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EDITORIAL

Note of clarification regarding data about the association between the interleukin-1β −31T>C polymorphism and breast cancer risk

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Recently, we read with great interest a paper entitled "Three polymorphisms in interleukin-1beta gene and risk for breast cancer: a meta-analysis", which was published online in Breast Cancer Research and Treatment 124: 821–825, 2010 [1]. In this paper, Liu et al. performed a meta-analysis to examine the association between the interleukin-1beta (IL-1β) −31T>C (rs1143627) polymorphism and breast cancer risk based on four studies including 1543 cases and 1165 controls [1]. Their results indicated that the variant CC genotype of rs1143627 was associated with a significantly increased breast cancer risk (CC versus TT: odds ratio (OR) = 1.37, 95 % confidence interval (CI) 1.10–1.70, $P = 0.22$ for heterogeneity; CC versus TT/TC: OR = 1.40, 95 % CI 1.17–1.67, $P = 0.49$ for heterogeneity) [1]. It is an interesting study.

Nevertheless, after carefully examining the data reported by Liu et al. [1], we found two key issues that are worth noticing. First, the data reported by Liu et al. [1] for the study of Liu et al. [2] did not seem to agree with the data reported in Liu et al.'s original publication [2]. The numbers reported by Liu et al. [2] for the TT, CT and CC genotypes were 88, 175 and 102 among the cases and 185, 313 and 133 among the controls, respectively (shown in Table 2 of Liu et al.'s original publication) [2]. Interestingly, after carefully examining the data reported by Liu et al. [1], the numbers for TT, CT and CC were 185, 313 and 133 among the cases and 88, 175 and 102 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 reported by Akisik et al. [3] did not seem to agree with the data from Akisik et al.'s study [3] in their original publication. The numbers reported by Akisik et al. [3] for the TT and CC genotypes were 45 and 18 among the cases and 33 and 21 among the controls, respectively (shown in Table 2 of Akisik et al.'s original paper). Interestingly, after carefully examining the data reported by Liu et al. [1], the numbers for TT and CC were 18 and 45 among the cases and 21 and 33 among the controls, respectively (shown in Table 1 of Liu et al.'s paper) [1].

Thus, the above discrepancies imply that the association between the IL-1β −31T>C polymorphism and the risk of breast cancer is not entirely credible. The association between the IL-1β −31T>C polymorphism and breast cancer risk requires clarification. We reassessed this association by conducting an updated meta-analysis based on 1277 breast cancer cases and 1431 controls that could provide comprehensive evidence for the association of the IL-1β −31T>C polymorphism with breast cancer risk. A cumulative meta-analysis that accumulated the data according to the year of publication was simultaneously conducted.

The general information about the eligible studies is listed in Table 1. The summary ORs of the association between the

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Table 1 General information for the selected studies in this meta-analysis

Study	Country	Cases				Controls				*P* value of HWE
		TT	TC	CC	Total	TT	TC	CC	Total	
Ito LS (Jpn J Clin Oncol, 2002, 32: 398–402)	Japan	66	103	58	227	58	99	28	185	0.177362
Lee KM (Breast Cancer Res Treat, 2006, 96: 197–202)	Korea	153	259	147	559	122	270	113	505	0.117556
Liu J (Int J Cancer, 2006, 118: 2554–2558)	China	88	175	102	365	185	313	133	631	0.977145
Akisik E (J Clin Lab Anal, 2007 21: 97–102)	Japan	45	63	18	126	33	56	21	110	0.749492

HWE Hardy–Weinberg equilibrium

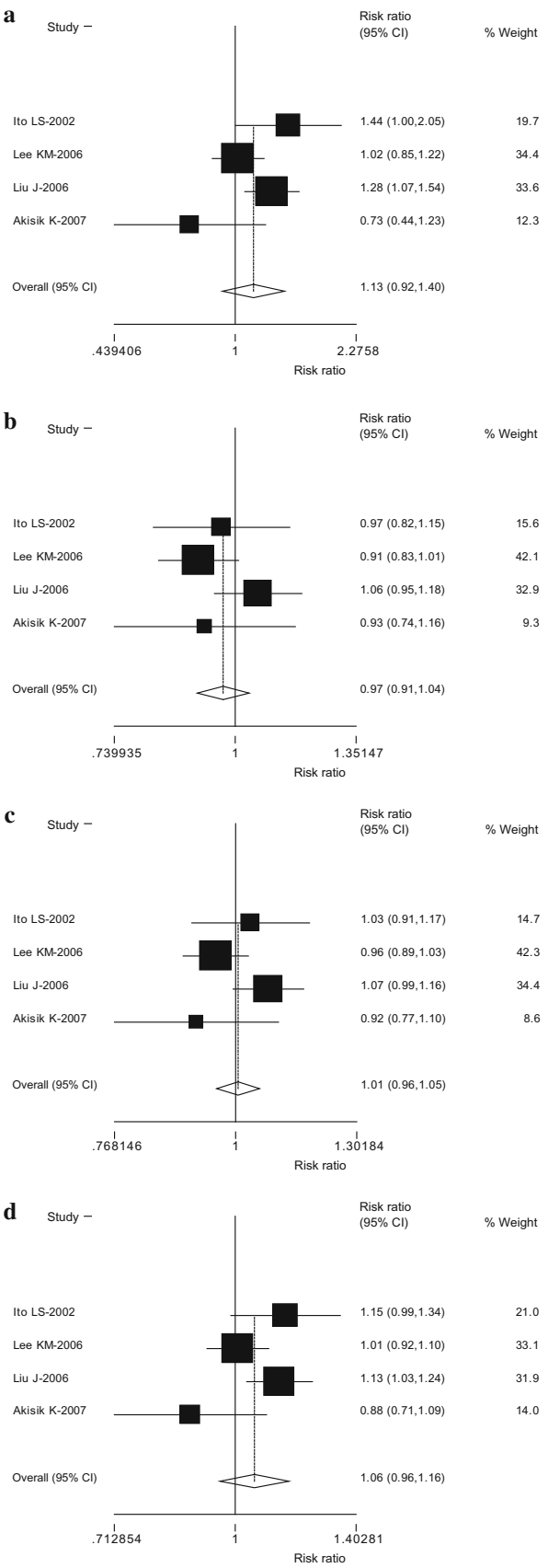
Table 2 Summary odds ratios of the association between the IL-1β −31T>C polymorphism and breast cancer risk

Genetic model	Number of studies	Heterogeneity test		Analysis model	Summary OR (95 % CI)	Hypothesis test		Begg's test		Egger's test	
		Q	*P*			*Z*	*P*	*Z*	*P*	*t*	*P*
CC versus TT	4	7.55	0.056	Random-effects model	1.13 (0.92–1.40)	1.15	0.251	0.34	0.734	0.38	0.743
CT versus TT	4	4.06	0.255	Fixed-effects model	0.97 (0.91–1.04)	0.91	0.365	0.34	1.000	0.12	0.917
CT + CC versus TT	4	5.80	0.122	Fixed-effects model	1.01 (0.96–1.05)	0.22	0.827	0.34	1.000	0.29	0.800
C allele versus T allele	4	7.27	0.064	Random-effects model	1.06 (0.96–1.16)	1.10	0.272	0.34	0.734	0.43	0.707

OR odds ratio, *CI* confidence interval

IL-1β −31T>C polymorphism and breast cancer risk are listed in Table 2. Overall, we did not observe any significant association between the IL-1β −31T>C polymorphism and breast cancer risk. The summary ORs were 1.13 (95 % CI 0.92–1.40) for CC versus TT, 0.97 (95 % CI 0.91–1.04) for CT versus TT, 1.01 (95 % CI 0.96–1.05) for CT + CC versus TT and 1.06 (95 % CI 0.96–1.16) for the C allele versus the T allele, respectively (Fig. 1a–d). Similar results were found in our cumulative meta-analysis, which indicated that there was not any significant association between the IL-1β −31T>C polymorphism and breast cancer risk. The cumulative ORs were 1.24 (95 % CI 0.85–1.82) for CC versus TT, 0.92 (95 % CI 0.77–1.10) for CT versus TT, 1.02 (95 % CI 0.86–1.21) for CT + CC versus TT and 1.11 (95 % CI 0.92–1.33) for the C allele versus the T allele, respectively. These findings increased the reliability of our results to certain extent. The results of Begg's test and Egger's test revealed no evidence of publication bias in this study (Table 2).

In summary, the results reported by Liu et al. [1] should be expounded with caution. To reach a definitive conclusion, additional well-designed studies with larger sample sizes are still required to evaluate the association between the IL-1β −31T>C polymorphism and breast cancer risk. We hope that our remarks will contribute to more accurate elaboration and substantiation of the results reported by Liu et al. [1].



◀**Fig. 1** Forest plots for the odds ratios of the association between the IL-1β −31T>C polymorphism and breast cancer risk (**a** CC versus TT, **b** CT versus TT, **c** CT + CC versus TT, **d** C allele versus T allele)

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Compliance with ethical standards

Conflicts of interest None declared.

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

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