



Published in final edited form as:

*J Alzheimers Dis.* 2018 ; 65(4): 1055–1064. doi:10.3233/JAD-180585.

## The Influence of the Val66Met Polymorphism of Brain-Derived Neurotrophic Factor on Neurological Function after Traumatic Brain Injury

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### Abstract

Functional outcomes after traumatic brain injury (TBI) vary widely across patients with apparently similar injuries. This variability hinders prognosis, therapy, and clinical innovation. Recently, single nucleotide polymorphism (SNPs) that influence outcome after TBI have been identified. These discoveries create opportunities to personalize therapy and stratify clinical trials. Both of these changes would propel clinical innovation in the field. This review focuses on one of most well-characterized of these SNPs, the Val66Met SNP in the brain-derived neurotrophic factor (BDNF) gene. This SNP influences neurological function in healthy subjects as well as TBI patients and patients with similar acute insults to the central nervous system. A host of other patient-specific factors including ethnicity, age, gender, injury severity, and post-injury time point modulate this influence. These interactions confound efforts to define a simple relationship between this SNP and TBI outcomes. The opportunities and challenges associated with personalizing TBI therapy around this SNP and other similar SNPs are discussed in light of these results.

### Keywords

Brain-derived neurotrophic factor; precision medicine; single nucleotide polymorphism; traumatic brain injury

## INTRODUCTION

Traumatic brain injury (TBI) causes approximately 56,000 deaths, 282,000 hospitalizations, and 2.5 million emergency room visits in the United States every year [1]. Survivors of TBI may have prolonged or permanent deficits in social, emotional, cognitive, and motor function, depending on the severity of the injury and the location of the lesion. Functional outcomes vary widely across patients with TBI. This is true for both mild and severe TBI at both acute and chronic time scales. Several demographic and environmental factors are known to influence functional TBI outcomes, including age, gender, and history of TBI [2–4]. In addition, evidence is accumulating that genetic factors influence TBI outcomes [5–8].

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Authors' disclosures available online (<https://www.j-alz.com/manuscript-disclosures/18-0585r2>).

Understanding these genetic factors is perhaps the most important challenge in modern TBI research, with ramifications for prognosis, therapy, and clinical trial design. Prognosis is exceptionally difficult in TBI [9]. Some patients continue to make functional gains steadily for years after a severe TBI while others do not. Also, some patients decline several years after exposure to mild head impacts while others do not [10]. A genetic factor that partially explained these differences would be valuable to patients and clinicians attempting to plan around likely future neurological function. On the therapeutic front, genetic factors that influence pathology may also influence how that pathology responds to therapy. An understanding of these influences may enable more effective personalized therapy. On a related note, it is increasingly clear that future trials of TBI therapies must be stratified to have any chance of success. More than 30 phase III clinical trials of candidate therapeutics for TBI have been conducted and all have failed [11]. The consensus in the research community is that TBI trials fail in part because of the heterogeneity of the patient population [12]. This heterogeneity creates a signal-to-noise problem: the more outcomes vary within treatment groups, the more treatment effect is required to achieve statistical significance. The solution is to stratify patients according to likely outcome and a genetic outcome predictor would be invaluable in this regard. In order to be useful, the genetic predictor must be common and must exert a powerful influence on TBI outcomes. The Val66Met single nucleotide polymorphism (SNP) of brain-derived neurotrophic factor (BDNF) occurs in about 30% of the U.S. population [13]. It has been shown to influence neurological function in healthy subjects [14], TBI patients [15, 16], and stroke patients [17, 18]. In this review, we summarize what is known about how this SNP influences TBI outcomes and explore its potential to inform prognosis, therapy, and clinical trial design.

## **BDNF AND THE VAL66MET SNP**

The complex architecture of the human nervous system is established and maintained by local interactions between specialized neurons and their targets. Neurons require chemical signals called neurotrophins supplied by their targets for survival [19]. This simple mechanism organizes the nervous system during development and maintains this organization in adulthood. Neurons are generated in great excess during embryogenesis. However, only those neurons that enervate an appropriate target receive the neurotrophins they need to survive [20] so supernumerary neurons apoptose. In an analogous way, neurotrophins regulate the branching of surviving neurons and the formation of synapses so that neural circuits adapt to the requirements of their targets [21]. There are four neurotrophins: neural growth factor (NGF), BDNF, neurotrophin 3 (NT-3), and neurotrophin-4/5 (NT-4/5). Certain classes of neuron depend on certain neurotrophins for survival while remaining indifferent to others. This selectivity dynamically organizes neurons around their targets. BDNF plays a prominent role in hippocampal functions including learning and memory [22] because it regulates long term potentiation (LTP) [23]. Suppressing BDNF in mice by genetic knock out [24] or RNA interference [25] impairs performance in learning and spatial memory tasks. BDNF is well suited to its role in LTP because it is released in an activity-dependent fashion while all other neurotrophins are released at a constant rate [26]. Electrical stimulation triggers secretion of BDNF which then

promotes synapse formation and enhances synaptic transmission. These changes are the cellular basis of LTP.

When translated, the BDNF molecule contains three important domains: the signal peptide, the pro domain, and the functional BDNF molecule. The signal peptide sequesters the molecule in the endoplasmic reticulum and is then removed [27]. Subsequently removing the pro-domain produces mature BDNF. The pro-domain must interact with the sortilin receptor in the Golgi wall to allow proper folding of the mature domain. Proper folding allows a motif in the mature domain to connect to carboxypeptidase E, and then BDNF is sorted into large dense core vesicles to be released via the regulated secretory pathway [28]. The pro-domain may be removed intracellularly in the trans-Golgi network by enzymes such as furin [29] or extracellularly by enzymes such as plasmin [30] or matrix metalloproteinase 7 [30]. Mature BDNF and pro-BDNF function antagonistically to regulate neuroplasticity [30]. Mature BDNF binds to the tyrosine related kinase receptor (TrkB) to activate pathways involved in LTP [31], cell survival [32], and dendrite formation [33]. ProBDNF acts via the p75 neurotrophin receptor (p75NTR) and sortilin to activate pathways involved in long term depression [34], apoptosis [35], and reducing dendritic complexity [34].

There are several hundred known polymorphisms of the BDNF gene [36]. Of these, Val66Met (also known as rs6265) is the most widely studied. It is a SNP at nucleotide 196 that causes the substitution of the typical valine with methionine at codon 66 (Val66Met). About 30% of the population is at least heterozygous for this SNP in the United States [13], but this proportion varies widely across global populations [13, 37]. Val66Met occurs in the portion of the BDNF gene that encodes the pro-domain. Therefore, it does not alter the function of the mature protein. For example, the Val66Met allele does not modulate the neurotrophic effect of mature BDNF on PC12 cells in culture [14]. However, it does alter intracellular sorting and secretion of the protein. Specifically, the SNP occurs in a portion of the prodomain that interacts with sortilin [38]. BDNF proteins with methionine at codon 66 (mBDNF) do not sort from the Golgi into secretory vesicles as well as BDNF proteins with valine at codon 66 (vBDNF) [14]. As a result, mBDNF tends to accumulate in the soma while vBDNF accumulates in punctate vesicles in the dendrites. Neurons secrete vBDNF but not mBDNF in response to activity. Activity-dependent release of BDNF drives LTP [21] so Met carriers have impaired neuroplasticity [14]. Hippocampal volume has been reported to be reduced in Met carriers by several investigators [39–41], although this conclusion remains controversial [42]. The Met allele is also associated with reduced grey matter volume in other brain structures including the amygdala [43] and dorsolateral prefrontal cortex [40]. The Val66Met SNP has functional consequences in healthy subjects. Human Met carriers generally have worse episodic memory than matched Val carriers [14] and show less activation of the hippocampus during memory tasks as measured using magnetic resonance imaging techniques [44]. Met carriers have inferior motor function and motor learning compared to Val/Val subjects [45]. While the SNP is generally deleterious in healthy subjects, benefits emerge in some disease states, including TBI.

## VAL66MET IN TBI

The Met allele partially protects patients with severe TBI. In a study of male Vietnam veterans with penetrating TBI, TBI impaired executive function among Val/Val individuals but not among Met carriers [16]. In the same cohort, Val/Met individuals had better general intelligence, working memory, and processing speed than Val/Val individuals after TBI, although there was no difference between these groups before TBI [15]. It is worth noting that brain function was assessed in these individuals at very long-term time points, up to 40 years post injury. Met carriers secrete less of both mature BDNF and proBDNF in response to activity. The Met allele is protective after severe TBI, suggesting that the apoptotic action of proBDNF overcomes the survival signaling of mature BDNF in this context. Under these circumstances, impaired secretion would become neuroprotective [15, 16]. The Val allele may also aggravate the deleterious effects of proBDNF. *In vitro*, the Val form of proBDNF inhibits LTP and promotes tau hyperphosphorylation while the Met form does not [46]. Another possibility is that the Met allele improves long term outcomes because it shifts the excitatory / inhibitory balance of the brain toward excitation. The mouse model of the Val66Met SNP [47] has not been subjected to experimental TBI, to our knowledge, but it has been subjected to experimental stroke. The Met allele led to worse short term motor outcomes after stroke in this mouse model [48], due to inferior neuroplasticity and angiogenesis, but better long term outcomes [49], due to higher excitability in the striatum opposite the lesion.

The protective effect of the Met allele in severe TBI depends on age at chronic time points. A study of BDNF SNPs in severe TBI tested the hypothesis that the Met allele of Val66Met in conjunction with another putative high-risk polymorphism of BDNF, rs7124442, would increase the risk of death. In fact, the putative high-risk alleles reduced the risk of death at short time points (<7 days). At long time points (8–365 days), an interaction with age emerged. The Met allele along with the other hypothetical risk allele did indeed increase risk of death for patients under 45 years of age. However, for those over 45, these alleles were again protective [50]. Note that long term death rates were higher overall in the over 45 age group. This age dependence may arise because the balance of receptors that mediate pro-survival and pro-apoptotic effects of BDNF changes with age [51, 52]. Severe TBI uncouples the autonomic and cardiovascular systems [53] so the role of the Val66Met SNP in autonomic function is also important. Healthy Met/Met individuals have altered sympathovagal balance and less parasympathetic activity compared to Val/Val individuals [54]. Also, healthy Met/Met individuals had less cardiovascular reactivity to acute psychosocial stress than Val/Val individuals [55]. However, the effect of the Val66Met SNP on autonomic function after TBI is currently unknown.

The influence of the Val66Met SNP in mild TBI depends on gender and the post-injury time point. Female concussed athletes carrying a Met allele performed significantly better on assessments of olfactory function than their Val/Val counterparts [56]. Participants in this study were assessed an average of 27 months after their concussion. On the other hand, tests of mood conducted at 1 and 6 weeks post-injury in another cohort of patients with mild TBI found more depression and anxiety in Met carriers. The effect on depression was modulated by gender, being significant at both time points in males but only at the first time point in

females [57]. Mild TBI increased depressive rumination and reduced cognitive flexibility among Met carriers but not among Val/Val homozygotes. Unfortunately, no data about the time of injury was collected in this study [58]. In this context, it is worth noting that Met allele carriers are more prone to rumination than Val/Val homozygotes in the absence of TBI [59] and that this trend becomes more pronounced under stress in Met homozygotes [60]. The Val66Met SNP lowered performance among both injured subjects and uninjured controls in a study of reaction times after mild to moderate TBI (Glasgow Coma Score 9–15) but this effect did not interact with TBI. However, several other polymorphisms of BDNF did influence the effect of TBI in a gender dependent fashion with more influence in males [61]. Table 1 summarizes what is known about the influence of the SNP on acute and chronic TBI pathology in males and females for mild TBI.

In addition to modulating the pathology of TBI, the Val66Met SNP modulates the risk of sustaining a TBI according to two consistent but small studies in human subjects [62, 63]. The reasons for this trend may be behavioral or physiological or both. Behaviors modulated by this SNP include addiction [64, 65], aggression [66, 67], participation in high risk sports [68], and hyper-active impulsivity (in people with attention deficit hyperactivity disorder) [69]. Met carriers have greater hostility and aggression, supporting a behavioral explanation for this trend [63]. However, larger human studies are needed to fully explain this phenomenon [70].

## VAL66MET AND NEURODEGENERATION

One of the most important and mysterious questions in modern TBI research is how does TBI influence the likelihood of subsequent dementia. Striking evidence of early-life tauopathy has been discovered in athletes [10] and military veterans [71] with a history of repeated mild TBI. The unique spatial distribution of this tauopathy defines it as a distinct neuropathological entity: chronic traumatic encephalopathy [72]. Unfortunately, the prevalence of this condition is currently unknown. TBI also increases the risk of Alzheimer's disease (AD) [73, 74]. A recent study of a large population of U.S. military veterans found that all forms of TBI increased the risk of dementia with hazard ratios ranging from 2.36 for mild TBI without loss of consciousness to 3.77 for moderate to severe TBI [75]. The apolipoprotein E (APOE) gene exists in 3 isoforms, one of which, APOE s4, increases the risk of AD [76]. TBI amplifies the impact of APOE s4 on AD risk. One study reported that APOE s4 doubled the risk of AD absent a history of TBI but that the combination of APOE s4 with TBI history increased the risk of AD 10-fold [77]. Therefore, it is possible that other genetic risk factors for AD also synergize with TBI. The Val66Met SNP has been investigated as a genetic risk factor for AD. Early studies found that Met carriers had lower incidence of the disease [78] and, in the case of Met homozygotes, better reasoning skills in late life [79]. However, subsequent studies failed to replicate these findings [80, 81]. This inconsistency may arise in part from interactions of the Val66Met SNP with other factors. For example, the effect of the Val66Met SNP on phenotypes associated with AD was age dependent, with Met carriers being protected in late life but more susceptible in early life [82]. Gender also moderates the effect. The Met allele increased risk of AD in women but not in men in a Japanese cohort [83]. While both TBI and the Val66Met SNP influence the

risk of dementia, there is as yet no published evidence demonstrating synergy between them. Nevertheless, the possibility of such a synergy merits investigation.

## VAL66MET AND THERAPY

Determined efforts to discover a therapy that improves outcomes for all TBI patients have not yet succeeded. Therefore, the more modest goal of discovering a therapy that benefits a subset of TBI patients deserves attention. The Val66Met SNP may define such a subset because it has been shown to modulate the effectiveness of neurological drugs in a number of settings. For example, olanzapine for the treatment of schizophrenia is less effective in Met carriers [84]. Memantine was more effective as an add-on therapy for depressive symptoms in heterozygous bipolar disorder patients than in Val/Val homozygotes [85]. However, most of the pharmacogenetic investigation of the Val66Met SNP has addressed its influence on selective serotonin reuptake inhibitors (SSRIs), a popular class of anti-depressants. Two meta-analyses concluded that heterozygotes were more responsive to SSRIs than either Val or Met homozygotes. This effect was modulated by race, being stronger among Asians [86, 87]. However, TBI patients with depression were most likely to respond to citalopram (an SSRI) if they were Val homozygotes [88]. This discrepancy may indicate that post-TBI depression requires a different strategy for therapy personalization than other types of depression or it may reflect the fact that Val66Met was combined with another genetic predictor in this study (a polymorphism in the methylene tetrahydrofolate reductase gene). These results have immediate clinical relevance. Up to 53% of TBI patients experience depression in the first year after their injury [89] and SSRIs are a proven, first line therapy for this post-TBI depression [90].

The Val66Met SNP may also modulate the effectiveness of non-pharmaceutical therapies for TBI. Exercise improves emotional and cognitive outcomes after TBI [91, 92]. This effect depended on expression of BDNF [93]. Positive neurobiological effects of exercise in mice were diminished by the Met allele of the Val66Met SNP [94]. Since the Met allele impairs activity-dependent release of BDNF [14], it is reasonable to hypothesize that physical exercise does not promote recovery after TBI as readily in these individuals. This hypothesis has not as yet been tested directly in the literature. In a small study of spinal cord injury patients, Met carriers increased circulating BDNF less in response to physical exercise than Val/Val patients [95]. This trend approached but did not meet the threshold for statistical significance. Low levels of physical activity increased the risk of cognitive decline and dementia in an elderly Korean cohort and this effect was modulated by the Val66Met SNP, with Met alleles increasing risk [96]. In a study of healthy young adults, physical exercise improved performance on a memory task in Val/Val individuals but not in Met carriers [97]. A short period of motor training increased corticospinal output and motor map area in Val/Val human subjects but not in Met carriers, implying impaired experience-dependent plasticity in the motor cortex among Met carriers [98]. Val/Val subjects performed better on a motor learning task and retained more of what they learned. The Val66Met allele also caused differences in brain activation during motor activity as measured by functional magnetic resonance imaging [45]. However, persistent training overcame these deficits [99], suggesting that patience in motor rehabilitation of Met carriers will be rewarded.

## CONCLUSION

TBI has been described as “the most heterogeneous of all neurological disorders” [11]. Several different pathologies, including edema, ischemia, hemorrhage, and diffuse axonal injury may or may not occur [100]. The distribution of TBI patients by age has three widely separated peaks at 0–4, 15–19, and >65 years of age [101]. In addition to Val66Met, there are several other common polymorphisms in genes such as DRD2, COMT, and ANKK1 that modulate outcomes [5–8, 102]. This heterogeneity implies that precision medicine could have many benefits in TBI. Clinical trial stratification would make expensive trials more likely to detect treatment effects in spite of confounding factors. Personalized therapy would allow new medicines to benefit some patients even if they cannot benefit all patients. However, daunting challenges must be overcome to realize the potential of personalized medicine in TBI. Not only do multiple patient-specific factors influence outcome, but these factors interact with each other in ways that cannot be ignored. This review took a reductionist approach, focusing on one SNP known to influence outcomes in TBI. However, it proved impossible to fully describe the role of this SNP without also considering how it interacts with ethnicity, age, injury severity, post injury time point, and gender. New interactions are likely to emerge over time as investigations continue, including interactions with other genetic polymorphisms. These interactions create confusion in the field because they lead to conflicting results in human studies conducted in different populations [103]. It is very difficult to eliminate all potentially confounding interactions from a human study but human *in vitro* models can be used to reduce confounds in a human system. In these models, induced pluripotent stem cell (iPSC) technology is used to create neurons or other neural cell types from a patient. These cells retain the genetic identity of the donor patient. Furthermore, gene editing technology can be used to introduce genetic variants one at a time against a uniform genetic background [104]. In these experiments, genetic risk factors can be eliminated or introduced individually to test hypotheses definitively. While this approach eliminates some confounds associated with conventional human studies, it has its own limitations. As in any *in vitro* system, the normal architecture of the tissue is lost. Also, human iPSC-derived neurons are typically immature, resembling fetal or neonatal neurons more than adult neurons [105]. However, rapid progress is being made to address these limitations. Brain organoids have been developed that juxtapose several neural cell types derived from human iPSCs in biofidelic configurations [106]. Aging of iPSC-derived neurons can be accelerated by expressing progerin, a truncated form of lamin A associated with premature aging disorders [107], or by telomerase manipulation [108]. Human *in vitro* models have already made significant contributions in other neurological disorders, including amyotrophic lateral sclerosis [109, 110]. They have recently been introduced in neurotrauma [111, 112] where they may eventually provide a powerful complement to traditional pre-clinical tools. The challenges associated with personalizing TBI medicine around patient-specific traits such as the Val66Met SNP are great. However, the potential rewards are greater still and this type of personalization will be a vital frontier for innovation in the field in the near future.

## ACKNOWLEDGMENTS

The authors would like to acknowledge financial support from the National Institutes of Health (R21NS098129).

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**Table 1**

Influence of the Val66Met SNP on mild TBI pathology

	<b>Acute</b>	<b>Chronic</b>
Female	Deleterious [57]	Protective [56] Neutral [57]
Male	Deleterious [57]	Deleterious [57]

Note that different studies use different outcomes and different definitions of acute and chronic time periods.

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