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Data Article

Data on inflammasome gene polymorphisms of patients with sporadic malignant melanoma in a Brazilian cohort



Wanessa Cardoso da Silva^{a,*}, Telma M. Oshiro^a,
Daniel Coelho de Sá^b, Dilcilea D.G.S. Franco^b, Cyro Festa Neto^b,
Alessandra Pontillo^c

^a *Laboratory of Medical Investigation in Dermatology and Immunodeficiencies - LIM 56, Department of Dermatology, Faculty of Medicine, University of Sao Paulo, Avenida Dr. Eneas de Carvalho Aguiar, 470 - Prédio 2 - 3º andar - CEP:05403-000 - Cerqueira César, Sao Paulo, Brazil*

^b *Department of Dermatology, Faculty of Medicine, University of Sao Paulo, Avenida Dr. Eneas de Carvalho Aguiar, 500 - CEP: 05403-000 Cerqueira Cesar, Sao Paulo, Brazil*

^c *Laboratory of Immunogenetics, Department of Immunology, Institute of Biomedical Sciences, University of Sao Paulo, Avenida Prof. Lineu Prestes, 1730 - 05508-000 Cidade Universitaria, Sao Paulo, Brazil*

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ABSTRACT

This article presents data related to our another article entitled, **Genotyping and differential expression analysis of inflammasome genes in sporadic malignant melanoma reveal novel contribution of CARD8, IL1B and IL18 in melanoma susceptibility and progression** (W.C. Silva, T.M. Oshiro, D.C. Sá, D.D.G.S. Franco, C. Festa Neto, A. Pontillo, 2016) [2]. Data presented here refers to the distribution of selected inflammasome SNPs in a Brazilian case/control cohort. We have identified 4 inflammasome related Single Nucleotide Polymorphisms (SNPs) for *CARD8* (rs6509365); *IL1B* (rs1143643) and *IL18* (rs5744256 and rs1834481) related to melanoma susceptibility/protection. This data can serve as a potential prognostic marker in sporadic malignant melanoma.

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* Corresponding author.

E-mail address: wanessacardoso@yahoo.com.br (W.C. da Silva).

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Specifications Table

Subject area	Genetics
More specific subject area	Immunogenetics
Type of data	Tables, figures
How data was acquired	ABI Prism 7300 Real Time PCR equipment (Applied Biosystems, ThermoScientific, USA), SDS 2.3 software (Applied Biosystems, ThermoScientific, USA), R software (www.r-project.org), Haploview software
Data format	Raw, analyzed
Experimental factors	Determination of clinical data of patients, extraction of DNA from buffy coat and genetic polymorphism parameters
Experimental features	Analysis of polymorphism in inflammasome genes in sporadic malignant melanoma patients and healthy controls
Data source location	Sao Paulo, Brazil
Data accessibility	The data is available with this article

Value of the data

- Presence or absence of a particular polymorphism in inflammasome genes can drive an individual's susceptibility to melanoma.
- This dataset provides some selected inflammasome related SNPs' frequencies in a Brazilian case/control melanoma cohort and its association with clinical outcomes.
- Comparison of this dataset with other cohort dataset can help to elucidate the contribution of inflammasome genes in the development of and progression to sporadic malignant melanoma.

1. Data

A Brazilian case/control SMM cohort was studied concerning frequencies of selected inflammasome SNPs in *NLRP1*, *NLRP3*, *CARD8*, *IL1B* and *IL18* genes and minor allele frequencies (MAF) with respective Hardy–Weinberg *p*-values were calculated.

Case/control analysis were performed and distribution of alleles for each selected SNP, as well as Odd Ratios (OR), haplotypes, *Linkage disequilibrium* analysis were determined.

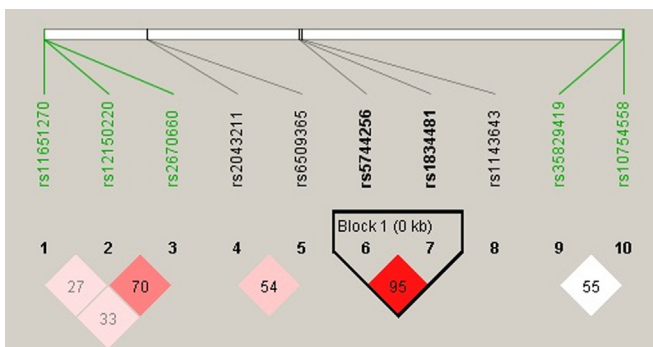


Fig. 1. Linkage disequilibrium results for single-nucleotide polymorphisms examined in case/control study. Haploview plot showed D'/LOD values.

Table 1

SNPs frequencies in case/control cohort. Minor allele frequencies (MAF) with respective Hardy–Weinberg p -values (HW p) for studied SNPs are reported in case (SMM) and controls (HC). Hapmap project MAF (or 1000 Genome MAF where indicated) for Caucasian and African population are included. MAF for SNPs studied by Verma et al., 2012^a [1] are also included with respective p -value for comparisons with SNPs frequencies in studied Brazilian cohort^a.

Gene	SNP ID	Allele	SMM	HW p	HC	HW p	CEU	YRI	SMM (Verma et al. [1])	HC (Verma et al. [1])
<i>NLRP1</i>	rs12150220	T	0.44	0.071	0.46	0.079	0.46	0.02	0.52 (0.020)	0.20 (< 2exp-16)
	rs2670660	G	0.51	0.180	0.46	0.485	0.35*	0.32*		
	rs11651270	C	0.50	0.059	0.41	0.216	0.47	0.50		
<i>NLRP3</i>	rs35829419	A	0.04	1.0	0.04	1.0	0.06	na	0.08 (4.2exp-8)	0.06 (1.0exp-6)
	rs10754558	G	0.41	0.878	0.38	0.070	0.36	0.23		
<i>CARD8</i>	rs2043211	T	0.29	0.203	0.38	0.855	0.27	0.16	0.34 (0.524)	0.36 (0.026)
	rs6509365	G	0.25	0.157	0.40	0.373	0.28	0.32		
<i>IL1B</i>	rs1143643	T	0.40	1.0	0.37	0.804	0.39	0.15		
<i>IL18</i>	rs5744256	G	0.18	0.803	0.20	0.177	0.22	na		
	rs1834481	G	0.17	0.628	0.20	0.103	0.23	na		

^a data from 1000 Genome.

Table 2

Association results for inflammasome polymorphisms in sporadic malignant melanoma. Genotype frequencies are reported as well as unadjusted p -values (p), p -values adjusted for age, sex and ethnicity (p_{adj}) and respective Odds Ratio (OR) and 95% confidence intervals (95% CI). Statistically significant results ($p < 0.005$) are indicated in bold characters. SMM: sporadic malignant melanoma; HC: healthy controls; Ref: reference genotype.

Gene	SNP ID	Genotypes	SMM ($n=198$)	HC ($n=142$)	p	OR (95%CI)	p_{adj}	OR (95%CI)
<i>NLRP1</i>	rs12150220	T/T	0.23	0.25	0.887	0.87 (0.48–1.58)	0.673	0.86 (0.43–1.69)
		A/T	0.42	0.42		0.98 (0.58–1.64)		1.15 (0.64–2.08)
		A/A	0.35	0.33		Ref		Ref
	rs2670660	G/G	0.28	0.19	0.145	1.54 (0.81–2.93)	0.166	1.69 (0.81–3.54)
		A/G	0.45	0.53		0.87 (0.51–1.49)		0.91 (0.49–1.69)
		A/A	0.27	0.28		Ref		Ref
rs11651270	C/C	0.28	0.19	0.155	1.84 (0.98–3.44)	0.132	1.97 (0.97–3.99)	
	T/C	0.43	0.43		1.25 (0.73–2.12)		1.11 (0.61–2.01)	
	T/T	0.29	0.37		Ref		Ref	
<i>NLRP3</i>	rs35829419	A/A	0	0	0.911	–	0.810	–
		C/A	0.07	0.07		1.05 (0.44–2.54)		1.13 (0.42–3.02)
		C/C	0.93	0.93		Ref		Ref
	rs10754558	G/G	0.17	0.18	0.310	1.14 (0.60–2.16)	0.467	1.20 (0.58–2.46)
		C/G	0.48	0.40		1.46 (0.89–2.40)		1.42 (0.81–2.48)
		C/C	0.35	0.42		Ref		Ref
<i>CARD8</i>	rs2043211	T/T	0.06	0.13	0.043	0.37 (0.16–0.83)	0.102	0.39 (0.15–0.98)
		A/T	0.45	0.49		0.73 (0.46–1.18)		0.69 (0.40–1.19)
		A/A	0.49	0.38		Ref		Ref
	rs6509365	G/G	0.08	0.18	3.1 exp-4	0.28 (0.13–0.58)	1.7 exp-4	0.35 (0.15–0.80)
		A/G	0.33	0.44		0.48 (0.29–0.78)		0.41 (0.24–0.72)
		A/A	0.59	0.38		Ref		Ref
<i>IL1B</i>	rs1143643	T/T	0.16	0.12	0.700	1.45 (0.59–3.56)	0.581	1.76 (0.56–5.53)
		C/T	0.48	0.49		1.06 (0.58–1.95)		1.02 (0.46–2.27)
		C/C	0.36	0.39		Ref		Ref
<i>IL18</i>	rs5744256	G/G	0.03	0.06	0.589	0.58 (0.19–1.72)	0.235	0.39 (0.12–1.29)
		A/G	0.29	0.28		1.03 (0.62–1.70)		0.77 (0.44–1.34)
		A/A	0.67	0.66		Ref		Ref
	rs1834481	G/G	0.05	0.07	0.755	0.64 (0.17–2.36)	0.244	0.40 (0.09–1.86)
		C/G	0.23	0.25		0.87 (0.43–1.74)		0.58 (0.27–1.28)
		C/C	0.73	0.69		Ref		Ref

Table 3

Association results for *IL18*rs5744256-rs1834481 haplotypes. Frequencies for SMM patients (case) and healthy donors (control) as well as *p*-values are reported for resulted rs5744256-rs1834481 haplotypes. Only haplotypes with frequency > 0.05 are included in GLM analysis. SMM: sporadic malignant melanoma; HC: healthy controls.

Haplotypes Rs5744256-rs1834481	Case/Control Frequencies	<i>p</i>	<i>P</i> _{adj}
C-A	0.79/0.80	ref	ref
G-G	0.17/0.19	0.8647	0.8512
rare	0.04/0.01	0.1663	0.1381

Table 4

Association results for inflammasome polymorphisms in melanoma patients stratified for histological tumor type. Gene symbol, polymorphism identification number (SNP ID), *p*-values adjusted for sex, age and ethnicity are reported for three comparisons: superficial spreading melanoma (SSM) versus nodular melanoma (NM), SSM versus lentigo malignant melanoma (LMM) and SSM versus melanoma “*in situ*”. Statistically significant values are indicated in bold characters. nd: not determined.

Gene	SNP ID	SSM (<i>n</i> =77)/ NM (<i>n</i> =30) Dominant model of inheritance	SSM (<i>n</i> =77)/ LMM (<i>n</i> =21) Recessive model of inheritance	SSM (<i>n</i> =77)/ <i>in situ</i> (<i>n</i> =29) Recessive model of inheritance
<i>NLRP1</i>	rs12150220	0.018	0.109	0.639
	rs2670660	0.229	0.475	0.820
	rs11651270	0.003	0.060	0.08
<i>NLRP3</i>	rs35829419	nd	nd	nd
	rs10754558	0.303	0.020	0.952
<i>CARD8</i>	rs2043211	0.005	0.108	0.792
	rs6509365	0.040	0.983	0.600
<i>IL1B</i>	rs1143643	0.815	0.904	0.020
<i>IL18</i>	rs5744256	0.903	0.937	0.050
	rs1834481	0.176	0.946	0.030

Table 5

Association results for inflammasome polymorphisms in melanoma patients according to invasiveness and skin type. Gene symbol, polymorphism identification number (SNP ID), multivariate analysis *p*-values adjusted for sex, age at diagnosis and ethnicity are reported for SMM patients according to invasiveness (Breslow index), with less invasive (< 2 mm) or more invasive (≥ 2 mm) tumors; or with sun-sensitive or less sun-sensitive skin types. Statistically significant values are indicated in bold characters. nd: not determined.

Gene	SNP ID	Tumor invasiveness ≥ 2 mm (<i>n</i> =30)/ < 2 mm(<i>n</i> =133)	Skin type Sun-sensitive (<i>n</i> =94)/Less sun-sensitive (<i>n</i> =57)
<i>NLRP1</i>	rs12150220	0.690	0.880
	rs2670660	0.645	0.950
	rs11651270	0.616	0.836
<i>NLRP3</i>	rs35829419	nd	nd
	rs10754558	0.537	0.986
<i>CARD8</i>	rs2043211	0.256	0.692
	rs6509365	0.409	0.624
<i>IL1B</i>	rs1143643	0.004	0.978
<i>IL18</i>	rs5744256	0.970	0.003
	rs1834481	0.455	0.027

Patients were stratified according to histological tumor type, invasiveness and skin type were represented (Fig. 1).

2. Experimental design, materials and methods

Refer to the associated article [2] for detailed methods (Table 1–5).

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.11.053>.

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- [2] W. Silva, T. Oshiro, D. Sá, F.DDGS, C. Festa Neto and A. Pontillo Genotyping and differential expression analysis of inflammasome genes in sporadic malignant melanoma reveal novel contribution of *CARD8*, *IL1B* and *IL18* in melanoma susceptibility and progression. *Cancer Genetics*. Submitted.