LETTER to the EDITOR

Comment on: "Association Between the XRCC3 Thr241Met Polymorphism and Risk of Colorectal Cancer: A Meta-Analysis of 5,193 Cases and 6,645 Controls"

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Dear Editor

We read with great interest the recent article by Namazi and colleagues, "association between the XRCC3 Thr241Met polymorphism and risk of colorectal cancer: a meta-analysis of 5,193 cases and 6,645 controls"(Namazi et al., 2015). There are some important negative points decrease the reliability of the article.

Firstly, some contradictory findings exist in this meta-analysis. The author found a significant association between the XRCC3 Thr241Met polymorphism and colorectal cancer under the overall dominant and heterozygous model in Caucasian descent. Our review demonstrated inconsistent results in texture (CC+CT vs. TT: OR=0.575, 95%CI=0.498-1.665, P<0.001, $P_{heterogeneity}$=0.00, I2=83%) and diagram of overall dominant model (CC+CT vs. TT: OR=0.904, 95%CI=0.796-1.027, P=0.120). On the other hand, in a stratified analysis by ethnicity, the P value of heterozygous model in Caucasian descent is more than 0.05 (CT vs. TT: OR=0.929, 95%CI=0.806-1.070, P=0.308, $P_{heterogeneity}$=0.002, I2=57%). Therefore, it seems to exist no significant association between the XRCC3 Thr241Met polymorphism and colorectal cancer under mentioned genetic models. Moreover, the author reported that the dominant and allelic genetic models of the XRCC3 Thr241Met polymorphism were significantly correlated with increasing risk of CRC in Asian population (Dominant model: CC+CT vs. TT: OR=0.609, 95%CI=0.411-0.902, P=0.013, $P_{heterogeneity}$=0.54, I2=0.00%; Allelic model: C vs. T: OR=0.708, 95%CI=0.605-0.829, P=0.000, $P_{heterogeneity}$=0.000, I2=92%). Conversely, the OR of dominant and allelic models in Asian descent represent decreasing CRC risk.

Secondly, Namazi et al. mentioned to the extracted genotyping method, the source and genotype distribution of control groups from all included studies and they acclaimed that the allele frequencies among populations of these studies conformed to Hardy-Weinberg equilibrium (HWE). However, the reviewing of the original studies showed contrary to this entry. The allele frequencies among populations of six articles (Krupa and Blasiak, 2004; Jin et al., 2005; Canbay et al., 2011; Krupa et al., 2011; Zhao et al., 2012; Nissar et al., 2014) demonstrated the deviation from HWE (Table 1) and there is no data about the genotyping method and source of the control groups. Furthermore, the author has been mentioned analysis of data was performed by Comprehensive Meta-Analysis software (version 5), while the latest released version of this software is 3.

According to the mentioned points, the results of this meta-analysis study may be not reliable, and the re-evaluating of the relevant studies of the association between XRCC3 Thr241Met polymorphism and the risk of colorectal cancer requires a closer look.

References

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Table 1. The Included Studies That Deviated from HWE

			Genotype distribution in controls				
First author	Country	Ethnicity	CC	CT	TT	P HWE	Deviated from HWE
Nissar et al. 2014	Kashmir	Asian	118	22	10	<0.001	Yes
Zhao et al. 2012	China	Asian	846	81	43	<0.001	Yes
Krupa et al. 2011	Poland	Caucasian	50	47	3	0.039	Yes
Canbay et al. 2011	Turkey	Caucasian	74	146	27	<0.001	Yes
Jin et al. 2005	China	Asian	268	11	1	0.025	Yes
Krupa and Blasiak et al. 2004	Poland	Caucasian	11	81	8	<0.001	Yes

HWE, Hardy-Weinberg Equilibrium

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