Significant association of BDNF rs6265 G>A polymorphism with susceptibility to epilepsy: a meta-analysis

Introduction: Previously published articles have suggested that BDNF rs6265 G>A polymorphism is a potential risk factor for epilepsy. However, the results were not consistent.

Methods: We conducted a meta-analysis to explore the association between BDNF rs6265 G>A polymorphism and epilepsy risk. Four online databases were searched, and related studies were reviewed from their inception up to June 20, 2017. ORs and corresponding 95% CIs were used to calculate the associations of each genetic model. Overall, 10 case–control publications involving 9,512 subjects were included in this meta-analysis.

Results: Significant associations were found between BDNF rs6265 G>A polymorphism and epilepsy (A vs G: OR=0.88, 95% CI=0.83–0.94, P<0.01, I^2=0%); GA vs GG: OR=0.88, 95% CI=0.79–0.97, P=0.01, I^2=0%; AA vs GG: OR=0.79, 95% CI=0.70–0.90, P<0.01, I^2=0%; GA+AA vs GG: OR=0.85, 95% CI=0.77–0.94, P<0.01, I^2=0%; AA vs GG+GA: OR=0.85, 95% CI=0.76–0.95, P=0.01, I^2=0%). Subgroup analysis also showed similar results in an Asian population.

Conclusion: Our meta-analysis indicated that BDNF rs6265 G>A polymorphism might be involved in epilepsy susceptibility, especially in the Asian population.

Keywords: brain derived neurotrophic factor, epilepsy, seizure, polymorphism, variant, rs6265, case–control

Introduction

Epilepsy is a complex neurological disease that involves transient disturbances in cerebral function, which is mostly caused by pathologic neuronal discharges and characterized by recurrent and spontaneous seizures. To date, more than 50 million people worldwide have epilepsy. The prevalence of epilepsy is approximately 0.5%–1%, with a total annual incidence of 50–70 or 190 cases per 100,000 individuals in industrialized and developing countries. At least 80% of epilepsy patients live in a developing country, and only 25% of patients receive basic treatment. In 2017, the International League against Epilepsy (ILAE) published a revised operational classification of seizure types with focal onset, generalized onset, and unknown onset.

Morbidity due to epilepsy is more common in children and the elderly. The brain has been proven to be more “seizure susceptible” in childhood and old age. The immature brain mechanisms and degenerative changes may lead to an increased risk of epileptic seizures. Epilepsy is a serious threat to health and will lead to a significant economic burden for the patients and their families, as well as decreased quality of life. Today, epilepsy is not only a disease but also a serious problem in terms of public health, social stability, and economic development. However, current treatments focus on managing...
symptoms with a lot of antiepileptic drugs because the patho-
genesis of epilepsy remains unclear. In addition, the treatment
and prognosis for epilepsy are not yet satisfactory.

In the past decade, BDNF has been recognized as one of
the important neurotrophic factors that could regulate the
morphology of neurons and synapse formation, playing a
neuroprotective role in the central nervous system. Animal
model studies with transgenic mice also demonstrated that
overexpression of BDNF in the brain can interfere with
increased excitability and epilepsy risk. Single-nucleotide polymorphisms (SNPs) are drawing
increased attention in current studies, because they are one
of the most important genetic mutations and could regulate
BDNF expression and metabolism. A large amount of
research has proven that rs6265 G>A (with a nucleotide
change from guanine deoxyribonucleotide to adenine deoxy-
ribonucleotide) is the most common polymorphism located
in the BDNF gene that causes an amino acid change from
valine (Val) to methionine (Met), which may contribute to
various central nervous system diseases, such as Alzheimer’s
disease, Parkinson’s disease, depression, and bipolar
disorder. In 2003, Kanemoto et al published the first study
on the association between BDNF rs6265 G>A polymor-
phism and epilepsy risk and did not find any
significant association in a Japanese population. To date,
subsequent studies have been published about the relationship
between BDNF rs6265 G>A polymorphism and epilepsy
susceptibility, but the results were controversial. We there-
fore conducted this meta-analysis to more precisely assess
the association between BDNF rs6265 G>A polymorphism
and epilepsy susceptibility.

Methods
This meta-analysis was conducted under the guidance of
the Preferred Reporting Items for Systematic Reviews and
Meta-Analyses (PRISMA) statement. All included data
were collected from published studies, and there were no
ethical issues.

Search strategy
Four online databases (PubMed, Embase, CNKI, and
Wanfang) were searched for relevant studies with the follow-
ing search strategy on the association between BDNF rs6265
G>A polymorphism and epilepsy risk from their inception up
to June 20, 2017. The bibliographies of the collected studies
and relevant reviews were retrospectively assessed to identify
additional articles. Only studies that were written in English
and Chinese were included. The following search terms and
strategy were used (for example in PubMed):

#1 Brain Derived Neurotrophic Factor
#2 BDNF
#3 rs6265
#4 #1 OR #2 OR #3
#5 polymorphism
#6 variant
#7 mutation
#8 #5 OR #6 OR #7
#9 epilepsy
#10 seizures
#11 #9 OR #10
#12 #4 AND #8 AND #11.

Study selection and exclusion
All selected studies shared the following inclusion criteria:
1) case–control and cohort studies; 2) studies focused on BDNF
rs6265 G>A polymorphism and epilepsy risk; 3) all data
were based on human subjects; and 4) selected with adequate
genotype information or completed OR and 95% CIs. The
exclusion criteria included: 1) case report or review articles;
2) molecular biology research; 3) articles without enough data
or that could not be calculated to corresponding OR and a 95%
CI; and 4) articles with duplicated or overlapping data.

Data extraction
Two reviewers (Xu and Li) retrieved, read, and extracted
the relevant data from selected studies independently. This
information was collected and listed in Table 1: author,
study publication year, country or ethnic distribution of
the subjects, control design, genotyping method, subtype
of epilepsy, the distributed number of genotypes in cases
and controls, the group and patient age, and the minor allele
frequency in the control group.

Statistical analysis
The Hardy-Weinberg equilibrium (HWE) in controls of
each study was calculated by using a chi-square test first.
Pooled ORs with 95% CIs were calculated to evaluate the
strength of the relationship between BDNF rs6265 G>A
polymorphism and epilepsy risk. Five genotype models were
used, including allele contrast (A vs G), co-dominant (GA
vs GG and AA vs GG), dominant (GA+AA vs GG), and
recessive (AA vs GG+GA) models. Subgroup analyses were
also conducted according to stratified design, such as ethnic
distribution, control design, disease type, age distribution,
and genotyping method. Cochran’s Q statistic was used to
assess the between-study heterogeneity. The fixed-effect model (the Mantel-Haenszel method) was used when the I² index was less than 40%; otherwise, a random effects model (the DerSimonian and Laird method) was applied. Furthermore, cumulative analyses and sensitivity analyses were conducted to examine the trends and the stability of the results. Publication bias was conducted with Begg’s funnel plot and Egger’s test. Statistical analyses were performed with STATA version 14.0 (StataCorp LP, College Station, TX, USA). P<0.05 was statistically significant.

Results

Study characteristics

In general, 211 studies were identified by a systematic literature search. Figure 1 presents the selection process of the studies. After screening the titles, abstracts, and full articles, 201 articles were excluded. A total of 10 studies involving 2,941 patients and 6,571 controls were included in this meta-analysis.19,21–29 Among these studies, five studies focused on adult patients,19,21,22,26,27 four studies focused on pediatric patients,23–25,28 and one study focused on mixed patients.29 Six studies researched Asian populations21,22,26,27,28 and four researched Caucasian populations.21,22,25,29 Five studies focused on the subtype of temporal lobe epilepsy.19,21,22,24,27 In the genotyping method subgroup, four studies used polymerase chain reaction-restriction fragment length polymorphism,19,22,23,25,28 two studies used applied biosystems,21,29 one study adopted direct sequencing,24 one study used Illumina HumanHap,26 and the last study applied the Taqman method.27 In terms of the genotype distributions in control groups, only one study deviated from HWE.27 All included characteristics of each study are summarized in Table 1.

Meta-analysis

Meta-analysis was conducted for the combined studies, and the results demonstrated some significant protective effects between rs6265 G>A polymorphism and epilepsy susceptibility in all five genotype models (A vs G: OR=0.88, 95% CI=0.83–0.94, P<0.01, I²=0%; GA vs GG: OR=0.88, 95% CI=0.79–0.97, P=0.01, I²=0%; AA vs GG: OR=0.79, 95% CI=0.70–0.90, P<0.01, I²=0%; GA+AA vs GG: OR=0.85, 95% CI=0.77–0.94, P<0.01, I²=0%, Figure 2; AA vs GG+GA: OR=0.85, 95% CI=0.76–0.95, P=0.01, I²=0%) (Figure S1 shows other models). Subsequently, analysis excluding the study by Shen et al, which deviated from HWE, also indicated decreased risks in the five genotype models (Table 2).

Table 1 Characteristics of case-control studies on BDNF rs6265 G>A polymorphism and epilepsy risk included in the meta-analysis

| First author       | Year  | Country/ethnicity | Control |
|--------------------|-------|-------------------|---------|
| Kanemoto et al     | 2003  | Japan/Asian       | Hospital control |
| Chou et al         | 2004  | China/Asian       | Healthy control |
| Lohoff et al       | 2005  | Germany/Asian     | Healthy control |
| Bragatti et al     | 2011  | Italy/Asian       | Healthy control |
| Gkampeta et al     | 2012  | Greece/Asian      | Hospital control |
| Shen et al         | 2016  | China/Asian       | Hospital control |

Notes: HWE in control. Abbreviations: AD, age distribution; HWE, Hardy-Weinberg equilibrium; MAF, minor allele frequency in control group; NA, not available; PCR-RFLP, polymerase chain reaction-restriction fragment length polymorphism; TLE, temporal lobe epilepsy.
Figure 1: Flow diagram of the study selection process.

| Study ID       | OR (95% CI)       | % weight |
|----------------|-------------------|----------|
| Asian          |                   |          |
| Kanemoto et al (2003)19 | 1.11 (0.76–1.60) | 6.03     |
| Chou et al (2004)20 | 0.61 (0.30–1.22) | 2.36     |
| Chen et al (2011)21 | 0.96 (0.55–1.68) | 2.84     |
| Fu et al (2014)22 | 0.69 (0.26–1.83) | 1.10     |
| Sha’ari et al (2016)23 | 0.85 (0.75–0.96) | 59.94    |
| Shen et al (2016)24 | 0.84 (0.67–1.06) | 18.06    |
| Subtotal (I²=0.0%, P=0.678) | 0.86 (0.78–0.95) | 90.33    |

| Caucasian      |                   |          |
| Lohoff et al (2005)25 | 0.74 (0.46–1.17) | 4.71     |
| Bragatti et al (2010)26 | 0.95 (0.52–1.74) | 2.41     |
| Tondo et al (2011)27 | 0.45 (0.09–2.33) | 0.55     |
| Gkampeta et al (2014)28 | 0.66 (0.32–1.37) | 2.00     |
| Subtotal (I²=0.0%, P=0.790) | 0.76 (0.55–1.04) | 9.67     |

| Overall        |                   |          |
| (I²=0.0%, P=0.859) | 0.85 (0.77–0.94) | 100      |

Figure 2: OR and 95% CIs of the associations between BDNF rs6265 G>A polymorphism and epilepsy susceptibility in GA+AA vs GG model.
Table 2: Summary ORs and 95% CIs of BDNF rs6265 G>A polymorphism and epilepsy risk

| rs6265 G>A | N* | A vs G | GA vs GG | AA vs GG | GA+AA vs GG | AA vs GG+GA |
|------------|----|--------|----------|----------|-------------|-------------|
|            |    | OR     | 95% CI   | P-value  | OR     | 95% CI   | P-value  | OR     | 95% CI   | P-value  | OR     | 95% CI   | P-value  |
| Total      | 10 | 0.88   | 0.83–0.94 | <0.01    | 0.88   | 0.79–0.97 | 0.01    | 0.79   | 0.70–0.90 | <0.01    | 0.85   | 0.77–0.94 | <0.01    |
| HWE-yes    | 9  | 0.90   | 0.84–0.96 | 0.01     | 0.87   | 0.77–0.97 | 0.01    | 0.82   | 0.71–0.95 | 0.01     | 0.85   | 0.77–0.95 | <0.01    |
| Ethnicity  |    |        |          |          |        |          |         |        |          |          |        |          |         |
| Asian      | 6  | 0.89   | 0.83–0.95 | <0.01    | 0.89   | 0.80–0.99 | 0.04    | 0.79   | 0.69–0.90 | <0.01    | 0.86   | 0.78–0.95 | <0.01    |
| Caucasian  | 4  | 0.82   | 0.62–1.08 | 0.15     | 0.73   | 0.52–1.03 | 0.07    | 0.92   | 0.40–2.08 | 0.84    | 0.76   | 0.55–1.04 | 0.09     |
| Design     |    |        |          |          |        |          |         |        |          |          |        |          |         |
| Hospital base | 4 | 0.88   | 0.79–0.99 | 0.04     | 13.2   | 0.97   | 0.80–1.17 | 0.75    | 0.77   | 0.61–0.98 | 0.03    | 0.90   | 0.76–1.08 | 0.27     |
| Healthy base** | 5 | 0.88   | 0.82–0.95 | <0.01    | 0.84   | 0.75–0.95 | 0.01    | 0.80   | 0.69–0.94 | 0.01    | 0.83   | 0.74–0.93 | <0.01    |
| NA         | 1  | 0.68   | 0.18–2.53 | 0.57     | NA     | 0.26   | 0.03–2.29 | 0.23    | NA     | 1.50   | 0.14–16.36 | 0.74     |
| Subtype    |    |        |          |          |        |          |         |        |          |          |        |          |         |
| TLE        | 5  | 0.88   | 0.78–0.99 | 0.04     | 39.3   | 0.89   | 0.74–1.07 | 0.23    | 0.80   | 0.62–1.02 | 0.07    | 0.86   | 0.72–1.03 | 0.10     |
| AD         |    |        |          |          |        |          |         |        |          |          |        |          |         |
| Adult      | 5  | 0.89   | 0.83–0.95 | <0.01    | 0.89   | 0.80–0.99 | 0.03    | 0.80   | 0.70–0.92 | <0.01    | 0.86   | 0.78–0.95 | <0.01    |
| Children   | 4  | 0.82   | 0.66–1.03 | 0.09     | 0.78   | 0.54–1.13 | 0.20    | 0.71   | 0.45–1.12 | 0.14    | 0.75   | 0.53–1.07 | 0.11     |
| Mixed      | 1  | 0.68   | 0.18–2.53 | 0.57     | NA     | 0.26   | 0.03–2.29 | 0.23    | NA     | 1.50   | 0.14–16.36 | 0.74     |
| Type       |    |        |          |          |        |          |         |        |          |          |        |          |         |
| PCR-RFLP   | 5  | 0.94   | 0.79–1.10 | 0.43     | 0.94   | 0.73–1.21 | 0.63    | 0.88   | 0.61–1.26 | 0.48    | 0.92   | 0.73–1.17 | 0.52     |
| Other      | 5  | 0.87   | 0.82–0.94 | <0.01    | 0.86   | 0.77–0.97 | 0.01    | 0.78   | 0.68–0.90 | <0.01    | 0.84   | 0.75–0.93 | <0.01    |

Notes: Statistically significant values are shown in bold. *P-value for heterogeneity test. **Numbers of comparisons. Healthy base refers to control groups that consist of healthy persons who may be from the hospital or from the general population.

Abbreviations: AD, age distribution; HWE, Hardy-Weinberg equilibrium; NA, not available; PCR-RFLP, polymerase chain reaction-restriction fragment length polymorphism; TLE, temporal lobe epilepsy.
Furthermore, the subgroup analyses were stratified by ethnicity, control design, disease type, age distribution, and genotyping method. All these findings presented consistent effects with the overall analysis results, such as in Asians (A vs G: OR = 0.89, 95% CI = 0.83–0.95, P < 0.01, I² = 0%; GA vs GG: OR = 0.89, 95% CI = 0.80–0.99, P = 0.04, I² = 0%; AA vs GG: OR = 0.79, 95% CI = 0.69–0.90, P < 0.01, I² = 0%; GA+AA vs GG: OR = 0.86, 95% CI = 0.78–0.95, P < 0.01, I² = 0%; AA vs GG+GA: OR = 0.85, 95% CI = 0.76–0.95, P = 0.01, I² = 0%) and adults (A vs G: OR = 0.89, 95% CI = 0.83–0.95, P < 0.01, I² = 0%; GA vs GG: OR = 0.89, 95% CI = 0.80–0.99, P = 0.03, I² = 0%; AA vs GG: OR = 0.80, 95% CI = 0.70–0.92, P < 0.01, I² = 0%; GA+AA vs GG: OR = 0.86, 95% CI = 0.78–0.95, P < 0.01, I² = 0%; AA vs GG+GA: OR = 0.86, 95% CI = 0.76–0.96, P = 0.01, I² = 0%) (Table 2).

Sensitivity analyses were performed by removing each study one-by-one according to the publication date, and the results did not show significant changes (Figure 3 for GA+AA vs GG model and Figure S2 for other models). Cumulative analysis was also performed and presented an apparent protective effect in 2016 from the report by Sha’ari et al (Figure 4 for GA+AA vs GG model and Figure S3 for other models).

Publication bias was evaluated with Begg’s tests, and no significant asymmetry was found (Figure 5 for GA+AA vs GG model and Figure S4 for other models). The Egger’s test also confirmed these results (A vs G, P = 0.39; GA vs GG: P = 0.33; AA vs GG, P = 1.00; GA+AA vs GG, P = 0.39; AA vs GG+GA, P = 0.99).

**Discussion**

Epilepsy is one of the most common neurological conditions triggered by the disruption of the abnormal electrochemical activities of the brain’s neurological system, thereby resulting in a seizure. Epilepsy affects approximately 0.5% to 1% of the general population. Epilepsy can be controlled, but not cured, and more than 30% of patients have a poor response to medical treatment.30

Goldberg and Coulter suggested that the etiology of epilepsy in most patients is still unclear, especially for idiopathic epilepsies, which, without any specific cause, contributed to more than 70% of seizure symptoms.31 However, Scheffer et al postulated that idiopathic epilepsies, nowadays, are known to be of genetic origin, particularly those with early onset – in the first or second decade of life. On the other hand, many symptomatic epilepsies are now classified as structural, metabolic, genetic, post-inflammatory, post-traumatic, or a combination of these etiologies.32

BDNF is one of the crucial nerve growth factors in the family of neurotrophins and plays an important role in the maintenance, regulation, and differentiation of peripheral and central nervous system neurons.33 A large amount of research has indicated that abnormal
expression of BDNF plays a critical role in the pathological process of epilepsy development. Martínez-Levy et al and de Souza Bernardino et al found an increased expression of BDNF transcription in patients with epilepsy, which also supported the idea that the high expression of BDNF in some brain areas may contribute to limbic seizures.\(^{34,35}\) Moreover, transgenic mice with high expression of BDNF also indicated an increased seizure risk combined with a hippocampal hyperexcitability.\(^{13}\) This cumulative evidence prompted the idea that the abnormalities in the BDNF gene may be responsible for epileptogenesis.

The human BDNF gene is located at the short arm of chromosome 11p13.\(^{36}\) Today, several SNP loci of the BDNF gene have been found, and the rs6265 variant is the most common site. This polymorphism substitutes a guanine to adenine (G>A) change at the nucleotide 196 site and results in a Val to Met substitution at amino acid residue 66 of the pro-BDNF protein.\(^{37}\) Bhang et al found that the Met allele of the BDNF val66met polymorphism contributed to a significantly lower serum level of BDNF.\(^{38}\) In addition, some studies indicated that the variant-type BDNF (BDNF Met) would create negative effects to alter the trafficking paths with two important aspects: 1) decreased variant BDNF distributed into neuronal dendrites and targeted to secretory granules, 2) contributed to the impairment of regulated secretion of BDNF.\(^{39,40}\) Furthermore, other researchers also found that this change reduces the activity-dependent secretion of BDNF and influences cortical processing,\(^{40–42}\) such as low BDNF expression, and protects against seizures with the Met allele of this polymorphism.\(^{40,43}\) In 2003, Kanemoto et al conducted the first case–control study to explore the association between the BDNF rs6265 G>A polymorphism and epilepsy susceptibility in the Japanese population, and the results indicated no statistically significant differences between the epilepsy patients and control groups.\(^{19}\) Similarly, Lohoff et al and Bragatti et al did not find any significant association between BDNF rs6265 G>A polymorphism and epilepsy risk.\(^{21,22}\) Since then, a series of studies have been published, but the results were controversial and inconsistent. Sha’ari et al performed a case–control study on an East Asian population and found that the population had a higher risk of developing epilepsy compared with G carriers in all subjects (dominant model, OR=1.18, 95% CI=1.04–1.33).\(^{26}\)

| Study ID                  | OR (95% CI)     |
|---------------------------|-----------------|
| Kanemoto et al (2003)\(^{19}\) | 1.11 (0.76–1.60) |
| Chou et al (2004)\(^{28}\)    | 0.97 (0.70–1.34) |
| Lohoff et al (2005)\(^{31}\)  | 0.88 (0.68–1.15) |
| Bragatti et al (2010)\(^{22}\) | 0.89 (0.70–1.14) |
| Chen et al (2011)\(^{23}\)    | 0.90 (0.72–1.13) |
| Tondo et al (2011)\(^{29}\)   | 0.89 (0.71–1.11) |
| Fu et al (2014)\(^{34}\)      | 0.88 (0.71–1.09) |
| Gkampeta et al (2014)\(^{35}\) | 0.86 (0.70–1.06) |
| Sha’ari et al (2016)\(^{26}\) | 0.85 (0.77–0.95) |
| Shen et al (2016)\(^{27}\)    | 0.85 (0.77–0.94) |

Figure 4 Cumulative meta-analyses according to publication year in GA+AA vs GG model of BDNF rs6265 G>A polymorphism.

Figure 5 Funnel plot analysis to detect publication bias for GA+AA vs GG model of BDNF rs6265 G>A polymorphism.

Note: Circles represent the number of the studies.
Conversely, Shen et al suggested that the A allele might play a protective role against epilepsy risk.27

These inconsistent results create confusion. How can we conduct a more precise assessment of the association between BDNF rs6265 G>A polymorphism and epilepsy risk? Few studies and small sample size may be the most important factors that contributed to the confusing results. Meta-analysis is a statistical method that combines the results of multiple studies focused on one topic. Therefore, we conducted this meta-analysis with published studies involving a total of 9,512 subjects and found that the A allele mutation of BDNF rs6265 G>A polymorphism plays an important protective role against epilepsy development, especially in the Asian population. This result might be due to the greater number of studies conducted in Asian populations with large sample sizes, thereby providing increased statistical efficiency. Moreover, the subgroup analyses based on control design, disease type, age distribution, and genotyping method also indicated some protective effect against epilepsy. Interestingly, the mechanism of BDNF rs6265 G>A polymorphism was more effective in the adult group compared with the pediatric group. It was supposed that the accumulative protective effect of BDNF rs6265 G>A mutation would present gradually along with aging.

To the best of our knowledge, this is the first meta-analysis to assess the association between BDNF rs6265 G>A polymorphism and epilepsy susceptibility.

Limitations
Some limitations need to be addressed in the present analysis. First, although we conducted a systematic review and collected eight published studies, the sample size was still small, which could have influenced the results, thereby resulting in some deviations from the truth. Second, only one polymorphism locus (BDNF rs6265 G>A) was assessed in our analysis. Some influencing factors, such as brain trauma; cigarette smoking, alcohol, and drug use during pregnancy; environmental deterioration; and other gene mutations, could not be comprehensively evaluated. Third, all the included studies were conducted in Caucasian and Asian population. Ethnicity bias may have affected the results and might not be applicable to all people. Despite these flaws, the findings further help us understand the potential associations between BDNF rs6265 G>A polymorphism and epilepsy susceptibility. Furthermore, some positive aspects have been addressed: 1) no heterogeneity exists between the included studies, 2) the results of sensitivity analysis and cumulative analysis are all fairly consistent, and 3) Egger’s test and Begg’s funnel plots did not present any significant publication bias.

Conclusion
In summary, this meta-analysis indicated that the BDNF rs6265 G>A polymorphism is associated with epilepsy development, especially in Asian population. More studies with large sample sizes and in-depth research on the mechanism are needed to explore the role of BDNF rs6265 G>A polymorphism.

Acknowledgments
This study was supported by the Foundations of the Science and Technology Department of Hubei Province (no 2016CFB567) and Taihe Hospital (2016BSQD02). These organizations had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Disclosure
The authors report no conflicts of interest in this work.

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### Supplementary materials

#### Figure S1

| Study ID | OR (95% CI) | % weight |
|----------|-------------|----------|
| **A**    |             |          |
| Asian    |             |          |
| Kanevski et al (2003) | 1.04 (0.81–1.33) | 6.25 |
| Chou et al (2004) | 0.72 (0.47–1.08) | 2.67 |
| Chen et al (2011) | 1.06 (0.71–1.61) | 3.23 |
| Fu et al (2014) | 0.70 (0.36–1.31) | 1.18 |
| Shi et al (2014) | 0.56 (0.33–0.97) | 12.11 |
| Shen et al (2016) | 0.63 (0.11–0.36) | 18.04 |
| Subtotal (A+G, P=0.488) | 0.88 (0.53–0.99) | 94.44 |
| **C**    |             |          |
| Asian    |             |          |
| Kanevski et al (2003) | 1.05 (0.63–1.76) | 5.37 |
| Chou et al (2004) | 0.53 (0.26–1.19) | 3.16 |
| Chen et al (2011) | 1.00 (0.49–2.02) | 2.96 |
| Fu et al (2014) | 0.53 (0.16–1.74) | 1.44 |
| Shi et al (2014) | 0.81 (0.09–0.95) | 64.29 |
| Shen et al (2016) | 0.88 (0.50–0.99) | 23.46 |
| Subtotal (A+G, P=0.546) | 0.79 (0.69–0.90) | 97.78 |
| **B**    |             |          |
| Asian    |             |          |
| Kanevski et al (2003) | 1.13 (0.76–1.66) | 6.17 |
| Chou et al (2004) | 0.67 (0.32–1.41) | 2.20 |
| Chen et al (2011) | 0.94 (0.52–1.70) | 2.94 |
| Fu et al (2014) | 0.81 (0.28–2.35) | 0.98 |
| Shi et al (2016) | 0.86 (0.36–2.09) | 59.96 |
| Shen et al (2016) | 0.63 (0.73–1.88) | 17.44 |
| Subtotal (A+G, P=0.804) | 0.89 (0.50–1.60) | 90.93 |
| **D**    |             |          |
| Asian    |             |          |
| Kanevski et al (2003) | 0.98 (0.62–1.54) | 5.46 |
| Chou et al (2004) | 0.70 (0.37–1.33) | 3.41 |
| Chen et al (2011) | 1.04 (0.58–1.87) | 3.22 |
| Fu et al (2014) | 0.83 (0.22–3.03) | 1.47 |
| Shi et al (2016) | 0.89 (0.78–0.99) | 63.94 |
| Shen et al (2016) | 0.71 (0.55–0.91) | 20.85 |
| Subtotal (A+G, P=0.358) | 0.85 (0.76–0.96) | 96.34 |

#### Figure S2 (Continued)

**A**

| Study ID | Meta-analysis estimates, given named study is omitted |
|----------|------------------------------------------------------|
| Kanevski et al (2003) | Lower CI limit | Estimate | Upper CI limit |
| Chou et al (2004) |          |          |              |
| Lohoff et al (2005) |          |          |              |
| Bragati et al (2010) |          |          |              |
| Chen et al (2011) |          |          |              |
| Tondo et al (2011) |          |          |              |
| Fu et al (2014) |          |          |              |
| Gkampatsa et al (2014) |          |          |              |
| Shari et al (2016) |          |          |              |
| Shen et al (2016) |          |          |              |

**B**

| Study ID | Meta-analysis estimates, given named study is omitted |
|----------|------------------------------------------------------|
| Kanevski et al (2003) | Lower CI limit | Estimate | Upper CI limit |
| Chou et al (2004) |          |          |              |
| Lohoff et al (2005) |          |          |              |
| Bragati et al (2010) |          |          |              |
| Chen et al (2011) |          |          |              |
| Tondo et al (2011) |          |          |              |
| Fu et al (2014) |          |          |              |
| Gkampatsa et al (2014) |          |          |              |
| Shari et al (2016) |          |          |              |
| Shen et al (2016) |          |          |              |
**Figure S2** Sensitivity analysis through deleting each study to reflect the influence of the individual dataset to the pooled ORs in BDNF rs6265 G>A polymorphism and epilepsy susceptibility (A for A vs G model; B for GA vs GG model; C for AA vs GG model; and D for AA vs GG+GA model).

**Figure S3** Cumulative meta-analyses according to publication year in BDNF rs6265 G>A polymorphism and epilepsy susceptibility (A for A vs G model; B for GA vs GG model; C for AA vs GG model; and D for AA vs GG+GA model).
Figure S4 Funnel plot analysis to detect publication bias in BDNF rs6265 G>A polymorphism and epilepsy susceptibility. (A for A vs G model; B for GA vs GG model; C for AA vs GG model; and D for AA vs GG+GA model).

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