99)	85.53 (9.93)	0.215	89.10 (12.99)	90.46 (13.15)	90.00 (12.15)	0.386
Conicity index	1.27 (0.09)	1.25 (0.10)	1.26 (0.08)	1.25 (0.06)	0.491	1.27 (0.10)	1.26 (0.09)	1.28 (0.09)	0.311

SD: Standard Deviation.
[a] Chi-square test between genotypes.
[b] Minimum wage R$678.00.
[c] Alcohol consumption in the last month.

study of Lee et al. with Taemin, there was just 15 T genotype, since this allele is found in some Asian population. There is no isolated factor (environmental or genetic) responsible for the obesity prevalence. Obesity is a multifactorial disease that could be investigated in different measures and adjusted models with others variables. However, factors associated with obesity might potentially interact each other. For example, the Manica-Cattani et al. (2010) adjusted the test to gender and age. However, the obesity is related to many others variables like food intake, lifestyle habits, like the present study.

Still, because the obesity is a frequent outcome, the Poisson regression is the better strategy for analyzing the relation between variables in the multivariate model. Lastly, from our knowledge that is

Table 2
Genetic sociodemographic and lifestyle habits and adiposity traits in *Quilombolas* in northern Minas Gerais. 2013.

Variables	Male % (n)[a]			Female % (n)[a]		
	Abdominal obesity (WC)	Overweight (BMI)	High CI	Abdominal obesity (WC)	Overweight (BMI)	High CI
Genotype						
CC	53.8(7)	59.1(55)	56.6(69)	63.9(154)	61.7(148)	66.4(251)*
CT	30.8(4)	29(27)	30.3(37)	23.7(57)	26.2(63)	21.4(81)
TT	15.4(2)	11.8(11)	13.1(16)	12.4(30)	12.1(29)	12.2(46)
Skin color/ethnicity						
Caucasian. Asiatic. *Pardos*. Indigenous	21.4(3)	14.3(15)	16.3(22)	13.5(35)	16.7(43)	15.2(61)
African-descendents	78.6(11)	85.7(90)	83.7(113)	224(13.5)	214(16.7)	339(15.2)
Age group (years)						
18–19	35.7(5)	3.8(4)	22.2(30)	20.1(52)*	1.2(3)	23.5(94)*
20–29	28.6(4)	22.9(24)	23.7(32)	32.8(85)	26.1(67)	30.8(123)
30–39	28.6(4)	29.5(31)	24.4(33)	29(75)	31.9(82)	28.2(113)
40–49	7.1(1)	25.7(27)	17.8(24)	11.2(29)	25.7(66)	11.8(47)
50–59	0(0)	10.5(11)	11.9(16)	6.9(18)	10.1(26)	5.8(23)
≥ 60	35.7(5)	7.6(8)	22.2(30)	20.1(52)	5.1(13)	23.5(94)
Marital status						
Single/widower	28.6(4)	29.5(31)	34.8(47)	30.5(79)	26.1(67)*	32.2(129)
Married/consensual	71.4(10)	70.5(74)	65.2(88)	69.5(180)	73.9(190)	67.8(271)
Schooling (years)						
Illiterate	21.4(3)	18.1(19)*	32.6(44)*	24.3(63)*	17.9(46)	22.2(89)*
1–4	21.4(3)	24.8(26)	31.1(42)	17(44)	19.1(49)	16.8(67)
5–8	28.6(4)	31.4(33)	25.2(34)	31.3(81)	31.1(80)	32(128)
≥ 9	28.6(4)	25.7(27)	11.1(15)	27.4(71)	31.9(82)	29(116)
Income (Minimum wage)[b]						
< 0.5	0(0)	10.5(11)*	16.3(22)	19.3(50)*	24.9(64)	23.5(94)*
≥ 0.5–1	64.3(9)	50.5(53)	38.5(52)	48.6(126)	45.9(118)	46.8(187)
≥ 1	35.7(5)	39(41)	45.2(61)	32(83)	29.2(75)	29.8(119)
Smoking						
Never smoke	21.4(3)	44.8(47)*	26.7(36)*	68.7(178)*	73.9(190)	69.5(278)*
Ex-smoker	14.3(2)	22.9(24)	28.1(38)	17.4(45)	14.8(38)	15(60)
Smoker	64.3(9)	32.4(34)	45.2(61)	13.9(36)	11.3(29)	15.5(62)
Alcohol consumption[c]						
Yes	50(7)	52.4(55)	54.8(74)	20.5(53)	19.5(50)	21.5(86)*
No	50(7)	47.6(50)	45.2(61)	79.5(206)	80.5(207)	78.5(314)
Regular consumption of red meat with fat						
No	38.5(5)	40.8(42)	43.3(58)	72.4(186)	70.7(181)	68.9(272)
Yes	61.5(8)	59.2(61)	56.7(76)	27.6(71)	29.3(75)	31.1(123)
Regular consumption of chicken with skin						
No	23.1(3)	37.5(39)	30.1(40)	69(178)	68.8(176)	66.4(265)*
Yes	76.9(10)	62.5(65)	69.9(93)	31(80)	31.2(80)	33.6(134)
Regular soft drink consumption						
No	64.3(9)	70.5(74)	66.7(90)	80.3(208)	81.3(209)	81(324)*
Yes	35.7(5)	29.5(31)	33.3(45)	19.7(51)	18.7(48)	19(76)
Regular fruit consumption						
No	21.4(3)	28.6(30)	25.4(34)	38.6(100)	40.9(105)	36.8(147)
Yes	78.6(11)	71.4(75)	74.6(100)	61.4(159)	59.1(152)	63.2(253)

We showed just numbers related to presence of overweight (BMI ≥ 25 kg/m^2), abdominal obesity (WC ≥ 88 cm for women and ≥ 102 cm for men) and high Conicity Index (IC ≥ 1.18 cm or women e ≥ 1.25 cm for men).

[a] Chi-square test between genotypes, socioeconomic and lifestyle variables by higher adiposity traits for each sex separately.

[b] Minimum wage R$678.00.

[c] Alchol consumption in the last month.

* p-value < 0.05.

the first study with a sampling in a based population study with regression models carefully adjusted. Besides that, it was done in *Quilombolas*, what is a particular population.

5. Conclusions

In conclusion, after socioeconomic and lifestyle adjustment T variant of rs1143634 is a protection factor for central obesity in *Quilombola* communities.

Declaration of interest

There are no conflicts of interest.

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Table 3
Multivariate Poisson regression model (prevalence ratio and 95% CI) for IL1-β (rs11143634) polymorphism and adiposity traits in *Quilombolas* in north de Minas Gerais. 2013 (n = 708).

Genetic variant	PR	CI95%	p-value	Ajusted PR[a]	CI95%	p-value	Adjusted R^2 (p-value)
Abdominal obesity (WC ≥ 88 cm for women and ≥ 102 cm for men)							
CC	1	–		1	–		0.1539
CT	0.95	0.75–1.20	0.687	0.59	0.37–0.92	0.021	(< 0.001)
TT	1.05	0.78–1.41	0.722	0.31	0.11–0.84	0.021	
Overweight (BMI ≥ 25 kg/m^2)							
CC	1	–		1	–	–	0.0211
CT	1.11	0.93–1.32	0.245	1.03	0.66–1.62	0.867	(< 0.001)
TT	1.04	0.81–1.33	0.719	0.81	0.32–2.02	0.661	
High conicity index (IC ≥ 1.18 cm or women e ≥ 1.25 cm for men)							
CC	1	–		1	–		0.0290
CT	0.92	0.82–1.04	0.197	1.07	0.84–1.36	0.550	(< 0.001)
TT	1.02	0.90–1.17	0.678	1.31	0.83–2.08	0.243	
Regular soda consumption* rs11143634				0.88	0.77–0.99	0.045	

PR: Prevalence ratio. Schooling (illiterate, 1–4, 5–8 and > 9 years). Smoker status (never, ex and current smoker). Alchool consumption (yes/no in the last month). Regular consumption of red meat with fat, regular consumption of chicken with skin, and regular consumption of soda, interaction rs11143634*regular consumption of soda, interaction rs11143634*regular consumption of red meat, interaction rs11143634* regular consumption of chicken with skin.

[a] Adjusted for age (years), Sex (female/male), Marital status (Single/Widower vs Married/consensual), Income (< 0.5, 0.5–1.0, > 1.0 minimum wages).

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