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Association between *FcεRIB* Polymorphisms and Asthma in Asian Population: a Meta-analysis

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DEAR EDITOR

With great interest, we read the article entitled "Association between FcεRIβ and IFN-γ Polymorphisms and Asthma in Asian Population: a Meta-analysis" published in Iranian Journal of Allergy, Asthma and Immunology, 2015, 14(1):1-14.[1] In the study, Yao YS et al preformed a meta-analysis to explore the association between E237G polymorphism in the exon 7 of the β subunit of the high affinity receptor for IgE (*FcεRIβ*) gene and asthma risk based on 19 case-control studies in 16 articles with 4030 asthmatics and 3373 controls. They also examined -109 C/T polymorphism in *FcεRIβ* promoter region on the basis of 1859 cases and 1640 controls. In overall analysis, no statistically significant association between *FcεRIβ* E237G polymorphism and asthma risk was found in Asians [EG+GG vs. EE: odds ratio (OR)=1.14, 95% confidence interval (CI)=0.94-1.40; G versus E: OR (95%CI)=1.13(0.95-1.34)]. In subgroup analysis by age and atopic status of asthmatic cases, no significant association was observed, either.

A statistically decreased risk of asthma in Asians was observed in allelic model for *FcεRIβ* -109 C/T polymorphism [C vs. T: OR (95% CI)=0.88(0.80-0.98)].

Keywords: Asthma; *FcεRIB*; Meta-analysis; Polymorphism

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The findings reported by Yao YS et al are interesting. However, after carefully rechecking the data provided by Yao YS[1] et al (Shown in Table 1 and 2 in their original article), we found several issues that are worth noticing. Firstly, two studies should be removed from the meta-analysis because of duplicated data.[2,3] Wang L and Cui TP reported the association between *FcεRIβ* gene polymorphisms and childhood asthma susceptibility in Hubei, China.[2] These data were also included in another study by Cui TP et al.[4] Similarly, both Kim SH's and Palikhe NS's asthmatic population were recruited by the same research group in Ajou University Hospital, Suwon, Korea.[3,5] Thus Palikhe NS's study [3] with smaller sample size should be excluded from the meta-analysis. Secondly, Chan IH's study[6] should be excluded from Yao YS et al's study because a biallelic polymorphism in the untranslated region of exon 7 of *FcεRIβ* gene rather than the coding E237G polymorphism was reported. Thirdly, 5 eligible studies focusing on the association of *FcεRIβ* E237G or -109C/T polymorphisms with asthma risk in Asian population were not included in Yao YS et al's study.[7-11] Ishizawa M et al[7] reported the association of E237G polymorphism with childhood atopic asthma risk in a Japanese population with 90 cases (number with genotype EE /EG/ GG =70/19/1) and 102 controls (EE /EG/ GG =81/21/0), respectively; Takabayashi A e al[8] reported the association of E237G polymorphism with childhood atopic asthma risk in a Japanese population with 100 cases (EE /EG/ GG =69/27/4) and 100 controls (EE /EG/ GG =65/33/2),

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Table 1. Summary of odds ratios for relationship between the *FcεRIB* E273G or C-108T polymorphisms and asthma risk

Comparisons	Sample size	No. of studies	Hypothesis tests			Heterogeneity tests			Publication bias test (*p*)	
	Case/control		OR (95% CI)	*Z*	*p*	χ^2 (df)	*p*	I^2 (%)	Begg' test	Egger'test
Overall (*FcεRIB* E237G)										
G vs. E	7790/7500	20	1.142 (0.968-1.349)	1.57	0.116	45.73 (19)	0.001	58.5	0.018	0.004
GG+GE vs. EE	3895/3750	20	1.154 (0.953-1.396)	1.47	0.142	47.84 (19)	<0.001	60.3	0.025	0.010
Atopic asthma(*FcεRIB* E237G)										
G vs. E	3368/3694	9	1.349 (1.003-1.815)	1.98	0.048	24.59 (8)	0.002	67.5	0.118	0.062
GG+GE vs. EE	1684/1847	9	1.392 (0.999-1.941)	1.95	0.051	24.96 (8)	0.002	67.9	0.118	0.091
Childhood asthma (*FcεRIB* E237G)										
G vs. E	4212/3972	11	1.172 (0.935-1.469)	1.37	0.170	26.75 (10)	0.003	62.6	0.020	0.002
GG+GE vs. EE	2106/1986	11	1.158 (0.900-1.491)	1.14	0.254	25.96 (10)	0.004	61.5	0.029	0.003
Adult asthma (*FcεRIB* E237G)										
G vs. E	3320/3442	8	1.126 (0.859-1.476)	0.86	0.389	17.02 (7)	0.017	58.9	0.386	0.245
GG+GE vs. EE	1660/1771	8	1.204 (0.886-1.635)	1.19	0.235	21.69 (7)	0.006	63.1	0.917	0.241
Overall (*FcεRIB* C-108T)										
T vs. C	3586/3278	7	0.979 (0.751-1.275)	0.16	0.873	40.15 (6)	<0.001	85.1	0.764	0.868
TT vs. TC+CC	1793/1639	7	0.988 (0.731-1.334)	0.08	0.936	26.92 (6)	<0.001	77.7	0.764	0.482
TT+TC vs. CC	1793/1639	7	0.996 (0.593-1.672)	0.01	0.989	32.66 (6)	<0.001	81.6	1.000	0.340
East Asians (*FcεRIB* C-108T)										
T vs. C	3112/2836	6	1.116 (1.001-1.244)	1.97	0.049	6.16 (5)	0.291	18.9	1.000	0.765
TT vs. TC+CC	1556/1418	6	1.122 (0.889-1.415)	0.97	0.331	12.02 (5)	0.034	58.4	1.000	0.912
TT+TC vs. CC	1556/1418	6	1.256 (0.982-1.607)	1.82	0.069	3.05 (5)	0.692	<0.1	0.707	0.830

OR, odds ratio; CI, confidence interval; df, degree of freedom.

respectively; Sharma S et al[9] studied the association between E237G polymorphism and Indian adult atopic asthma risk with 329 cases (EE /EG/ GG =300/29/0) and 266 controls(EE /EG/ GG =250/16/0), respectively; Li M et al[10] examined the correlation between E237G polymorphism and childhood asthma risk in a Chinese population with 50 cases (EE /EG/ GG =43/7/0) and 30 controls(EE /EG/ GG =30/0/0), respectively. Sharma S and Ghosh B[11] explored the association of -109C/T polymorphism with adult atopic asthma risk in an Indian population with 237 cases (number with genotype CC/CT/TT=89/108/40) and 221 controls (CC/CT/TT=34/118/69), respectively. Fourthly, the data reported by Yao YS for the study of Tang Y et al[12] were not in line with the data in their original publication. The reported number of by Tang Y for cases and controls, are 60 (EE /EG/ GG =49/11/0) and 65 (EE /EG/ GG =61/4/0), respectively.[12] The fore-mentioned reports led to inaccuracy of total sample size, selection bias and unreliability of conclusion supplied by Yao YS et al.[1] To clarify objectively the association between *FcεRIβ* polymorphisms and asthma risk in Asian population, we performed an updated meta-analysis based on a total of 20 studies with 3895 cases and 3750 controls for E237G, seven studies with 1793 cases and 1639 controls.

Table 1 listed the summary odds ratios of the association between *FcεRIβ* polymorphisms and

asthma risk in Asian population. Overall, we did not find statistically significant association between E237G polymorphism and asthma risk in Asian population under the allelic genetic model (OR=1.142, 95% CI=0.968-1.349) or under the dominant genetic model (OR=1.154, 95% CI=0.953-1.396 for 237GG+GE versus 237 EE). In stratified analysis on the basis of atopic status, a significant increased atopic asthma risk was observed under the allelic genetic model (OR=1.349, 95% CI=1.003-1.815), implying that *FcεRIβ* 237G-allele carriers have a 34.9% enhanced risk of atopic asthma compared with 237E-allele carriers. We also examined a marginally significant association between *FcεRIβ* E237G polymorphism and atopic asthma risk under the dominant genetic model (OR=1.392, 95% CI= 0.999-1.941). No significant associations between E237G polymorphism and asthma risk were found in the stratified analyses by age of asthma cases. As shown in Table 1, no significant associations between *FcεRIβ* C-108T polymorphism and asthma risk were observed in overall Asian population. However, a significantly elevated asthma risk was associated with *FcεRIβ* -108T allele in the East Asian population (OR=1.116, 95% CI=1.001-1.244) when summarizing the studies from China, South Korea and Japan.

In summary, the findings of the study by Yao YS et al should be interpreted with caution.[1] Well-designed studies with large sample size are necessary to make a definitive conclusion about the correlation between *FcεRIβ* polymorphisms and asthma risk. We hope that this remark will contribute to a more accurate elaboration and interpretation of the results presented by Yao YS et al.

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