



## Letter

The association between interleukin-1 $\beta$  gene rs1143634 polymorphism and the risk of breast cancer

## ARTICLE INFO

**Keywords:**  
IL-1 $\beta$   
Polymorphism  
Breast cancer  
Rs1143634

## ABSTRACT

We're confused about some data in a recent article entitled "Polymorphic variation in IL-1, IL-6 and IL-10 genes, their circulating serum levels and breast cancer risk in Indian women", which was published online in Cytokine. A clarification of data in this article is needed.

With great interests, we have read a recent article entitled "Polymorphic variation in IL-1, IL-6 and IL-10 genes, their circulating serum levels and breast cancer risk in Indian women", which was published online in Cytokine [1]. In this article, Pooja et al found the mutant allele and genotype at IL-1 $\beta$ [+3954C > T rs1143634] associated with the increased risk of breast cancer.

The article written by Pooja stated that the control group genotype data for all SNPs were analyzed for fitness in HWE with no significant deviation observed in any case. Nevertheless, careful examinations of data reported by Pooja et al reveal a key issue that is worth mentioning. From the data supplied by Pooja (Tables 1 and 2), we obtained data of the genotype distribution (Table 3). Obviously, the control groups of +3954C > T rs1143634 deviated from HWE ( $P < 0.05$ ), which led an unconvincing conclusion about the association between rs1143634 polymorphism and the risk of breast cancer.

The polymorphism +3954C > T rs1143634 of IL-1 $\beta$  has been widely investigated for its effect on protein production. The presence of the T allele at this site has already been associated with the increased IL-1 $\beta$  secretion in vitro [2]. So far, emerging studies have been conducted to investigate relations between rs1143634 polymorphism and the risk of breast cancer. For an instance, Snoussi et al only found that +3954C > T rs1143634 of IL-1 $\beta$  was highly connected with aggressive forms of breast cancer while no significant difference between polymorphism in +3954C > T rs1143634 of IL-1 $\beta$  and the risk of breast cancer was observed [3]. The results reported by Balasubramanian et al. also indicated that +3954C > T rs1143634 polymorphism was not a predisposition to the breast cancer susceptibility [4]. The data of Hefler deviated from HWE and no conspicuous link was found between +3954C > T rs1143634 polymorphism and the presence of breast cancer [5]. Generally speaking, the conclusions drawn by Pooja should

Table 1

Allele and genotype distribution of rs1143634 among cases and controls.

Alleles	Wide (C)	Mutated (T)	Genotype	Wide (CC)	Mutated (CT+TT)
Cases (200)	340	60	Cases (200)	147	53
Controls (200)	364	36	Controls (200)	176	24

Table 2

Allele and genotype distribution of rs1143634 in cases and controls as per menopausal status.

	Premenopause Patients (107)	Controls (200)	Postmenopause Patients (93)	Controls (200)
Alleles				
C	178	364	160	364
T	36	36	26	36
Genotype				
CC	75	176	71	176
CT+TT	32	24	22	24

Table 3

Genotype distribution of rs1143634 in cases and controls as per menopausal status.

	Genotype distribution										HWE
	Patients					Controls					
	C	T	CC	CT	TT	C	T	CC	CT	TT	
Premenopause	178	36	75	28	4	364	36	176	12	12	< 0.001
Postmenopause	160	26	71	18	4	364	36	176	12	12	< 0.001
Total	340	60	147	46	7	364	36	176	12	12	< 0.001

be interpreted with caution. In the future, we need further large-scale and rigorous studies to assess associations between +3954C > T rs1143634 polymorphism and the risk of breast cancer.

## Acknowledgements

We give thanks to Miss Dandan Chen for providing language help.

## Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

### Conflict of interest

The authors declare that they have no conflict of interest.

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Bei Wang\*, Fenlai Yuan

Department of Central Laboratory, Third Hospital Affiliated to Nantong University, Wuxi, Jiangsu 214041, China

E-mail address: [xuewuhewang@126.com](mailto:xuewuhewang@126.com) (B. Wang)

\* Corresponding author.