LETTER to the EDITOR

Note of Clarification of Data in the Meta-analysis of XPC 939A>C and 499C>T Polymorphisms in Skin Cancer

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Dear Editor

We read with great interest the paper (Ji et al., 2012). The author conducted a meta-analysis of eight case–control studies (3,892 cancer cases and 4,287 controls) to estimate the association of Ala499Val and Lys939Gln polymorphisms in XPC gene with skin cancer. His meta-analysis suggested no significant differences for association of Ala499Val and Lys939Gln polymorphisms with skin cancer. It is a valuable study.

Nevertheless, careful examination of the data provided by the author (Table 1 in the original text) revealed an issue that is worth noticing. There is one data is inconsistent with the original study (Blankenburg et al., 2005). The original text never referred to Lys939Gln polymorphism. However, another site Arg492His (exon 8) was used as Lys939Gln for data analysis.

We reassessed the association between XPC Ala499Val, Lys939Gln polymorphisms and skin cancer. This meta-analysis consisted of 5,914 cancer cases and 6,496 controls. In addition to the above eight studies, other three case–control reports were considered (Millikan et al., 2006, Kietthubthew et al., 2006, Paszkowska-Szczur et al., 2013), And we add another hotspot PAT polymorphism in XPC gene to our meta-analysis(Shen et al., 2001, Nelson et al., 2005, Yang et al., 2005, Sugimura et al., 2006). However, one group (Millikan et al., 2006) of deviation from Hardy–Weinberg equilibrium in control was not included. Therefore, we analyzed 14 studies in this meta-analysis (Table 1). This meta-analysis also showed that there was no significant difference for association of XPC Ala499Val, Lys939Gln, PAT polymorphisms with melanoma or nomelanoma under the additive model, dominant model and recessive model (Table 2) after

Table 1. The Distribution of the XPC Variants for Cases and Controls

Author	Publication	Case			Control			P^a	Type of
Lys939Gln	year	A/A	A/C	C/C	A/A	A/C	C/C		cancer
Paszkowska S K.	2013	227	314	94	480	647	209	0.711	melanoma
Goncalves, F. T.	2011	61	93	38	102	85	21	0.598	melanoma
Maider I V	2011	196	289	114	127	198	54	0.098	melanoma
Figl, A.	2010	420	568	197	460	597	216	0.348	melanoma
An, J.	2007	312	399	118	315	425	114	0.117	SCC
Li, C.	2006	223	281	98	195	311	97	0.144	melanoma
Thirumaran, R K.	2006	179	258	92	179	262	92	0.817	BCC
Kietthubthew, S.	2006	59	37	10	87	67	10	0.538	SCC
Festa, F.	2005	86	94	17	260	230	55	0.694	BCC
Ala499Val		C/C	C/T	T/T	C/C	C/T	T/T		
Paszkowska S K	2013	245	240	34	548	563	177	0.094	melanoma
Maider I V	2011	323	227	49	198	158	23	0.245	melanoma
Figl, A.	2010	626	477	81	670	516	88	0.398	melanoma
An, J.	2007	445	293	91	454	342	58	0.553	SCC
Li, C.	2006	338	214	37	318	248	50	0.866	melanoma
Blankenburg, S.	2005	219	146	8	185	95	14	0.689	melanoma
PAT		-/-	-/+	+/+	-/-	-/+	+/+		
Goncalves, F. T.	2011	65	85	42	114	73	21	0.077	melanoma
Kietthubthew, S.	2006	60	36	10	89	66	9	0.472	SCC
Sugimura, T..	2006	42	63	17	78	128	35	0.131	SCC
Yang, M.	2005	35	29	9	38	33	11	0.379	SCC
Nelson, H. H.	2005	278	333	121	211	303	99	0.574	BCC
Nelson, H. H.	2005	205	294	73	211	303	99	0.574	SCC
Shen, H. B.	2001	102	135	50	141	133	37	0.514	SCC

[a]*P*-value for Hardy–Weinberg equilibrium in control group

Table 2. ORs and 95% CI for Skin Cancer and XPC Polymorphisms under Different Genetic Models

SNP	Type of cancer	Genetice model								
		Additive			Recessive			Dominant		
		OR [95% CI] *P*	*P**	*P***	OR [95% CI] *P*	*P**	*P***	OR [95% CI] *P*	*P**	*P***
	Melanoma	1.085[0.931~1.264]0.297	0.002	0.327	1.071[0.941~1.22]0.299	0.036	0.05	1.073[0.873~1.32]0.502	0.005	0.327
939A>C	Nomelanoma	1.011[0.918~1.113]0.827	0.98	0.497	1.04[0.859~1.259]0.689	0.684	1	1.002[0.875~1.147]0.982	0.744	0.497
	Total skin cancer	1.045[0.956~1.143]0.329	0.023	0.233	1.061[0.953~1.182]0.279	0.16	0.112	1.035[0.916~1.169]0.583	0.037	0.233
499C>T	Total skin cancer	0.943[0.835~1.064]0.339	0.012	0.851	0.867[0.555~1.357]0.533	0	0.573	0.934[0.857~1.018]0.12	0.268	0.851
PAT	Total skin cancer	1.123[0.902~1.399]0.299	0	0.453	1.205[0.873~1.664]0.256	0.01	0.453	1.124[0.854~1.479]0.404	0	0.176

**P*-value for heterogeneity test; ***P*-value for Begg's test (Publication bias); Random-effects model was used when *P* value for heterogeneity test < 0.05

adding new genotyping data.

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