



Association between Maternal and Fetal MTHFR C677T and MTRR A66G Polymorphisms with the Risk of NTDs: A Systematic Review and Meta-Analysis Study

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Received 2021 June 25; Revised 2021 September 25; Accepted 2021 November 09.

Abstract

Background: Neural tube defects (NTDs) are classed as multifactorial birth defects of the brain and spinal cord that arise during embryonic development. Although the etiology is not well understood, NTDs are reported to be prevented by maternal folic acid supplementation before and during early pregnancy.

Objectives: This meta-analysis study aimed to assess the association between fetal and maternal methylenetetrahydrofolate reductase (MTHFR) C677T and methionine synthase reductase (MTRR) A66G polymorphisms with the risk of NTDs.

Methods: The PubMed, Scopus, and Springer Link databases were searched (from March 2000 to November 2020) for the literature on the association between MTHFR C677T and MTRR A66G polymorphisms with the risk of NTDs.

Results: In total, 33 studies were reviewed in the present study, and it was revealed that, unlike MTRR A66G polymorphism, MTHFR C677T was statistically associated with the risk of NTDs in the overall population. The results of subgroup analysis showed that the Indian subcontinent subgroup with maternal MTHFR C677T polymorphism and the European subgroup with fetal MTHFR C677T polymorphism was significantly susceptible to NTDs.

Conclusion: The obtained results revealed that, unlike MTRR A66G, maternal and fetal MTHFR C677T polymorphisms were significantly associated with NTDs. Subgroup analysis also demonstrated that folic acid deprivation can be considered the main cause of MTHFR C677T polymorphism in some areas.

Keywords: Methionine synthase reductase, Methylenetetrahydrofolate reductase, Neural tube defects, Polymorphism

1. Background

The neural tube defects (NTDs) are among the most important congenital malformations occurring during the early stage of embryogenesis. NTDs occurs by a failure in neural tube closure and its prevalence is about 1 per 1000 birth (1, 2). The NTDs are classified into two major groups including anencephaly and spina bifida. The precise mechanism of NTDs is not fully elucidated; however, it has been suggested that environmental and genetic factors are involved in its incidence (3). The results of previous studies revealed that folic acid deficiency and high levels of homocysteine might be associated with the risk of NTDs (4, 5). Based on epidemiological studies, hyperhomocysteinemia is an emerging risk factor for cardiovascular diseases and neural tube abnormalities. In addition, the consumption of folic acid supplementation by pregnant women reduces the risk of NTDs in fetuses. Considering the role of folic acid in the occurrence of NTDs, the enzymes involved in folate metabolism might be important in NTDs pathogenesis and single nucleotide polymorphisms (SNPs) (4, 6, 7). One of these enzymes is methylenetetrahydrofolate reductase

(MTHFR) which prompts the conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate and has a key role in folic acid metabolism (8). This enzyme has also a pivotal role in the synthesis of DNA and RNA, and protein metabolism (9). MTHFR gene is located on chromosome 1 (1p36.3) and has been documented for 14 rare and one common mutation (C677T, rs1801133) (10). C677T polymorphism is a point mutation at nucleotide 677 of the MTHFR gene which triggers the conversion of C nucleotide to T nucleotide and substitution of alanine with valine in MTHFR protein (8, 11).

Methionine synthase reductase (MTRR) is another enzyme maintaining methylcobalamin (cofactor of methionine synthase) in sufficient levels. This enzyme catalyzes the methylation of cobalamin using S-adenosylmethionine as a methyl donor and ultimately restores methionine synthase activity (12, 13). MTRR gene is mapped on chromosome 5p15.2-p15.3 (14). A66G is a single nucleotide polymorphism (rs1801394) in the MTRR gene that provokes the substitution of isoleucine with methionine at position 22 (13). It has been previously documented that MTRR polymorphism increases the risk of NTDs (15-17).

2. Objectives

Regarding the potential role of mentioned polymorphisms on folate metabolism pathway and level, and considering the existing controversy in previous studies, the present meta-analysis study aimed to investigate the association of maternal and fetal MTHFR C677T and MTRR A66G with the risk of NTDs.

3. Methods

3.1. Search strategy

The association of maternal or fetal MTHFR C677T and maternal or fetal MTRR A66G polymorphisms with the risk of NTDs was evaluated independently by two authors who performed a comprehensive literature search in PubMed, Scopus, and Springer Link databases. The keywords used for systematic search in databases included MTHFR C677T, methylenetetrahydrofolate reductase, polymorphism OR variant OR SNPs, MTRR A66G, methionine synthase reductase, NTDs, neural tube defect, and spina bifida. Two authors independently reviewed literature from each study according to the name of the first author, the year of publication, a sample size of case and control groups, and allelic and genotype frequencies. Any conflict between the two authors was resolved by consultation with a third reviewer.

3.2. Inclusion criteria

The inclusion criteria in the present meta-analysis study included case-control studies which assessed the association of maternal or fetal MTHFR C677T and maternal or fetal MTRR A66G polymorphisms with NTDs risk. The literature was supposed to provide enough data for genotype or allelic frequencies in case and control groups. Eventually, only full texts studies with human subjects written in English were included in the present meta-analysis study.

3.3. Exclusion criteria

The exclusion criteria in the present study included 1) Studies conducted before 2000; 2) Animal studies; 3) Studies with insufficient information for allelic and genotype frequencies in case and control groups; 4) Non-English articles; and 5) Letters, reviews, hypothesis studies, and short communication articles.

3.4. Statistical analysis

The data were analyzed using STATA software (Version 16.0). The odds ratio (OR) with a 95% confidence interval (CI) was used to assess the association of maternal and fetal MTHFR C677T and MTRR A66G polymorphism with susceptibility to NTDs. The pooled ORs were calculated by the Random-effects model (Mantel-Hansel method) for allelic, homozygous, heterozygous, dominant, and recessive models. The heterogeneity in the present meta-analysis study was evaluated using I^2 , χ^2 , and τ^2 . The Forest plots were used to visualize the overall effects, and the Egger's test, Beggs's test (18), and funnel plot were adopted for the assessment of publication bias. Eventually, the literature was geographically subdivided into different sub-groups.

4. Results

4.1. Literature characteristics

The 573 articles were identified in PubMed, Scopus, and Springer link databases. According to the inclusion and exclusion criteria, authors reviewed the records based on their titles and their abstracts, and 531 literatures were excluded from the study. The selected studies were reviewed according to their full text and nine studies were removed subsequently. Ultimately, 33 articles were included in the present meta-analysis study (Figure 1). Tables 1 and 2 present the main characteristics of the included studies.

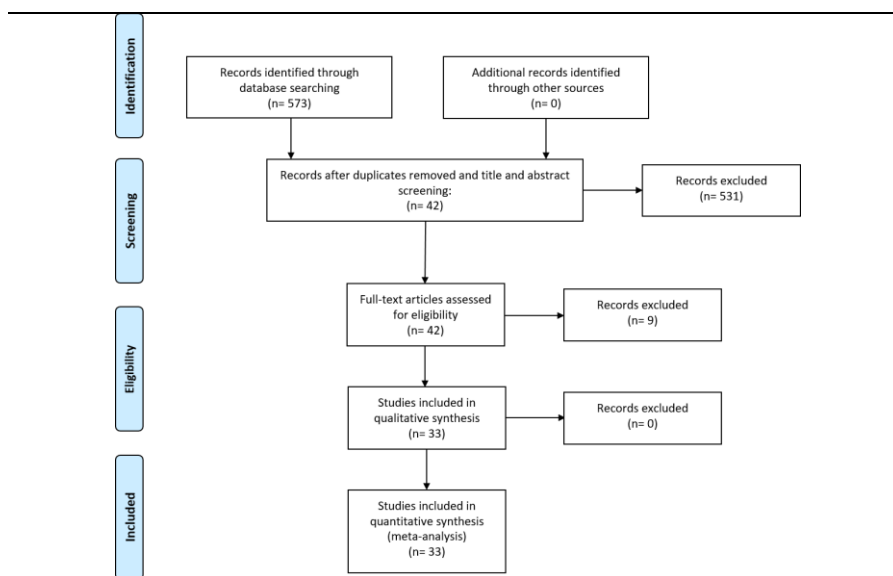


Figure 1. Flowchart of the procedure for literature search

Table 1. Characteristics of included studies for the association of maternal and fetal MTHFR C677T with neural tube defect risk

Characteristics of included studies on the association of maternal and fetal MTHFR C677T with neural tube defect risk										
Author's name	Year	Country	Case (N)	Control (N)	CC	Case CT	TT	CC	Control CT	TT
Da'valos (34)	2000	Mexico	68	101	19	35	14	31	51	19
Lucock (15)	2000	United Kingdom	19	31	8	9	2	11	17	3
Lucock (35)	2001	United Kingdom	21	28	9	9	3	12	13	3
martinez (36)	2001	Mexico	38	31	11	12	15	12	16	3
Garcia-Fragoso(37)	2002	Puerto	37	100	7	23	7	41	50	9
Arbour (38)	2002	Canada	74	101	32	31	11	52	38	11
Parle-McDermott (27)	2003	Ireland	277	255	105	138	36	125	104	26
Alvarez Perez (39)	2003	Brazil (white)	81	52	37	38	6	30	16	6
Alvarez Perez (39)	2003	Brazil (nonwhite)	50	74	37	12	1	51	20	3
Relton (40)	2004	United Kingdom	186	512	86	78	22	191	254	67
Felix (41)	2004	Brazil	41	44	19	15	7	16	22	6
Grandone (42)	2006	Italy	57	143	10	35	12	38	79	26
Dalal (43)	2007	India	101	60	56	21	26	45	12	3
Houcher (44)	2009	Algeria	48	147	14	25	9	67	59	21
Erdogan (45)	2010	Turkey	26	48	5	14	7	18	21	9
Naushad (46)	2010	India	50	80	33	11	6	64	16	0
Godbole (47)	2011	India	305	684	238	62	5	521	158	5
Husna (25)	2013	Malaysia	24	14	15	8	1	11	3	0
Zhi-zhen (48)	2013	China	51	66	10	25	16	22	22	7
Kondo (49)	2014	Japan	230	9034	47	56	12	1763	2060	694
Wang (50)	2015	China	144	300	31	73	40	96	159	45
Bourouba (51)	2018	Algeria	48	82	25	17	6	33	35	14
Nasri (32)	2018	Tunisia	77	71	21	41	15	31	34	6
Nauman (52)	2018	Pakistan	109	100	67	31	11	72	26	2
Cai (53)	2019	China	61	61	5	30	26	15	27	19
Characteristics of included studies on the association of fetal MTHFR C677T with neural tube defect risk										
Garcia-Fragos (37)	2002	USA	31	100	10	18	3	41	50	9
Parle-McDermott (27)	2003	Ireland	279	255	108	118	53	125	104	26
Alvarez Perez (39)	2003	Brail (white)	81	51	35	38	8	29	15	7
Alvarez Perez (39)	2003	Brazil (nonwhite)	50	75	32	16	2	52	22	1
Relton (40)	2004	United Kingdom	200	578	92	78	30	267	247	64
Grandone (42)	2006	Italy	15	143	0	11	4	38	79	26
Erdogan (45)	2010	Turkey	33	48	13	16	4	18	21	9
Behunova (54)	2010	Slovakia	93	290	47	36	9	164	106	20
ESER(55)	2010	Turkey	39	34	18	14	7	19	17	8
Husna MZ (25)	2013	Malaysia	24	13	18	6	0	11	2	0
Fang (56)	2018	China	152	169	22	67	64	40	77	52

Table 2. Characteristics of included studies on the association of maternal and fetal MTRR A66G with neural tube defect risk

Characteristics of included studies on the association of maternal MTRR A66G with neural tube defect risk										
Author's name	Year	Country	Case N	Control N	AA	Case AG	GG	AA	Control AG	GG
LUCOCK (35)	2001	United Kingdom	21	28	5	10	6	8	14	6
Relton (40)	2004	United Kingdom	203	532	208	107	68	58	263	211
Relton (57)	2004	United Kingdom	89	176	12	42	35	20	82	74
O'Leary (24)	2005	Ireland	447	476	149	215	83	178	222	76
Van an derLinden(58)	2006	Netherlands	116	264	18	45	53	53	135	76
Candito (24)	2008	France	77	61	16	39	22	22	25	14
Naushad(46)	2010	India	50	80	0	33	17	0	52	28
Abbas (31)	2016	Algeria	38	67	10	20	8	15	43	9
Nasri (32)	2018	Tunisia	62	64	16	34	12	7	44	13
Cai (53)	2019	China	61	61	22	31	8	33	24	4
Characteristics of included studies on the association of fetal MTRR A66G with neural tube defect risk										
Relton (40)	2004	Tunisia	201	601	23	125	53	28	265	308
O'Leary (26)	2005	Ireland	470	476	149	240	81	178	222	76
Wang (59)	2015	China	165	280	45	91	29	105	139	36
Abbas (31)	2016	Algeria	48	66	20	25	3	14	43	9
Fang (56)	2018	China	151	169	66	67	18	95	62	11

4.2. Evaluation of the association between maternal MTHFR C677T polymorphism and NTDs risk

In total, 25 literature, including 2,225 cases and 12,204 controls were analyzed in the present meta-analysis study to assess the association of maternal MTHFR C677T polymorphism with the risk of NTDs.

The random-effects model was used to evaluate the pooled OR. As indicated in Table 3 and Figure 2A, alleles and genotypes of maternal MTHFR C677T polymorphism were statically associated with NTDs. The allelic (log (OR)=1.344, 95% CI=1.147, 1.574) (P<0.001), homozygous (log (OR)=1.880, 95%

CI=1.360, 2.598) (P<0.001) and heterozygous (log (OR) =1.237, 95% CI=1.036, 1.477) (P=0.019) models showed significant correlation with the risk of NTDs. On the other hand, same results were observed in dominant (log (OR)=1.384, 95% CI=1.136, 1.689) (P<0.001) and recessive models (log (OR)=1.536, 95% CI=1.194, 1.977) (P<0.001).

4.3. Evaluation of the association of fetal MTHFR C677T polymorphism with NTDs risk

In total, 11 studies with 997 cases and 1,756 controls were included in the present meta-analysis to evaluate the association of fetal MTHFR C677T polymorphism with risk of NTDs. As presented in Table 3 and Figure 2 B, allelic (log (OR)=1.261, 95% CI=1.072, 1.485) (P=0.005), homozygous (log (OR)=1.6644, 95% CI=1.263, 2.140) (P<0.001), and heterozygous models (log (OR)=1.212, 95% CI=1.008,

1.456) (P=0.040) were associated with the risk of NTDs. In addition, the dominant (log (OR)=1.297, 95% CI=1.092, 1.540) (P=0.003) and recessive models (log (OR)=1.467, 95% CI=1.163, 1.850) (P<0.001) were significantly associated with the risk of NTDs.

4.4. Evaluation of the association between maternal and fetal MTRR A66G polymorphism with NTDs risk

In total, 10 literatures with 1,164 cases and 1,809 controls were included to assess the maternal MTRR A66G polymorphism with NTD risk. In the following, five articles with 1,035 cases and 1,592 controls were included in the present study to analyze fetal MTRR A66G polymorphism with NTD risk. As presented in Table 4 and Figure 3 A and B, it was revealed that alleles and genotypes of maternal and fetal MTRR A66G had no significant association with NTD risk.

Table 3. Meta-Analysis of pooled association of maternal and fetal MTHFR C677T polymorphism with neural tube defect risk

Meta-Analysis of the pooled association between maternal MTHFR C677T polymorphism with the risk of neural tube defect							
Variation	Number of Studies	Case frequency	Control frequency	OR (95% CI)	OR P-value	I ² , heterogeneity P-value	Publication Bias (Begg's Test, P-value; Egger's Test, P-value)
C	25	2738	10041	-	-	-	-
T	25	1482	5323	-	-	-	-
CC	25	947	3368	-	-	-	-
CT	25	849	3312	-	-	-	-
TT	25	316	1007	-	-	-	-
T vs. C	25	-	-	1.344 (1.147, 1.574)	<0.001	64.4%, P< 0.001	(z= -.28,P-value =0.005, z=.76, P-value =0.083)
TT vs. CC	25	-	-	1.880 (1.360, 2.598)	<0.001	54.4%, P< 0.001	(z=-.39,P-value =0.003, z=1.2,P-value =0.140)
CT vs. CC	25	-	-	1.237 (1.036, 1.477)	0.019	38.5%, P= 0.027	(z=1.12,P-value =0.088, z=.86,P-value =0.088)
TT+CT vs. CC	25	-	-	1.384 (1.136, 1.689)	<0.001	55.8%, P< 0.001	(z=1.24P-value =0.021, z=-.98P-value =0.047)
TT vs. CT+CC	25	-	-	1.536 (1.194, 1.977)	<0.001	40.5%, P= 0.020	(z=1.43,P-value <0.001, z=.46,P-value =0.200)
Meta-Analysis of the pooled association between fetal MTRR A66G polymorphism and neural tube defect risk							
C	11	1206	2348	-	-	-	-
T	11	797	1208	-	-	-	-
CC	11	395	804	-	-	-	-
CT	11	418	740	-	-	-	-
TT	11	184	222	-	-	-	-
T vs. C	11	-	-	1.261 (1.072, 1.485)	0.005	31.2%, P= 0.150	(z=1.53,P-value =0.534, z=-1.37P-value =0.533)
TT vs. CC	11	-	-	1.644 (1.263, 2.140)	< 0.001	0.0%, P= 524	(z=1.69,P-value =0.527, z=-1.32P-value =0.429)
CT vs. CC	11	-	-	1.212 (1.008, 1.456)	0.040	0.0%, P= 0.601	(z=1.45.P-value =0.321, z=1.62,P-value =0.125)
TT+CT vs. CC	11	-	-	1.297 (1.092, 1.540)	0.003	0.0%, P= 0.569	(z=-.78,P-value =0.706, z=.88,P-value =0.460)
TT vs. CT+CC	11	-	-	1.467 (1.163, 1.850)	< 0.001	0.0%, P= 0.700	(z=1.3,P-value =0.016, z=.6,P-value =0.090)

Log (OR): Logarithm of odds ratio, I2: relative heterogeneity, OR P<0.05 was considered statistically significant

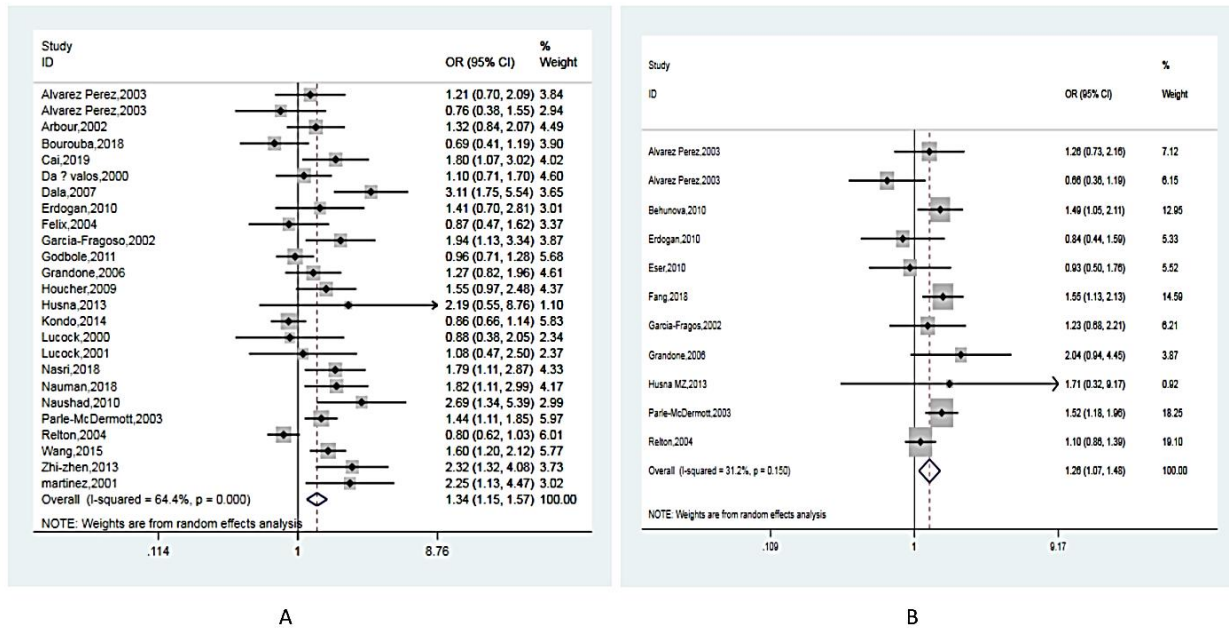


Figure 2. Forest plot of the association between maternal (A) and fetal (B) MTHFR C677T polymorphism with neural tube defect risk using T versus C allelic model in total population

4.5. Subgroup analysis of the pooled association between maternal and fetal MTHFR C677T and MTRR A66G polymorphisms with NTDs risk

As specified in Table 5, maternal MTHFR C677T polymorphism in Indian subcontinent subgroup had

a significant association with NTDs risk in allelic (log(OR)=1.875, 95% CI=1.023, 3.434) (P=0.042), homozygous (log(OR)=4.920, 95% CI=2.387, 10.13) (P<0.001), and recessive models (log(OR)=4.745, 95% CI=2.313, 9.734) (P<0.001).

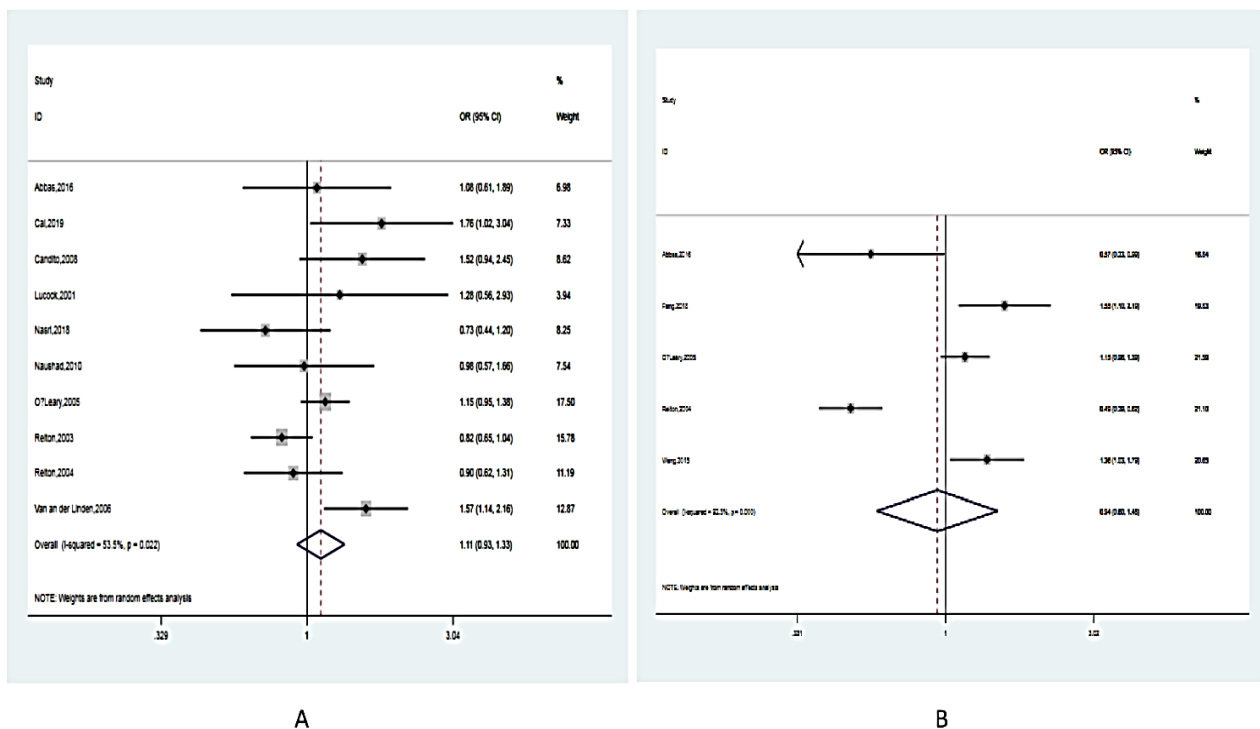


Figure 3. Forest plot of association of maternal (A) and fetal (B) MTRR A66G polymorphism with neural tube defect risk using A versus G (allelic model) in total population

Table 4. Meta-analysis of the pooled association between maternal and fetal MTRR A66G polymorphism with neural tube defect risk

Meta-Analysis of the pooled association between maternal MTRR A66G polymorphism and neural tube defect risk							
Variation	Number of Studies	Case frequency	Control frequency	OR (95% CI)	OR P-value	I ² , heterogeneity P-value	Publication Bias (Begg's Test, P-value; Egger's Test, P-value)
A	10	1126	1692	-	-	-	-
G	10	1198	1926	-	-	-	-
AA	10	456	394	-	-	-	-
AG	10	576	904	-	-	-	-
GG	10	312	511	-	-	-	-
G vs. A	10	-	-	1.110 (0.926, 1.331)	0.259	53.5%, P= 0.022	(z=-.7, P-value =0.027, z=-.88, P-value =0.127)
GG vs. AA	10	-	-	0.947 (0.362, 2.474)	0.912	93.3%, P<0.001	(z=1.47, P-value =0.323, z=2.03, P-value =0.220)
AG vs. AA	10	-	-	0.772 (0.353, 1.690)	0.518	92.7%, P<0.001	(z=1.5, P-value =0.405, z=-.001, P-value =0.461)
GG+AG vs. AA	10	-	-	0.825 (0.356, 1.911)	0.653	94.5%, P<0.001	(z=1.36, P-value =0.351, z=-0.16, P-value =0.408)
GG vs. AG+AA	10	-	-	1.106 (0.675, 1.813)	0.689	85.0%, P<0.001	(z=2.06, P-value =0.273, z=1.002, P-value =0.129)
Meta-Analysis of the pooled association between fetal MTRR A66G polymorphism and neural tube defect risk							
A	5	1572	1154	-	-	-	-
G	5	1610	916	-	-	-	-
AA	5	420	303	-	-	-	-
AG	5	731	548	-	-	-	-
GG	5	440	184	-	-	-	-
G vs. A	5	-	-	0.940 (0.599, 1.477)	0.790	92.3%, P<0.001	(z=.13, P-value =0.982, z=-.29, P-value =0.849)
GG vs. AA	5	-	-	0.831 (0.334, 2.068)	0.691	89.5%, P<0.001	(z=1.2, P-value =0.789, z=-1.26, P-value =0.480)
AG vs. AA	5	-	-	1.033 (0.683, 1.562)	0.879	73.2%, P= 0.05	(z=1.4, P-value =0.349, z=1.28, P-value =0.162)
GG+AG vs. AA	5	-	-	0.933 (0.548, 1.588)	0.798	85.3%, P<0.001	(z=1.29, P-value =0.621, z=-1.85, P-value =0.170)
GG vs. AG+AA	5	-	-	0.873 (0.427, 1.786)	0.710	88.9%, P<0.001	(z=1.88, P-value =0.834, z=3.2, P-value =0.551)

Log (OR): Logarithm of odds ratio, I²: relative heterogeneity, OR P<0.05 was considered statistically significant

Table 5. Subgroup meta-analysis of the pooled association between maternal and fetal MTHFR and MTRR polymorphisms and neural tube defect risk

Subgroup meta-analysis of the pooled association between maternal MTHFR C677T polymorphism with neural tube defect risk						
	T vs. C OR (95%CI), P-value	TT vs. CC OR (95%CI), P-value	CT vs. CC OR (95%CI), P-value	TT+CT vs. CC OR (95%CI), P-value	TT vs. CT+CC OR (95%CI), P-value	
Africa	1.260 (0.727, 2.186), 0.410	1.631 (0.571, 4.657), 0.361	1.338 (0.667, 2.685), 0.413	1.383 (0.638, 2.996), 0.411	1.370 (0.674, 2.786), 0.385	
East Asia	1.489 (0.959, 2.312), 0.076	2.290 (0.860, 6.093), 0.097	1.528 (0.965, 2.420), 0.071	1.807 (0.985, 3.316), 0.056	1.545 (0.794, 3.007), 0.200	
Europe	1.090 (0.797, 1.490), 0.589	1.177 (0.765, 1.812), 0.458	1.075 (0.655, 1.763), 0.776	1.097 (0.671, 1.794), 0.712	1.103 (0.799, 1.523), 0.552	
Indian subcontinent	1.875 (1.023, 3.434), 0.042	4.920 (2.387, 10.13), <0.001	1.011 (0.778, 1.314), 0.935	1.547 (0.917, 2.609), 0.102	4.745 (2.313, 9.734), <0.001	
South America	1.138 (0.832, 1.557), 0.419	1.258 (0.650, 2.433), 0.496	1.032 (0.688, 1.547), 0.880	1.099 (0.773, 1.543), 0.598	1.289 (0.609, 2.727), 0.506	
Mixed	1.544 (1.141, 2.089), 0.005	2.361 (1.239, 4.498), 0.009	1.784 (1.121, 2.840), 0.015	1.859 (1.200, 2.878), 0.005	1.681 (0.950, 2.977), 0.075	
Subgroup meta-analysis of the pooled association between fetal MTHFR C677T polymorphism and neural tube defect risk						
Europe	1.375 (1.107, 1.707), 0.004	1.784 (1.235, 2.576), 0.002	1.147 (0.859, 1.531), 0.353	1.274 (0.944, 1.720), 0.114	1.643 (1.210, 2.231), 0.001	
Mixed	1.121 (0.864, 1.455), 0.390	1.444 (0.932, 2.236), 0.100	1.407 (1.022, 1.939), 0.036	1.407 (1.042, 1.899), 0.026	1.258 (0.880, 1.797), 0.208	
Subgroup meta-analysis of the pooled association between maternal MTRR A66G polymorphism and neural tube defect risk						
	G vs. A OR (95%CI), P-value	GG vs. AA OR (95%CI), P-value	AG vs. GG OR (95%CI), P-value	GG+AG vs. G OR (95%CI), P-value	GG vs. AG+AA OR (95%CI), P-value	
Europe	1.132 (0.905, 1.417), 0.278	0.902 (0.253, 3.221), 0.874	0.781 (0.269, 2.266), 0.649	0.831 (0.266, 2.602), 0.751	1.026 (0.524, 2.011), 0.940	
Mixed	1.067 (0.740, 1.539), 0.728	1.066 (0.406, 2.801), 0.896	0.792 (0.319, 1.963), 0.614	0.855 (0.341, 2.146), 0.739	1.186 (0.747, 1.885), 0.469	

Log (OR): Logarithm of odds ratio, P<0.05 was considered statistically significant

In addition, maternal MTHFR C677T polymorphism in the mixed subgroup was connected to NTDs risk in allelic (log (OR)=1.544, 95% CI=1.141, 2.089) (P=0.001) model. Same results were associated with the risk of NTDs in homozygous (log (OR)=2.361, 95% CI=1.239, 4.498) (P=0.009), heterozygous (log (OR) =1.784, 95% CI=1.121, 2.840) (P=0.015), and dominant models (log (OR)=1.859, 95% CI=(1.200, 2.878) (P=0.005).

As for the fetal MTHFR C677T polymorphism in the Europe sub group, a significant association with NTDs risk was observed in the allelic (log (OR)=1.375, 95% CI=(1.107, 1.707) (P=0.004), homozygous (log(OR)=1.784, 95% CI=1.235, 2.576) (P=0.002) and recessive models (log(OR)=1.634, 95% CI=(1.210, 2.231) (P=0.001).

No significant association was observed in the maternal MTRR A66G polymorphism with the risk of NTDs in different subgroups (Table 5).

4.6. Publication bias

The Egger's test and Begg's funnel plot were performed to evaluate the publication bias between the studies. However, since Egger's test could indicate publication bias better than Begg's test, the results of Egger's test were assessed to determine the publication bias. Based on the results of Egger's test, no publication bias was detected in different genetic models, except for the maternal MTHFR C677T dominant model (TT+CT vs. CC P=0.047) (Table 3 and 4).

5. Discussion

The NTD, as a congenital malformation of the central nervous system, occurs in the early stage of embryogenesis (about 28 days after conception) and is caused by a defect in neural tube closure (19, 20). Different major types of NTDs include anencephaly, encephalocele, and spina bifida. Anencephaly is the fetal type of NTDs, while spina bifida causes severe disability in affected children (3). The results of previous studies revealed that the consumption of folic acid supplementation during pregnancy reduced the risk of NTDs in the offspring of these women. This indicates the crucial function of folic acid in the pathogenesis of NTDs (4, 6). As a coenzyme for DNA synthesis and DNA methylation enzymes, folic acid has a central role in the neurulation process during embryogenesis (21-23). Regarding the role of folic acid in the pathogenesis of NTDs, the enzymes involved in the folic acid metabolism can be targeted for NTDs-related studies. MTHFR and MTRR are among the enzymes that are involved in folate metabolism (8, 16). The SNPs in the genes of these enzymes can change their activity and cause NTDs by altering folate levels. The results of previous studies revealed that MTHFR C677T and MTRR A66G polymorphisms might be related to NTDs incidence (24-27). Considering the statistical power of the

meta-analysis, the present study aimed to investigate the relation of maternal and fetal MTHFR C677T and MTRR A66G with susceptibility to NTDs.

The results of 25 literatures with 2,225 cases and 12,204 controls were combined to assess the association of maternal MTHFR C677T with the NTDs risk. With no publication bias, it was revealed that maternal MTHFR C677T polymorphism was linked to the occurrence of NTDs in newborns. In addition, the results of subgroup analysis indicated that there was a significant correlation between the maternal MTHFR C677T polymorphism and NTDs risk in the Indian subcontinent and mixed subgroups.

In the present meta-analysis study, the association of fetal MTHFR C677T polymorphism with the risk of NTDs was investigated in 11 studies with 997 cases and 1,756 controls that have been selected based on the inclusion and exclusion criteria. The findings showed that fetal MTHFR C677T polymorphism was associated with susceptibility to NTDs in the overall population and the European subgroup. This result was in line with the result of the study performed by Yang et al. (28), which showed that maternal and fetal MTHFR C677T polymorphism was associated with the risk of NTDs. In the same line, Yadav et al. also reported a positive association between maternal MTHFR C677T polymorphism and MTRR A66G polymorphism with the NTDs risk (29). According to this study, MTHFR C677T polymorphism was strongly associated with NTDs in Asian, European, and American subgroups. These results might be associated with variations in folate, vitamin B12, and vitamin B6 intake in different geographical areas. These findings were in line with those obtained in this study, except that in the present study a positive relation was observed between the fetal MTHFR C677T polymorphism in the European subgroup. The results of the present study indicated that there was no association between maternal and fetal MTHFR C677T polymorphism with the risk of NTDs in the East Asian population. Our results opposed those obtained in the previous studies which have verified the association of MTHFR polymorphism and the risk of NTDs in the Asian population (28, 30). This contradiction might be due to the omission of non-English language studies in this meta-analysis study which included only original articles and excluded letters, short communication articles, and reports.

Previous studies have introduced MTRR A66G polymorphism as another mutation contributing to both maternal and fetal NTDs (31, 32). This theory was assessed with a combination of the results of 10 literatures (including 1,164 cases and 1,809 controls) and 5 studies (including 1,035 cases and 1,592 controls). The obtained results reported a negative correlation of the maternal and fetal MTRR A66G polymorphisms with NTDs risk in offspring. In contrast to the results of this study, Yadav et al. (29)

showed that maternal MTRR A66G was associated with the occurrence of NTD. Although the adopted inclusion and exclusion criteria in this study were similar to those used in other studies, the discrepancies in the results could be attributed to the number of original publications included in this study.

In another meta-analysis study conducted by Shengrong Ouyang et al., 10 studies (including 1,358 cases and 2,169 controls) were analyzed to explore the association of MTRR A66G polymorphisms and NTDs risks in Caucasian children. The result of this study reflected a negative association between the MTRR A66G polymorphisms and NTDs risks (33). These results could be related to the limited number of publications in the Caucasus area. The results of this study were consistent with these results; however, a negative relation between the MTRR A66G polymorphisms and NTDs risk during embryonic development was observed in this meta-analysis study.

The contradictory results in different meta-analysis studies can be explained by limited publications, different inclusion and exclusion criteria, and various folate supplementation in different countries. In addition, gene to gene interaction, epigenetic factors, and family history are important factors that were not involved in assessing the link of MTHFR and MTRR polymorphisms with the NTDs risks. All previous studies agreed on the importance of folate supplementation before and during the pregnancy and confirmed its relation with MTHFR and MTRR polymorphisms.

6. Conclusion

The present meta-analysis study revealed the possible association of maternal and fetal MTHFR polymorphisms and MTRR polymorphisms with NTDs risk by pooling the available data. Based on the obtained results in the present meta-analysis study, maternal and fetal MTHFR C677T polymorphism is associated with susceptibility to NTDs. Moreover, the results of the association of maternal and fetal MTRR A66G with the risk of NTDs suggested that there was no significant statistical association between maternal and fetal MTRR A66G with the risk of NTDs.

Acknowledgments

This study was partially supported by Zanjan University of Medical Sciences, Zanjan, Iran. The authors would like to thank colleagues at Shahid Beheshti University of Medical Sciences for their knowledge contribution during this study.

Footnotes

Authors' contributions: Dr. Reza Mahdian Joibari

designed and wrote the manuscript draft. Dr. Abolfazl Movafagh revised the draft, and Alireza Molaie performed the statistical analysis.

Ethical Approval: Not applicable.

Funding/Support: The authors received no financial support for this research.

Conflicts of Interest: Authors declare that they have no conflict of interest, regarding the publication of the present study.

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