Understanding the role of inflammatory-related pathways in the pathophysiology and treatment of psychiatric disorders: evidence from human peripheral studies and CNS studies

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Abstract
Many lines of evidence now support the hypothesis that inflammation-related pathways are involved in the pathophysiology of psychiatric disorders. Much of the data underpinning this hypothesis has come from the study of inflammation-related proteins in blood of individuals with mood disorders and schizophrenia. Significantly, recent data have emerged to suggest that changes in inflammation-related pathways are present in the CNS of subjects with psychiatric disorders. It is therefore timely to overview how such data, plus data on the role of inflammation-related proteins in CNS function, is contributing to understanding the pathophysiology of mood disorders and schizophrenia. In addition, it has been suggested that antidepressants, mood stabilizers and antipsychotic drugs act on inflammation-related pathways and therefore measuring levels of inflammation-related proteins in blood may be useful in monitoring treatment responsiveness. Despite these important neuropsychopharmacological discoveries, there is no clear understanding as to how inflammatory-related pathways can precipitate the onset of psychiatric symptoms. This review will focus on data suggesting that acute-reactive proteins and cytokines are affected by the pathophysiology of mood disorders and schizophrenia, that levels of blood inflammation-related proteins before and after treatment might be useful in the diagnosis of psychiatric disorders or measuring responsiveness to drug treatment. Finally, it will be postulated how changes in these proteins affect CNS function to cause psychiatric disorders.

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Introduction
Changes in inflammatory-related pathways have long been suggested to have a role in the pathophysiology of mood disorders (Maes et al. 1992) and schizophrenia (Sz) (Lin et al. 1998). After a great deal of effort to test this important hypothesis, the mechanisms by which inflammatory-related pathways can precipitate the symptoms of psychiatric disorders, presumably by affecting CNS function, is beginning to be understood. This review will therefore consider the evidence, at the molecular level, that supports the hypothesis that inflammatory-related pathways are involved in the pathophysiology of psychiatric disorders. In addition, by extrapolating from this and other evidence, potential mechanisms by which inflammatory-related processes in the CNS could cause the symptoms of psychiatric disorders will be presented.

The peripheral inflammation/immune system
The peripheral inflammation/immune system has been extensively studied. The immune system consists of two processes, the innate system that recognizes and responds to pathogens but does not give long-lasting immunity and the adaptive immune system which allows a long-lasting recognition of specific
Peripheral inflammatory markers in psychiatric disorders: diagnostic potential

The majority of data supporting a role for inflammatory pathways in the pathophysiology of psychiatric disorders comes from the measurement of circulating inflammatory markers. A review of these studies shows that there is considerable evidence to suggest there are changes in inflammatory-related proteins (IRPs) in blood from individuals with major depressive disorder (MDD), bipolar disorder (BD) and Sz (Supplementary Table 1). However, as is common in many areas of psychiatric research, the data on whether changes in IRPs occur in blood from subjects with psychiatric disorders is not consistent. This is perhaps not surprising given that IRP levels in blood vary with many factors which include sleep disturbance (Ryan et al., 2005), body weight (Wellen & Hotamisligil, 2003), glycaemic state (Huerta & Nadler, 2002), diurnal variation (Miller et al., 2003) and even sample storage conditions (Flower et al., 2000; Friebe & Volk, 2008). Therefore the lack of standardization across studies measuring IRPs in the blood from subjects with psychiatric disorders could be the simple explanation as to why outcomes are not consistent.

To better understand the usefulness of IRP blood levels as a diagnostic aid it will be necessary to complete well controlled multi-centre trials using well considered standardized blood collection processes. Standardization will need to begin by agreeing on anticoagulant use, blood processing and storage as these factors all seem to influence cytokine stability. In addition, it will be critical to determine if ‘apparent’ changes in IRPs in a single blood sample are actually reflecting a shift in diurnal secretion of these proteins (Petrovsky et al., 1998) rather than a change in the amount of IRPs in blood over prolonged periods. Therefore studies are required to determine the nature of cytokine diurnal secretion in humans and if this is altered in people with psychiatric disorders. In addition, given the relationship between blood IRPs and body weight (Wellen et al., 2003), care should be taken to exclude individuals who have experienced significant weight changes prior to blood sampling. To control for diurnal variation (Petrovsky et al., 1998) in cytokine secretion, once this is shown not to have phase-shifted, and the effect of glycaemic variation (Huerta & Nadler, 2002) blood collection should be in the fasting state and at a standardized time of day. Finally, given the potential for variation in blood IRPs during the menstrual cycle (O’Brien et al., 2007a), this variable should also be controlled for in any study of blood IRPs in psychiatric disorders. It might be that a working group is required to consider all of these parameters and issue guidelines similar to those used in many endocrine protocols examining hormones in blood.

Peripheral inflammatory markers in psychiatric disorders: treatment monitoring and response prediction

Whilst many studies have tested the validity of measuring levels of inflammatory-related markers in the blood of subjects with MDD, BD and Sz (Supplementary Table 1) as a diagnostic aid, some studies have attempted to determine if changing levels of IRPs in blood before and after drug treatment could provide a measure of drug responsiveness. One novel study showed that treatment with paroxetine prior to treatment with cytokine interferon-α2B in subjects with malignant melanoma reduced levels of depression induced by that inflammatory cytokine (Musselman et al., 2001). These data would suggest that...
antidepressant drugs can interfere with the mechanisms that allow inflammatory-related pathways to generate depressive symptoms. However, it is less clear whether measuring IRPs in blood may be an indicator of treatment responsiveness in psychiatric disorders because recent studies have reported that levels of circulating IRPs are either changed [tumour necrosis factor-α (TNF-α) and CRP (Tuglu et al. 2003); interleukin-6 (IL-6) (Basterzi et al. 2005); IL-12, transforming growth factor-β1 (TNF-β1) (Sutcigil et al. 2007); interleukin-2 receptor (IL-2R) (Eller et al. 2008); TNF, CRP (Tousoulis et al. 2009); IL-6, TNF (Yoshimura et al. 2009)] or not changed [TNF (Himmerich et al. 2004); TNF, IL-8 (Eller et al. 2008); TNF, IL-1β, CRP (Piletz et al. 2009)] after antidepressant drug treatment. In internally controlled studies, were IRPs were measured before and after treatment, it has been reported that antidepressants decrease levels of pro-inflammatory IRPs (Basterzi et al. 2005; Sutcigil et al. 2007) and increased levels of anti-inflammatory IRPs (Narayan et al. 2008), which is consistent with an overall anti-inflammatory effect. Finally, data from some studies suggests that elevated levels of IRP prior to (Eller et al. 2008) or after (O’Brien et al. 2007b; Yoshimura et al. 2009) antidepressant drug treatment may be indicative of treatment resistance. Unfortunately, despite some promising findings on levels of circulating IRPs as a marker of antidepressant responsiveness, it must be acknowledged that many of the current studies have been completed on small patient cohorts using different antidepressants and different treatment regimens. Therefore it is still not possible to conclude that measuring IRPs in blood is useful in monitoring antidepressant drug treatment.

Early evidence that mood stabilizers might influence IRP levels came from the finding that TNF and IL-6 were increased in the blood of individuals treated with lithium (Haack et al. 1999). The notion that lithium can affect cytokine levels is supported by in-vitro data using human blood cells showing exposure of the cells to lithium can affect cellular expression of IRPs (Rapaport & Manji, 2001). Moreover, in normal control subjects it has been reported that treatment with valproate increases levels of circulating IL-6 (Shiah et al. 2005), data that suggest increasing IRPs in blood may be a common feature of all mood stabilizers. However, studies to determine whether treatment with mood stabilizers alter levels of circulating IRPs and whether monitoring levels of these proteins may provide a useful indicator of treatment response are required to test such a hypothesis.

An early indicator that antidepressive drugs may alter IRP levels in blood came from a report that levels of IL-1α and IL-6, but not IL-1β, IL-2 or TNF, were increased in the blood from Sz subjects taking antipsychotic drugs (Xu et al. 1994). By contrast, another study showed that levels of IL-2 were decreased in drug-naive Sz subjects, that levels of IL-3α were decreased in the same individuals after antipsychotic drug treatment and that there was no changes in IL-1β levels either in the untreated or treated state (Bessler et al. 1995). These data suggest there must be a complex interaction between disease pathophysiology and drug action. Moreover, a study showing that clozapine treatment (10 wk) decreased levels of blood TNF without changing levels of IL-6 (Monteleone et al. 1997) suggests that changes in levels of blood cytokines may be drug specific. This hypothesis is supported by the differing outcomes from studies measuring blood cytokines before and after treatment in Sz subjects that reported IRP levels to be reduced [interferon-γ (IFN-γ), IL-2 – mixed treatment (Arolt et al. 2000); IFN-γ – risperidone (Cazzullo et al. 2002); IL-2 – risperidone and haloperidol (Zhang et al. 2004); IL-2, IL-6 – risperidone but not haloperidol (Zhang et al. 2005); IL-6, IL-13 – mixed treatment (Pae et al. 2006)], unchanged [mixed treatment, IL-2, IFN-γ (Rothermundt et al. 2000); IL-2, IL-8 – risperidone and haloperidol (Zhang et al. 2004); IFN-γ, transforming growth factor-β1 (TGFB1) – mixed treatment (Kim et al. 2004); TNF, IL-2, IL-10 (Pae et al. 2006)] or increased [IL-10 – risperidone (Cazzullo et al. 2002); IL-4 (Kim et al. 2004); IL-12 – mixed treatment (Crespo-Facorro et al. 2008)] after such treatments. Hence it seems clear that the conclusion, reached by the Clinical Antipsychotic Trials of Intervention and Effectiveness study (Meyer et al. 2009), that changes in IRP blood levels vary with different antipsychotic drug treatments was correct. Moreover, this conclusion is essentially proven by a longitudinal study showing drug-specific effects of risperidone and haloperidol on IRP levels in blood (Zhang et al. 2005). Finally, one study has suggested that neither IRP blood levels on admission nor after a standardized antipsychotic drug treatment regimen gave any insight into the likelihood of treatment responsiveness (Erbagci et al. 2001). This is a disappointing outcome as it suggests that IRP blood monitoring may not be useful in assessing drug responsiveness in subjects receiving antipsychotic drugs.

A recent study has suggested that the effects of drug treatment on circulating IRPs are regulated by genetics (Zai et al. 2006). If that is correct, variation in the genetic make-up of the cohorts used in the study of the effects of antipsychotic drug treatment on blood IRPs could be one confound that has contributed to some.
variation in study outcomes. From a theoretical viewpoint it is significant that there is evidence to suggest treatment with most psychotropic drugs has the potential to influence blood inflammatory markers. This raises the need for studies in drug-naive subjects to determine the true status of blood inflammatory markers in individuals with psychiatric disorders.

The effect of psychotropic drug treatment on inflammatory markers

The notion that measuring levels of circulating blood cytokines can be used as a marker of drug responsiveness is based on the hypothesis that treating with psychotropic drugs must affect the expression of such markers in the periphery and CNS. The ability to modulate inflammatory-related pathways has been a known mechanism of action of antipsychotic drugs for at least 50 years (Pollmacher et al. 2000). Significantly, antipsychotic drugs have drug-specific effects on IRP levels which could account for some of the different clinical benefit/side-effect profiles of the different antipsychotic drugs. Of importance are the recent clinical trials suggesting improved clinical benefits when using drugs such as celecoxib (Muller et al. 2006; Nery et al. 2008) and aspirin (Laan et al. 2010) as adjunctive treatments with antipsychotic drugs. These studies suggest that antipsychotic drugs alone are not an optimal way of modulating IRPs in Sz subjects.

Antidepressants have also long been known to affect the production of IRPs (Maes, 2001), however the effects of such treatments appear to be drug-specific and have complex temporal variability (Fazzino et al. 2009; Kubera et al. 2000). Current data show that antidepressants do not have class-specific effects and thus more research is required to better understand how antidepressants can alter IRP expression. Moreover, the recent finding that there are clinical benefits in using celecoxib as an adjunctive treatment to antidepressant drugs (Akhondzadeh et al. 2009) would suggest that, as with antipsychotic drugs, antidepressant drugs alone do not produce optimal effects on IRPs in people with depression.

There is some evidence that the mood stabilizers lithium (Beyaert et al. 1991) and valproate (Brouland et al. 1989; Ichiyama et al. 2000) effect IRP expression. Again, it has been suggested that celecoxib has some benefit as an adjunctive treatment with BD (Nery et al. 2008). However, such a combination of treatments has been suggested to run the risk of significant adverse events (Slordal et al. 2003) and therefore the use of cox-2 inhibitors in the treatment of BD may need to be pursued with caution.

Given that current data suggest that targeting inflammation-related pathways in psychiatric disorders seems to give therapeutic benefit, it is becoming more critical to understand how these pathways are affected by the pathophysiology of those disorders; in particular it is becoming important to know if these pathways are altered in the CNS.

Peripheral inflammatory markers in psychiatric disorders: CSF studies

Whilst the study of MDD, Sz, BD and various drug treatments give a broad indication that IRPs may be affected by the pathophysiology and treatment of psychiatric disorders, it was the demonstration of increased IL-1β in the blood and CSF of Sz subjects that provided the first indication that blood IRPs may reflect changes in those proteins in the CNS (Barak et al. 1995). In the same study, CSF and blood levels of TNF, IL-2 and IL-6 were reported as unaltered in Sz and that soluble IL-2R was increased in the CSF but not blood from subjects with the disorder. In another CSF study, levels of IL-6 were reported as increased in subjects with a delayed, but not poor, response to antipsychotic drugs (Garver et al. 2003). Thus, as with the study of blood, the study of CSF has yet to provide a clear indicator as to the likely changes in inflammation-related pathways in Sz subjects.

Changes in inflammatory pathways in psychiatric disorders – findings from the study of the human CNS transcriptome

The availability of technology that allows large-scale measurement of gene expression at the level of the transcriptome and proteome has impacted greatly on current understanding of the pathophysiology of psychiatric disorders (Dean et al. 2005). Therefore it is important to consider findings from such studies when trying to understand the pathophysiology of psychiatric disorders.

There have been a number of microarray studies examining changes in the transcriptome in MDD subjects. These have suggested that changes in pathways involved in the fibroblast growth-factor system (Evans et al. 2004), oligodendrocytes (Aston et al. 2005; Klempan et al. 2009), glutamate/neural amino-acid transport (Choudary et al. 2005), GABA neurotransmission (Choudary et al. 2005; Klempan et al. 2009), catabolism of polyamines (Sequeira et al. 2006) and cell proliferation (Tochigi et al. 2008) as being affected by the pathophysiology of MDD. Importantly, a
recent microarray study of the dorsolateral prefrontal cortex has now provided strong evidence that a significant number of genes involved in inflammatory-related pathways were altered in MDD (Shelton et al. 2010). These data show that the levels of mRNA for both pro- and anti-inflammatory genes (IL-1α, IL-2, IL-3, IL-5, IL-8, IL-9, IL-10, IL-12A, IL-13, IL-15, IL-18, IFN-γ, lymphotoxin-α) are increased in the CNS of subjects with the disorder. Significantly, the predominant changes in gene expression appear to involve the interleukins rather than a generalized up-regulation of all genes involved in inflammatory-related pathways. The failure of other microarray studies to detect altered expression of cytokines in the CNS of MDD subjects could be because of the use of tissue from different tissue collections, the use of different microarray platforms or, of more biological relevance, the use of different CNS regions.

Significantly, a meta-analysis of microarray studies using post-mortem tissue from BD subjects did not suggest a significant involvement of inflammatory-related pathways in the pathophysiology of the disorder at the level of gene expression (Elashoff et al. 2007). By contrast, microarray studies do support the notion that the pathophysiology of BD affects mitochondrial function (Iwamoto et al. 2005; Quiroz et al. 2008; Sun et al. 2006), apoptosis (Kato et al. 2007), signalling pathways (Nakatani et al. 2006), ubiquitination (Ryan et al. 2006) and synaptic function (Ryan et al. 2006).

There have been many microarray studies using post-mortem CNS from Sz subjects and an overview of these findings is beyond the remit of this review. Significantly, two of these studies have reported increased expression of immune pathway genes (Arion et al. 2007; Saetre et al. 2007) which is relevant to this review as perturbation of the immune processes is often linked to inflammation (Taub & Oppenheim, 1994). In addition, a study focused on the CNS microvasculature has identified perturbation of inflammatory-related pathways in tissue from Sz subjects (Harris et al. 2008). These data give rise to the possibility that changes in CNS IRPs may be due to blood IRPs crossing the blood–brain barrier (Banks & Erickson, 2010). In addition, a microarray study that focused on gene expression in the dorsolateral prefrontal cortex of Sz subjects at different durations of illness reported changes in levels of expression of genes involved in inflammation-related pathways, but only in tissue from subjects who had had the disorder for more than 20 years (Narayan et al. 2008). This finding argues that changes in inflammation-related pathways could be contributing to the progressive nature of the pathophysiology of Sz (Lieberman et al. 2001).

The conclusion that inflammation-related pathways were affected in long-duration Sz was based on a gene ontology analysis of microarray data and showed changed expression of 13 genes involved in such pathways. Gene ontology analysis is an in-silico approach to deriving biologically relevant meaning from a large microarray dataset and further manual curation is needed to begin to fully identify functional pathways within each gene ontology category. Thus a closer examination of the microarray data on genes involved in inflammation-related pathways in long-duration Sz, and data from other functional assays examining the expression of these genes, suggests that many of the changes in the expression of genes involved in inflammatory processes could result from the increased expression of TGFB1 in the CNS of subjects with long-duration Sz (Narayan et al. 2008). Thus, it has been shown that TGFB1 increases the expression of chemokine ligand 5 (CCL5) (Happel et al. 2008); a finding that reflects the complex nature of inflammatory pathways as TGFB1 is anti-inflammatory (Buisson et al. 2003) whereas CCL5 is an inflammatory cytokine (Soria & Ben-Baruch, 2008). Moreover, TGFB1 has been shown to increase the expression of the complement component 1, q subcomponent β chain (C1QB) (Morgan et al. 2000); the expression of which is associated with inflammation and is increased in the cortex of subjects with long-duration Sz. TGFB1 also increases prostaglandin-endoperoxide synthase 1 (PTGS1: COX1) expression in astrocytes, but not neurons (Luo et al. 1998); PTGS1 expression is increased in long-duration Sz. It should be noted that in the same in-vitro study (Luo et al. 1998), it was shown that TGFB1 increases prostaglandin-endoperoxide synthase 2 (PTGS2: COX2) expression in astrocytes and neurons but the expression of PTGS2 was decreased in the cortex of subjects with long-duration Sz. However, an inverse relationship between the expression of PTGS2 and prostaglandin E receptor 3 (PTGER3) has been reported in human chondrocytic cells (Abulencia et al. 2003) which is similar to the inverse relationship between the expression of those genes in the CNS of subjects with long-duration Sz. Combining the data from the changes in expression of
inflammation-related pathways in long-duration Sz and the effects of exogenous TGFB1 it would seem that TGFB1-related gene expression is probably associated with pro-inflammatory, rather than anti-inflammatory, outcomes in the CNS of individuals with long-standing Sz.

Supporting the hypotheses the TGFB1 is causing pro-inflammatory effects is in the CNS of long-standing Sz are data showing that increases in TGFB1 cause the exocytosis of matrix metallopeptidase 2 (MMP2) (Phillips et al. 2003). MMPs are zinc-dependent endopeptidases that are capable of degrading all kinds of extracellular matrix proteins (Jezierska & Motyl, 2009) and therefore have an active role in inflammation. Importantly, it has been shown that levels of gene expression of MMP2 are optimized to levels of exocytosis of that protein (Parekh & Wittrup, 1997); this means it is reasonable to postulate that increased levels of TGFB1 would cause increased exocytosis and expression of MMP2 in the CNS of subjects with long-duration Sz.

The involvement of PTGS1 and PTGS2 in the pathophysiology of Sz is significant because these genes encode proteins that synthesize prostaglandins by metabolizing arachidonic acid. A notable difference between PTGS1 and PTGS2 is that the former is a constitutively active enzyme whereas the latter is induced when required (Pairet & Engelhardt, 1996). In the periphery, PTGS2 inhibition is linked to the anti-inflammatory effects of non-steroidal anti-inflammatory drugs whereas PTGS1 is more involved in the gastric and renal side-effects associated with those drugs. Whilst, the effects of the two enzymes in the CNS are yet to be elucidated, the finding that the expression of both PTGSs is altered in the CNS of Sz subjects suggests changes in prostaglandin-related inflammatory activity (Kelly, 1996) and this could be contributing to the pathophysiology of long-duration Sz. Supporting this proposal is the data showing that the expression of the prostaglandin E receptor 3 (PTGER3) is increased in the cortex of Sz subjects. Significantly, PTGER3 has been shown to potently regulate CNS function (Momiyama et al. 1996) and therefore may regulate many of the CNS actions of prostaglandins. For example, PTGER3 is present on serotonergic neurons in the raphe suggesting it acts as an interface between prostaglandins and serotonergic pathways (Momiyama et al. 1996). This provides a potential mechanistic link between the changes in prostaglandin activity, as identified by gene expression changes in long-duration Sz (Narayan et al. 2008), and the well accepted notion that changes in

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**Fig. 1.** A schematic showing the genes that were identified as having changed levels of expression in the cortex of subjects with long-duration schizophrenia (direction of changes shown by solid arrows) which are also changed after the addition of exogenous transforming growth-factor β1 (TGFB1) in in-vitro experimental models (direction of changes shown by dotted arrows). Significantly, TGFB1 alters both the expression and secretion of matrix metallopeptidase 2 (MMP2) and secreted MMP is a potent pro-inflammatory protein. CCL5, Chemokine ligand 5; C1QB, complement component 1, q subcomponent β chain; PTGS1, prostaglandin-endoperoxide synthase 1; PTGS2, prostaglandin-endoperoxide synthase 2; PTGER3, prostaglandin E receptor 3; IL-1F5, interleukin-1F5.
serotonergic function are important in the pathophysiology of Sz (Dean, 2003).

There is further evidence for the notion that TGFB1-related pathways are important in the pathophysiology of long-duration Sz. In particular, it has been shown that levels of expression of CCL5 are directly related to levels of the expression of IL-1F5 in a mouse model of biliary atresia (Leonhardt et al. 2006) and the expression of both CCL5 and IL-1F5 are increased in long-duration Sz (Narayan et al. 2008). Whilst it has yet to be established whether there CCL5 directly controls the expression of IL-1F5, it is significant that IL-1F5 belongs to a family of proteins that have an important role in immune regulation and pro-inflammatory processes (Barksby et al. 2007). In addition, TGFB1⁻/⁻ have been shown to develop lethal immunopathology in multiple organs in conjunction with enhanced T-cell proliferation and activation with increased CD4⁺ T-cell differentiation into T helper 1 (Th1) and Th2 cells (Li et al. 2007). These data suggest that TGFB1-mediated changes in the CNS could involve multiple IRPs and inflammation-related pathways. Finally, TGFB1 has been shown to increase its own expression and to increase the expression of the TGFB1 receptor in the mouse hippocampus (Morgan et al. 2000). This means that changes in TGFB1 expression in the CNS could be related to an ongoing gain of function due to looping amplification processes (Gasser, 2009). Importantly, as the data on long-duration Sz do not show a change TGFB1 receptor, it is unlikely such a TGFB1 gain of function is involved in the pathophysiology of long-duration Sz.

Changes in inflammatory pathways in psychiatric disorders – findings from the study of the human CNS proteome

Whilst the majority of microarray studies do not seem to have added significantly to understanding the role of inflammatory-related pathways in the pathology of psychiatric disease, there are findings that raise the possibility of different inflammatory-related pathways contributing to the pathophysiology of MDD and long-duration Sz. However, when considering the implications of findings from the study of the human CNS transcriptome it must be remembered that there is not necessarily a strong correlation between changes in mRNA levels and in protein in the same tissue (Dean et al. 2007). This has lead to the use of technologies that can examine changes in the human proteome to attempt to understand the pathophysiology of psychiatric disease (Edgar et al. 2000), a technology suggested to be particularly suited to understanding the pathophysiology of disease of the human CNS that involves inflammatory processes (Suk, 2010). It is therefore significant that a recent review of the studies of the human CNS proteome of Sz subjects does not conclude that IRP levels are particularly affected in this disorder, rather pathways involved in brain energy metabolism, brain plasticity and synaptic function appear to be particularly affected (Martins-de-Souza et al. 2010). In addition, there appear to be few proteomic studies on BD and these do not suggest that there are significant changes in IRP levels associated with mood disorders (English et al. 2009).

In contrast to studies on the human proteome, a single protein study has recently reported increased levels of transmembrane (tmTNF), but not the soluble (sTNF), form of TNF in the dorsolateral prefrontal cortex, but not cingulate cortex of MDD subjects (Dean et al. 2010). To appreciate the significance of this finding it is necessary to understand the underlying biochemistry of TNF. In the CNS, TNF is expressed by microglia (Morganti-Kossman et al. 1997), astrocytes (Lieberman et al. 1989) and a limited population of neurons (Chung et al. 2005). All cells synthesizing TNF produce a monomeric type-2 transmembrane protein that is inserted into the cellular membrane as a homo-trimer termed tmTNF-α (McCoy & Tansey, 2008) (Fig. 2). In the membrane, tmTNF has a long leader sequence forming an intracellular domain, a 26-amino-acid transmembrane domain and a 20-amino-acid extracellular domain (Yan et al. 2009). The cleavage of tmTNF by TNF-α converting enzyme (ADAM17) gives rise to a soluble TNFα (sTNF) (McCoy et al. 2008). Significantly, data from TNF knock-in mice that have non-cleavable tmTNF, and hence cannot produce sTNF, shows that it is sTNF that is critical in activating inflammatory processes (Ruuls et al. 2001).

The two forms of TNF can activate two TNF receptors (TNFR1 and TNFR2) in cell membranes, with TNFR2 being preferentially activated by tmTNF and TNFR1 being preferentially activated by sTNF (McCoy et al. 2008). Significantly, TNFR1 appears to be expressed by most cells whereas TNFR2 is primarily expressed by immune cells (including microglia), endothelial cells and neurons (Eisner et al. 2004; McCoy et al. 2008). Notably, TNFR1 contains a cytoplasmic death domain that is critical in activating a complex receptor-signalling pathway (McCoy et al. 2008). TNFR1 can also indirectly recruit members of the TNF receptor-associated factor (TRAF) family of proteins to modulate cellular gene expression (Wajant et al. 2003). Currently it would appear that acute activation of TNFR1 is a cytoprotective process (Sato et al. 2005).
whereas prolonged activation leads to caspase-induced apoptosis (Tobiume et al. 2001). TNFR2 signals by a direct recruitment of TRAF proteins and can have protective and inflammatory effects (Wajant et al. 2003). In addition, TNFR2 is cleaved by ADAM17 and TNFR1 is cleaved by an unknown enzyme; this cleavage of TNFRs is important in controlling levels of TNFR activation (McDermott et al. 1999).

In beginning to interpret the potential outcomes of increased levels of tmTNF in the cortex of MDD subjects, it is clear the elevated levels of this protein could be associated with increased activity of inflammation-related pathways. However, increased TNF-mediated neurodegenerative processes are associated with increased levels of CD4+ and CD8+ T cells as well as astrocytosis, microgliosis and demyelination (Wajant et al. 2003). The notion that TNF-mediated neurodegeneration can be involved in the pathophysiology of disorders of human CNS is supported by an extensive literature showing abnormalities in CD4+ and CD8+-mediated outcomes in multiple sclerosis (Friese & Fugger, 2009). Therefore the absence of any evidence for neurodegenerative processes, such as astrocytosis or gliosis (Damadzic et al. 2001; Gilmore & Bouldin, 2002; Muller et al. 2001), in the CNS of MDD subjects could be an indicator that increased tmTNF is not activating inflammatory-related pathways. It is therefore important to acknowledge that until there is a better understanding of TNF-mediated processes in the human CNS it would be premature to suggested that the increased levels of tmTNF in the cortex of MDD subjects is indicative of increased activity within inflammatory-related pathways.

**The potential roles for cytokines in human CNS**

Whilst the exact mechanism and outcomes remain to be understood, there is a growing body of data suggesting a role for inflammatory-related pathways in disorders of the human CNS. Current evidence
from studies using human post-mortem CNS would suggest a role for cytokine-related pathways in the CNS of subjects with mood disorders. There is also evidence for a TGFB1-driven contribution to the pathophysiology of Sz. Therefore it is worth considering what is known about the function of these proteins and their associated pathways in the CNS, rather than the periphery.

There is a growing understanding of the complex role of TNF in the CNS. Thus, TNF can have diverse impacts on neurodevelopment processes including dendritic arborization which has been suggested to be the mechanism by which TNF can modulate behaviour and learning processes (Park & Bowers, 2010). It is also becoming clear that changed TNF signalling alone does not induce apoptotic processes, rather a secondary stimulus is required for TNF to induce a cell to move to an apoptotic state (Park et al. 2010). This indicates that changes in levels of TNF alone may not be sufficient to activate inflammation-related pathways. In addition, TNF has the capacity to modulate long-term potentiation, with late phase effects being modulated through changes in protein expression (Butler et al. 2004). TNF-mediated changes in protein expression can also regulate levels of ion channels and ligand-gated ion channel receptors in the CNS (Park et al. 2010). In addition, TNF can further affect neurotransmitter pathways by affecting the activity of serotonergic as well as glutamatergic neurons (Muller & Schwarz, 2007). Importantly, the communication between TNF and neurotransmitters is bidirectional as the activity of TNF can be controlled by neurotransmitters (Pavlov et al. 2006). Hence it is clear that TNF has effects on CNS function that go beyond modulating inflammation and some of these effects could be what causes the onset of the symptoms of psychiatric disorders. Therefore a better understanding of the overall affects of TNF is required to unravel the mechanisms by which TNF may be involved in the pathophysiology of disorders such as MDD.

From the current understanding of the roles of tmTNF, it can be postulated that aberrant signalling through three potential mechanisms could be involved in the pathophysiology of mood disorders (Fig. 3).

First would be aberrant signalling because of a disarrangements in a number of non-cell contact paracrine mechanisms (Fig. 3a) involving sTNF signalling through TNFR1 or TNFR2 (Eissner et al. 2004; McCoy et al. 2008) or sTNFR1 (Wajant et al. 2003), sTNFR2 (McDermott et al. 1999) acting at tmTNF. As levels of sTNF are not altered in the cortex of subjects with mood disorders over-activation of TNFR1 or TNFR2 by sTNF appears unlikely. The second mechanism could involve changes microglia-mediated cell–cell contact where tmTNF could be brought into contact with TNFR1 or TNFR2 (Fig. 3b). This model implies that the increased levels of tmTNF observed in the CNS of subjects with mood disorders are due to increased tmTNF expression by microglia or an increase in the number of microglia. The third model is based on cell–cell contact where tmTNF and TNFR1 or TNFR2 are expressed on adjacent cells (Fig. 3c). The latter two models would provide both forward and reverse signalling because of activation of TNFR1 or TNFR2 by tmTNF and TNFR1 or TNFR2 activation of tmTNF. Given that tmTNF is predominantly expressed by astrocytes (Lieberman et al. 1989) and TNFR2, the favoured receptor for tmTNF, is expressed by neurons and microglia (Eissner et al. 2004; McCoy et al. 2008) the latter two models would suggest a potential for astrocyte/microglia or astrocyte/neuron signalling. Thus, there is now a clear need to better understand tmTNF signalling mechanisms as these may have a pathophysiological role in mood disorders.

The interleukins also control many critical CNS processes such as the regulation of sleep (Krueger, 2008). Significantly, different members of the interleukin family are involved in inflammation-related and protective processes which, in part, depend on whether the interleukin is acting outside or inside a cell (Luheshi et al. 2009). The overall outcome of any change in interleukin levels in the CNS would therefore depend on the balance between the different family members, e.g. it is known that increased levels of the IL-1 family are associated with increased inflammatory-related pathway activity (Luheshi et al. 2009). To make the effects of interleukins even more complex some interleukins, such as IL-18, have a mixed inflammation-related and homeostatic role in the CNS (Alboni et al. 2010). Thus, given the potential for widespread changes in expression of interleukins in the CNS of subjects with psychiatric disorders (Shelton et al. 2010) it will be necessary to better define the changes in the balance and/or location of interleukins before it can be determined if their overall impact is indicative of an inflammation-related response.

Finally, there is the intriguing finding that TGFB1 pathways may be affected in the CNS of subjects with long-duration Sz. TGFB1 is generally regarded as an anti-inflammatory cytokine in the CNS (Saud et al. 2005) but it is argued here that the nature of expression changes in the CNS of long-duration Sz subjects would be pro-inflammatory. Significantly, ageing in humans
is associated with altered responsiveness to cytokines due to a fundamental change in the reactive state of microglia (Dilger & Johnson, 2008). Given that such an overall change in cytokine responsiveness is predicted to result in an increase in inflammatory-related pathways, it could be argued that the increase in the activity of TGFB1-related pathways in long-duration Sz (which by definition is in older individuals) represents some form of accelerated age-related inflammatory process. However, like other factors involved in inflammation-related pathways, TGFB1 has many diverse effects such as controlling overall astrocyte gene expression (Hamby et al. 2006), inhibiting neurogenesis (Buckwalter et al. 2006) and inducing the death of microglia (Kim et al. 2004). Thus, again it may be presumptive to assume that changes in TGFB1-driven pathways in the CNS of long-duration Sz subjects are associated with changes in an inflammatory-related status.

Conclusions

Peripheral studies have underpinned the notion that there are changes in inflammatory-related pathways in the CNS of subjects with psychiatric disorders (Lin et al. 1998; Maes et al. 1992). Importantly, the fold-change in levels of cytokines in blood from subjects with psychiatric diseases (Supplementary Table 1) do not seem to be of the same order of magnitude as those in the blood of subjects with an inflammatory-related disorder such as rheumatoid arthritis (Chen et al. 2009). This could suggest that the changes in cytokine-related pathways in individuals with psychiatric disorders are reflective of processes other than activation of peripheral inflammatory pathways. Moreover, many factors influence blood cytokine levels on a day-to-day basis which would argue that a standardized regimen is needed for the collection of blood in which IRPs are to be measured (Corsini & House, 2010) if the
true value of measuring circulating cytokines as a diagnostic aid or a predictor of treatment outcome is to be fully assessed in psychiatric disorders. Such studies are essential as it is important to assess any potential aid that may be helpful in assessing or treating psychiatric disorders.

Several lines of evidence are emerging to support the notion that changes in what have been classically regarded as immune-related pathways (Maes et al. 1992) are present in the CNS of subjects with psychiatric disorders. Natural end products of a chronic inflammatory process would be oedema, the presence of activated microglia, apoptosis and/or gliosis. Significantly, there is evidence to suggest that there are increased levels of activated microglia in the CNS of Sz subjects (van Berckel et al. 2008; Wierzbka-Bobrowicz et al. 2005) and that the presence of elevated levels of microglia may be associated with individuals with psychiatric disorders dying by suicide (Steiner et al. 2006). Therefore, understanding which inflammation-related pathways are affected in the CNS of subjects with psychiatric diseases should be a high priority. In this regard, there is growing evidence from animal studies that increases in pro-inflammatory pathways can lead to decreased availability of tryptophan with a concomitant increase in levels of kynurenine in the CNS due to increases in the activity of the enzyme indoleamine 2,3-dioxygenase. Whilst a critical analysis of this hypothesis is beyond the remit of this review, it is clear that changes in kynurenine pathways in the pathophysiology of psychiatric diseases; with these changes possibly being associated with the onset of psychoses rather than depression. More studies on kynurenine pathways in the CNS will be required to better elucidate the symptomological outcomes from changes in these pathways.

It is now acknowledged that a much better understanding of the pathophysiology of psychiatric disease is required as a basis for new drug design (Insel, 2009). This well-argued position underlies the urgency of understanding the role of cytokines and other IRPs in the pathophysiology of psychiatric disorders. Such knowledge will be particularly potent when the mechanisms involved in the genesis of the symptoms are unravelled. This is because the drug etanercept, which targets the TNF-related pathways (Esposito & Cuzzocrea, 2009), has been shown to have antidepressant effects (Tyring et al. 2006). This is strong data to support the premise that targeting and modulating inflammatory-related systems can have therapeutic benefits in subjects with psychiatric disorders.

Note

Supplementary material accompanies this paper on the Journal’s website (http://journals.cambridge.org/pnp).

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Statement of Interest

None.

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