Note of clarification regarding data on the association between the interleukin-1 β –511C>T polymorphism and breast cancer risk

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With great interest, we have read a recent article entitled “Three polymorphisms in interleukin-1 β gene and risk for breast cancer: a meta-analysis”, which was published online in Breast Cancer Research and Treatment [1]. In this article, Liu et al. conducted a meta-analysis to address the association between the interleukin-1 β (IL-1 β) gene –511C>T polymorphism and the risk of breast cancer [1]. Their results showed that the polymorphism of IL-1 β –511C>T was not associated with the risk of breast cancer. It is an extremely valuable study.

Nevertheless, careful examinations of the data reported by Liu et al. (shown in Table 1 of Liu et al.’s paper) [1] reveal two key issues that are worth mentioning. First, the data reported by Liu et al. [1] for the study of Smith et al. [2] did not seem in line with the data from Smith et al.’s original publication [2]. The numbers reported by Smith et al. for the CC and TT genotypes were 60 and 14 among the cases and 87 and 39 among the controls, respectively (shown in Table 2 of Smith et al.’s original publication) [2]. Interestingly, after carefully examining the data reported by Liu et al. [1], the numbers for the CC and TT genotypes were 14 and 60 among the cases and 39 and 87 among the controls, respectively (shown in Table 1 of Liu

et al.’s paper) [1]. Second, the data reported by Liu et al. [1] for the study of Liu et al. [3] did not seem in accord with the data from Liu et al.’s original publication [3]. The numbers reported by Liu et al. [3] for the CC, CT, and TT genotypes were 94, 170, and 101 among the cases and 197, 305, and 129 among the controls, respectively (shown in Table 2 of Liu et al.’s original paper) [3]. Interestingly, after carefully examining the data reported by Liu et al. [1], the numbers for the CC, CT, and TT genotypes were 197, 305, and 129 among the cases and 94, 170, and 101 among the controls, respectively (shown in Table 1 of Liu et al.’s paper) [1].

Therefore, the above discrepancies imply that the association between the IL-1 β –511C>T polymorphism and the risk of breast cancer is not entirely reliable. It is needed to clarify the association between the IL-1 β –511C>T polymorphism and the risk of breast cancer comprehensively and objectively. We re-evaluated this association by performing a cumulative meta-analysis based on five studies including 1678 breast cancer cases and 1808 controls.

Table 1 lists the general information of the eligible studies included in this cumulative meta-analysis. Table 2 lists the summary cumulative odds ratios (ORs) of the association between the IL-1 β –511C>T polymorphism and the risk of breast cancer. We did not observe any significant association between the IL-1 β –511C>T polymorphism and the risk of breast cancer under all four genetic models. The cumulative ORs were 0.934 [95 % confidence interval (CI) 0.797–1.093] for CT versus CC, 0.944 (95 % CI 0.593–1.505) for TT versus CC, 0.918 (95 % CI 0.697–1.208) for CT+TT versus CC, and 0.980 (95 % CI 0.809–1.187) for the T allele versus the C allele, respectively (Fig. 1a–d). The publication bias was evaluated by using Begg’s test and Egger’s test in this study. The

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Table 1 General information of the eligible studies included in this meta-analysis

First author	Year	Country	Cases				Controls				<i>P</i> value of HWE
			CC	CT	TT	Total	CC	CT	TT	Total	
Smith [2]	2004	Japan	60	67	14	141	87	135	39	261	0.253400
Hefler [4]	2005	Germany	124	114	31	269	88	111	28	227	0.438414
Liu [3]	2006	China	94	170	101	365	197	305	129	631	0.581862
Balasubramanian [5]	2006	UK	339	294	70	703	232	206	51	489	0.600124
Pooja [6]	2012	India	107*		93	200	119*		81	200	Not estimable

HWE Hardy–Weinberg equilibrium

* CC + CT

Table 2 Summary odds ratios of the association between the IL-1 β -511C>T polymorphism and breast cancer risk

Genetic model	Number of studies	Heterogeneity test		Analysis model	Summary OR (95 % CI)	Hypothesis test		Begg's test		Egger's test	
		<i>Q</i>	<i>P</i>			<i>Z</i>	<i>P</i>	<i>Z</i>	<i>P</i>	<i>t</i>	<i>P</i>
CT vs. CC	4	5.39	0.146	Fixed-effects model	0.934 (0.797–1.093)	0.836	0.403	0.34	0.734	1.31	0.321
TT vs. CC	4	10.49	0.015	Random-effects model	0.944 (0.593–1.505)	0.241	0.810	1.70	0.089	2.48	0.132
CT+TT vs. CC	4	9.67	0.022	Random-effects model	0.918 (0.679–1.208)	0.611	0.542	1.02	0.308	1.07	0.397
T allele vs. C allele	5	13.24	0.010	Random-effects model	0.980 (0.809–1.187)	0.206	0.837	0.73	0.462	1.25	0.299

OR odds ratio, *CI* confidence interval

results of Begg's test and Egger's test showed that there was no potential publication bias (Table 2). A sensitivity analysis was carried out to check the stability and reliability of our meta-analysis by sequentially deleting each eligible study. The summary OR was not substantially altered under the genetic model of the T allele versus the C allele (data not shown).

In summary, the results provided by Liu et al. [1] should be interpreted with caution. To reach a definitive conclusion, well-designed studies with larger sample sizes are still needed to examine the association between the IL-1 β -511C>T polymorphism and the risk of breast cancer. We hope that this remark will contribute to more accurate elaboration and substantiation of the results presented by Liu et al. [1].

Fig. 1 Cumulative meta-analysis to estimate the summary odds ratio of the association between IL-1 β -511C>T polymorphism and the risk of breast cancer (**a** CT vs. CC, **b** TT vs. CC, **c** CT+TT vs. CC and **d** T allele vs. C allele)

Compliance with ethical standards

Conflicts of interest None declared.

Ethical statement This article does not contain any studies with human participants or animals performed by any of the authors.

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