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## Neuroinflammation in animal models of traumatic brain injury

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### Abstract

Traumatic brain injury (TBI) is a leading cause of mortality and morbidity worldwide. Neuroinflammation is prominent in the short and long-term consequences of neuronal injuries that occur after TBI. Neuroinflammation involves the activation of glia, including microglia and astrocytes, to release inflammatory mediators within the brain, and the subsequent recruitment of peripheral immune cells. Various animal models of TBI have been developed that have proved valuable to elucidate the pathophysiology of the disorder and to assess the safety and efficacy of novel therapies prior to clinical trials. These models provide an excellent platform to delineate key injury mechanisms that associate with types of injury (concussion, contusion, and penetration injuries) that occur clinically for the investigation of mild, moderate, and severe forms of TBI. Additionally, TBI modeling in genetically engineered mice, in particular, has aided the identification of key molecules and pathways for putative injury mechanisms, as targets for development of novel therapies for human TBI. This Review details the evidence showing that neuroinflammation, characterized by the activation of microglia and astrocytes and elevated production of inflammatory mediators, is a critical process occurring in various TBI animal models, provides a broad overview of commonly used animal models of TBI, and overviews representative techniques to quantify markers of the brain inflammatory process. A better understanding of neuroinflammation could open therapeutic avenues for abrogation of secondary cell death and behavioral symptoms that may mediate the progression of TBI.

### BACKGROUND

Traumatic brain injury (TBI) is a leading cause of death and long-term disability in the developed world. Each year, approximately 10 million people suffer a TBI event worldwide

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(Hyder et al, 2007; Ruff et al, 2012). Predictive analyses indicate that TBI will constitute the third greatest portion of the total global disease burden by 2020 (Hyder et al, 2007). Within the US alone, some 1.7 million people sustain a TBI annually, and around 5.3 million people live with a TBI-associated disability (Langlois et al, 2006; Prins and Giza, 2012). Of those TBIs that occur, by far the majority are mild to moderate in nature and comprise 80–95 % of cases, with severe TBI accounting for the balance (Tagliaferri et al, 2006). Consequent to increases in survival rate after initial injury, TBI can give rise to substantial and lifelong cognitive, physical, and behavioral impairments that necessitate long-term access to health care and disability services (Tagliaferri et al, 2006; Shi et al, 2013). Exceptionally vulnerable are the elderly, in which the very same injury can cause greater disability and can induce a dramatic rise in the risk of neurodegenerative (Gardner et al, 2014; Barnes et al, 2014) and neuropsychiatric disorders (Chen et al., 2014). Although TBI symptoms can intermittently resolve within a year after injury, some 70–90% of patients endure prolonged and often permanent neurocognitive dysfunctions. It is now established that TBI represents a process, that once initiated can extend either silently or symptomatically to neurodegeneration. This process can lead to early onset of dementia (Gardner et al, 2014; Barnes et al, 2014) as well as Parkinson's disease (PD) and other degenerative conditions (Gardner et al., 2015; Gardner & Yaffe 2015). Particularly notable, TBI is a strong environmental risk factor for development of Alzheimer's disease (AD). Recent gene expression studies have delineated the up regulation of key pathways leading to AD and PD provoked by mild, let alone moderate or severe forms of TBI (Greig et al, 2014; Tweedie et al 2013 A&B; Goldstein et al, 2012). Consequent to a current lack of any available therapeutic options (Moppett, 2007), it is imperative to understand the mechanisms that underlie head injury and the ensuing neuronal dysfunction and cognitive impairments to successfully develop possible therapeutics.

## TBI-TRIGGERED PATHOLOGICAL PROCESSES

TBI instigates complex pathological processes that involve a broad spectrum of cellular and molecular pathways. TBI-associated brain damage can be classified into two main phases. First, an initial primary damage phase occurs at the moment of insult. This can involve contusion and laceration, diffuse axonal injury, brain swelling and intracranial hemorrhage, and invariably results in immediate (necrotic) cell death (Greig et al, 2014; LaPlaca et al, 2007, Cheng et al., 2012). This is followed by an extended secondary phase that involves cascades of biological processes initiated at the time of injury that may endure over much longer times, from days to numerous weeks (Maas et al., 2008; Zhang et al., 2008). This delayed phase, caused by a variety of cellular and molecular responses instigated in an effort to potentially restore the cellular homeostasis of the damaged tissue, is not particularly well controlled and often will lead to exacerbation of the primary injury damage, progressive neurodegeneration and delayed cell death (Kabadi and Faden, 2014; Lozano et al., 2015). Hallmarks of the secondary insult response can include blood-brain barrier (BBB) breakdown, oxidative stress, glutamate excitotoxicity, and neuroinflammation, which all can occur time-dependently following the primary mechanical insult (Bains and Hall, 2012; Das et al., 2012; Maas et al., 2008; Zhang et al., 2008).

Neuroinflammation is present in both primary (acute) and secondary (chronic) stages of TBI (Lozano et al., 2015) and appears to be responsible for both detrimental and beneficial effects, contributing to primary insult and secondary injury but also facilitating tissue repair (Woodcock and Morganti-Kossmann, 2013). In this regard, following the primary insult, cellular endogenous inflammatory responses are triggered at the injury site with the aim to repair the damaged tissue; however, the often excessive production of pro-inflammatory cytokines appear to become an important driving force for the pathological progression in TBI.

Consequent to recent medical and media interest in sport and military concussions, the concept of chronic neuroinflammation and white matter (WM) injury has been highlighted within the context of TBI. Historically, chronic neuroinflammation was generally associated with chronic neurological diseases, such as occurs in multiple sclerosis, rather than with acute injury, as occurs with TBI (Kutzelnigg & Lassmann, 2014). However, recent reports linking single and repeated TBI events to chronic WM outcomes have fortified association between TBI and neuroinflammation. Neuropathological studies of pre-clinical and clinical TBI cases has provided evidence that glial cells are a central component of the chronic WM degenerative process (Glushakova et al., 2014); (Mouzon et al., 2014); (Sajja et al., 2014).

## NEUROINFLAMMATION IN TBI

### TBI neuroinflammation is characterized by reactive gliosis

The development of neuroinflammation that follows TBI involves a complex process of cumulative changes that occur within the brain. Following a TBI insult, quiescent glial cells of multiple types become rapidly activated via a process termed “reactive gliosis”. This process involves activated microglia initiating and sustaining astrocytic activation via the generation and release of inflammatory mediators that, in turn, act on surrounding glia and neurons. Post-traumatic cerebral inflammation is characterized by glial activation, leukocyte recruitment, and upregulation and secretion of mediators such as cytokines and chemotactic cytokines (chemokines). (Morganti-Kossmann et al., 2001) (Figure 1).

These inflammatory mediators not only impact surrounding glia and neurons but additionally act to recruit peripheral immune cells, such as neutrophils, macrophages and lymphocytes, into brain. Thus acute neuroinflammation following an initial TBI insult not only functions to regulate both damaging and reparative events in the injured and recovering brain, but can also sensitize neurons to enable long-term degenerative processes (Mrak and Griffin, 2005; Streit et al., 2004; Tweedie et al., 2013, 2016). Glial activation induces morphological and functional alterations within the cells that impact neural–glial and glial–glial interactions. This change can cause dysfunction of synaptic connections, neurotransmitter homeostasis imbalance, and potential axonal degeneration and neuronal death ((Bal-Price and Brown, 2001). Astrocytes become activated (termed reactive astrogliosis) in response to CNS injury ((Buffo et al., 2010). Moreover, astrocytes are responsible for encapsulating damaged areas after injury, thereby partly separating injured from the healthy brain tissue ((Fitch and Silver, 2008); (Nimmerjahn, 2009). Astrocytic activation occurs consequent to a mechanism of hypertrophy and an upregulation of intermediate filaments, such as glial fibrillary acidic protein (GFAP) and vimentin ((Buffo et

al., 2010); (Gervasi et al., 2008); (Seker et al., 2010). Classically, reactive astrocytes form locally at the primary site of injury, but quite possibly also migrate from distant sites ((Seker et al., 2010); (Turner et al., 1999). In this regard, astrocyte migration historically has been determined from animal models as well as human postmortem studies. However, more recent in vivo studies have questioned whether or not astrocyte migration substantially occurs or, alternatively, if selective astrocyte proliferation at the injury site takes place (Bardehle et al., 2013). Studies have shown the presence of a variety of cytokines involved with either the initiation or modulation of reactive astrogliosis (Farina et al., 2007); (John et al., 2003); (Liberto, Albrecht, Herx, Yong, & Levison, 2004); (Rao et al., 2012). These include interleukin-1beta (IL-1 $\beta$ ), tumor necrosis factor- alpha (TNF- $\alpha$ ), and transforming growth factor beta- 1 $\beta$  (TGF-1 $\beta$ ), for which astrocytes express receptors and their interaction triggers an astrocytic reactive response. Astrocyte-derived cytokines such as IL-1 $\beta$  and TNF- $\alpha$  are considered to promote neurotoxicity whereas TGF- $\beta$ 1 is thought to be neuroprotective (Farina et al., 2007); (John et al., 2003); (Liberto et al., 2004); (Rao et al., 2012). Key studies demonstrating astrocyte activation in animal models of TBI are highlighted in Table 1

### **TBI, microglia and M1/M2 phenotypes**

Microglia, comprising some 15% to 20% of total cells within the brain, actively survey the CNS environment to orchestrate changes to maintain homeostasis, meet changing physiological needs and respond to pathological events by serving as brain immune cells to coordinate innate immune responses (Harry, 2013). Their physical association with synapses implicates microglia with synaptic refinement and scaling, which is achieved by continuous sampling of specific signals derived from neuronal and astrocyte-derived factors that are sensed by the presence of numerous receptors and ion channels present on microglia. Signaling through these receptors can induce changes in membrane potential, intracellular calcium, cellular motility and cytokine release, accompanied by potential changes in phenotype from their relatively quiescent state to the activated one, evident in TBI. Microglia are adept at exhibiting a M1 pro-inflammatory phenotype, as ensues immediately after TBI, or a M2 anti-inflammatory phenotype which can be induced by IL-4 and is typified by the release of trophic factors such as insulin like growth factor-1, anti-inflammatory IL-10 (Harry, 2013; Suh et al., 2013), and the incretin GLP-1 (Kappe et al., 2012). The ability to time-dependently change phenotype as a consequence of appropriate microenvironmental queues accounts for the heterogeneity of microglial function (Harry, 2013).

As pathological sensors of TBI, microglia rapidly become activated (activated microglia), undergoing essential morphological changes from a branched phenotype to active amoeboid cells (Aihara et al., 1995). Accompanying this, there is an upregulation of a variety of membrane receptors that include those to support phagocytosis. In this regard, microglia are considered to protect neurons by migrating to the site of injury surrounding damaged or dead cells with the purpose of clearing debris, such as myelin debris that can act as a rate-limiting factor in the process of remyelination, and stimulating an M1 inflammatory response to initiate the healing process (Harry, 2013; Kotter et al., 2011). Critically, a rapid transition of this M1 response to one of resolution and repair is required, to provide trophic support by the release of various growth factors (M2 response) followed by quiescence.

When appropriately queued, microglia can release nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), and neurotrophin-3(NT-3) to augment neuronal growth and survival (Parekkadan et al., 2008).

Deficits in the ability of microglia to optimally perform these functions or to appropriately switch between M1 and M2 phenotypes detrimentally impacts brain function. Altered microglial morphology associated with a more reactive/activated (M1) phenotype has been reported in rodent and human brain as a function of age (Vaughan and Peters, 1974; Schuitemaker A, et al., 2010), with elevated activated microglia markers and basal pro-inflammation cytokine levels (Harry, 2013). Data on the M2 anti-inflammatory cytokine response is less clear, but is suggested to be reduced (Ye and Johnson 2001; Fenn et al., 2012). Hence age (where, as discussed, TBI events occur more often and induce greater damage) as well as other factors (e.g., the presence of aberrant misfolded proteins) can elevate induction of proinflammatory cytokines, particularly TNF- $\alpha$  and IL-1 $\beta$ , and impair the normal time-dependent transition to the reparative M2 phase, leading to detrimental effects, neuronal dysfunction and demise (Streit et al., 2004; Greig et al., 2014). Key studies demonstrating microglial activation in animal models of TBI are highlighted in Table 2.

In contrast to microglial function, a central function of oligodendrocytes is to produce the myelin sheaths that surround CNS axons. Each oligodendrocyte may branch to form myelin on many axons within the surrounding tissue. Oligodendrocytes and their precursor cells (OPCs) are distributed throughout both gray and white matter of the CNS. They can provide trophic factors by the production of glial cell line-derived neurotrophic factor (GDNF), BDNF, and insulin-like growth factor-1 (IGF-1) (Dougherty et al., 2000; Du and Dreyfus, 2002). Oligodendrocytes, consequent to their multiple functions, have particularly high metabolic rates and are thus vulnerable to the molecular consequences of tissue insult (McTigue and Tripathi, 2008). Oligodendrocyte dysfunction and demise causes demyelination of WM tracts, resulting in impairment of axonal conduction, and eventually axon death that can underwrite memory impairment. Although phenotypically separate cells, oligodendrocytes, microglia and astrocytes collectively work together in a manner so that their combined dynamic responsibilities support the optimal functioning of the neuronal network. Subtle or blatant dysfunction of any or all of these glia, as occurs following TBI, is accompanied by morphological and functional changes that can impact both neural-glia and glial-glia interactions, and can thereby, result in a loss of homeostasis, imbalances of neurotransmitters and impaired synaptic function.

In synopsis, neuroinflammation is considered to have both beneficial and detrimental roles. Significant benefits can be achieved when the inflammation is controlled in a regulated manner and for a defined period of time. When sustained or excessive, however, inflammation can become a major cause of numerous neuropathologies and, thereby, drive neurodegenerative processes. Time-dependence is hence highly important when considering neuroinflammatory responses, as is their induction by specific experimental paradigms. This may explain the negative outcomes of anti-inflammatory agents in clinical trials of both head injury and other neurodegeneration diseases. Additionally, physiological and biochemical responses to TBI, including inflammation, may differ based on the species or strain, as well as the injury models used in the laboratory (Ziebell and Morganti-Kossmann, 2010). Finally,

time-dependent changes ascertained in animal models may not necessarily directly translate in to humans (on a 1:1 ratio – quite possibly they may be slower in humans).

### **Neuroinflammation and acute production of inflammatory mediators in TBI**

Within minutes of a traumatic insult, a robust neuroinflammatory response is generally provoked within the site of injury. The presence of a number of soluble markers of neuroinflammation is not only evident in the region of brain trauma but also in CSF, as typified by proinflammatory cytokines and chemokines (Karve et al., 2015; Kou and VandeVord, 2014; Lozano et al., 2015). As described, under pathological conditions in the CNS, chemokines are generated by activated resident local astrocytes and microglia and act to aid recruit peripheral immune cells into the brain parenchyma (Das et al., 2012; Semple et al., 2010b; Ziebell and Morganti-Kossmann, 2010). In addition to chemokines, various cytokines are also generated and secreted by activated glia following TBI (Das et al., 2012; Kumar and Loane, 2012; Ziebell and Morganti-Kossmann, 2010). These important chemokines and cytokines have been summarized in Tables 3 & 4.

Cytokines represent a diverse group of small proteins synthesized by a wide variety of cell types that act as autocrine and paracrine mediators of the inflammatory response to injury or infection. Notably, tumor necrosis factor- $\alpha$  (TNF $\alpha$ ) is synthesized as a type II transmembrane protein (tmTNF $\alpha$ ) of 26 kD. The metalloprotease, TNF $\alpha$  converting enzyme (TACE/ADAM17), can cleave tmTNF $\alpha$  from the plasma membrane of glia to release a soluble form (sTNF- $\alpha$ ) of 17 kDa into the brain interstitial fluid (Frankola et al., 2011). Both tmTNF $\alpha$  and sTNF $\alpha$  can then assemble in biologically active homotrimers to bind and activate TNF $\alpha$  receptors (R), which exist in either of two distinct forms on the cell surface. TNF-R1 (p55 or p60) is ubiquitously and constitutively expressed, except on erythrocytes, whereas TNF-R2 (p75 or p80) expression is limited to myeloid and endothelial cells, myocytes, thymocytes, microglia, astrocytes, oligodendrocytes, and selected neurons (Speeckaert et al., 2012). Whereas the two receptors were originally attributed with opposing actions with TNF-R1 providing pro-apoptotic and TNF-R2 pro-survival roles, more recent research has demonstrated that both receptors are capable of driving cell survival and apoptosis depending on the microenvironment, cell type, intracellular signaling pathway and other factors present (Woodcock and Morganti-Kossmann, 2013; Ziebell and Morganti-Kossmann, 2010). Early experimental studies in models of brain injury have demonstrated that TNF $\alpha$  is upregulated in the brain within a few hours (Fan et al., 1996; Knoblach et al., 1999; Shohami et al., 1996; Trembovler et al., 1999), and our more recent studies have confirmed this (Baratz et al., 2015). Notably, the upregulation of TNF $\alpha$  mRNA is reported to occur prior to the time of peripheral immune cell infiltration into the injured site (Riva-Deputy et al., 1994; Ziebell and Morganti-Kossmann, 2010), indicating that resident brain immune cells (e.g., microglia, astrocytes and oligodendrocytes) are the source of cytokines, independent of peripheral immune cell activation. The dual role of TNF $\alpha$  as a pro-apoptotic and pro-survival cytokine in CNS inflammation remains controversial, and studies with TNF $\alpha$  as well as TNF-R1 and -R2 knockout mice suggest that a deficiency of TNF $\alpha$  is beneficial early after experimental brain injury but may be deleterious at a late stage (Scherbel et al., 1999) after TBI. Such time-dependence of lowering TNF $\alpha$  in brain

can potentially be optimized pharmacologically by the early administration of a TNF $\alpha$  synthesis inhibitor following a TBI (Baratz et al., 2015).

## **ANIMAL MODELS OF TBI TO METHODOLOGICALLY EVALUATE NEUROINFLAMMATION**

Three widely used TBI rodent models (fluid percussion injury, controlled cortical impact injury, and weight-drop impact acceleration injury) are also evaluated in this article, and these can reasonably mimic key parts of the diverse pathophysiology of human TBI. Each model has individual advantages and disadvantages, and although originally developed in rats, they have subsequently been effectively utilized in mice either with or without modifications. Clearly, mice are smaller, often less expensive, easier to handle, and provide a wide opportunity for genetic manipulations to understand mechanisms, using knock out and knock in technology. By contrast, rats have larger brains, and more readily allow time-dependent plasma as well as CSF sampling. Of note, rodent models of TBI require the use of anesthetic agents that clearly limit immediate postinjury behavioral evaluations in relation to orientation, memory, and level of consciousness. Although no single animal TBI model perfectly mimics the human condition (Marklund and Hillered 2011), cross-validation across animal models has demonstrated that neuroinflammation is a consistent feature of TBI and its early mitigation has benefits. In light of the lack of effective pharmacological treatments for TBI, developing drug-like compounds that safely and effectively achieve this and can translate their actions to the human condition is a critical current unmet medical need, and an increasing armamentarium of methodologies exist to support such work.

### **The weight drop (WD) injury model**

The WD model is a clinically relevant animal model, which mimics cerebral contusion by dropping a fixed amount of weight from a pre-determined height onto the exposed dura (open skull WDI) or onto the intact calvarium (closed skull WD), which causes a shearing injury to the brain. The WD model was developed initially for use in the rat and has subsequently been applied to the mouse, either with or without modification(s) from the rat system. To prevent skull fractures caused by the dropped weight, a metallic disc is placed over the skull (generally in the rat) to dissipate the force over a larger area. The injury severity may be manipulated by adjusting the amount of weight as well as the height from which it is dropped. This model has been modified by some users by supporting the head with either a foam cushion, resin mold, or stereotactic frame that creates different pathological and behavioral outcomes. Whereas the weight of the mass, the height of its drop, and the mode of head support may be standardized, the magnitude of the brain injury may also be influenced by the skull thickness and degree of calcification. Slight differences in the drop angle and resultant skull fractures may influence the brain injury characteristics. In an effort to limit the injury variability caused by differences in the skull anatomy, the injury may be produced through a craniotomy using the direct fluid percussion (FP) or lateral FP (LFP) technique to the brain (Xiong et al., 2013). The application of the WD model to mice as a closed skull injury results in diffuse neuronal loss, neuroinflammation, elevation of markers of apoptosis, and both short- and long-term cognitive impairments across a range of behavioral paradigms (Deselms et al., 2016).

### **The lateral fluid percussion (LFP) model**

First established for use in rabbit and cats, the midline FP model of brain injury was later adapted to the rat (Dixon et al., 1987; McIntosh et al., 1987) and subsequently adapted to produce injury within a single hemisphere in rats and mice (McIntosh et al., 1989a). The technique involves a fluid pulse against the intact dural surface of the brain, which is applied through a small trephine opening in the parietal bone to generate a diffuse brain injury. The FP or LFP injury model generates vascular and axonal damage within the brain that is not influenced by either skull thickness or the degree of bone calcification. FP can create complex patterns of brain deformity, contingent on the location of the craniotomy and the path of the percussion waves. In rats, LFP injury generates an amalgamation of focal cortical contusion and diffuse subcortical neuronal injury (that includes injury within the hippocampus and thalamus). This occurs within minutes of the impact and progresses to neuronal loss within 12 hours, but does not markedly expand into other brain regions - as evaluated 7 days post-injury. Reproducibility of results with this model requires extensive and precise animal preparation and operative experience in order to replicate pressure and resulting injury. The LFP model has become one of the most widely used and well characterized models of experimental TBI (Laurer et al., 2002). Changes in injury severity can be achieved by adjusting the pendulum height, which defines the force of the fluid pressure pulse transmitted through the saline reservoir that impacts the dura over the brain. Modification of the injury device has included substitution of a high pressure pump to replace the pendulum and saline reservoir in order to create more reproducible patterns of brain compression. The model requires creation of a craniotomy of a precise shape, size, and location. Small differences in the craniotomy site or the angle of the trajectory can result in different FPI forces and variable brain injury. When undertaken optimally the method is ideal for studies of diffuse axonal injury (DAI) following. Injury is generally accompanied by ipsilateral cortical contusions, with axonal injury to the internal and external capsule and corpus callosum that are similar to those seen in humans (Xiong et al., 2013; Galgano et al., 2015).

### **The controlled cortical impact (CCI) model**

The CCI model induces a measurable brain displacement by effectively utilizing a mechanical solid percussion device that is applied to the dura through a cranial opening. Briefly, in an anesthetized animal a craniectomy is undertaken to gain access to the animal's brain for deformation brain injury induced using a pneumatic or electromechanical CCI device. This system manifests a strong correlation between the magnitude of cortical deformation that is produced and the resulting histological damage to the brain, as well as longer-term behavioral changes. The method is relatively simple to employ, and thus widely used in TBI research. Whereas the majority of CCI studies have been undertaken in rats, numerous also have been published in mice (Xiong et al., 2013; Galgano et al., 2015). Several parameters, including the impactor velocity and depth of the brain deformation produce a precise focal brain injury that may be accurately controlled. In this regard, the impactor can be relatively small tipped – and make a precise and well defined lesion, or it can be of a larger diameter (e.g., 5 mm) to induce DAI and its long-term functional deficits.



A midline CCI lesion using a large 5 mm diameter impactor can induce readily measurable neurological deficits, as assessed by cognitive dysfunction, foot drop, reduced Rotarod test scores, an increased latency in the water maze test, and clumsiness when removing small adhesive paper circles placed on the forelimb paw. Hence, changing the impactor size can create a diversity of clinically relevant models. A limitation of the CCI model is the occasional occurrence of a dural laceration, which is more frequent in the mouse consequent to the delicacy of the dura and its vulnerability to puncture at the plunger impact site. Relatively severe swelling can occur when a large contusion is created through a large craniotomy. When the bone flap is not replaced an open craniotomy provides a release mechanism for the contused and swollen brain, detrimentally affecting the reproducibility of the model. Nevertheless, the model is both widely and effectively utilized in brain injury research, and the relatively mild to moderate forces associated with the CCI model generally do not produce significant brainstem injury to cause high mortality. Subsequent to its development in rats (Dixon et al., 1991), CCI has been commonly applied across species (from large to small) as the quantitative control it permits over injury force and velocity, and thus graded tissue deformation, allows the model's adaption to numerous research questions. Specifically, CCI has been successfully modified for use across mice, rats, swine, and primates in a manner that perhaps few other methodologies have.

### Concussion models (mild TBI)

As sports injuries, particularly with American football, are common in humans, models of such injuries are critical to evaluate the effects of concussion related injuries. Experimental methodologies that cause a cerebral concussion in rodents are essentially similar to those that generate a cerebral contusion (e.g., WD, LFP and CCI models), but are used with decreased force. Cerebral concussion in rodents is characterized by behavioral changes in the forced swimming test, depression-like behavior, and cognitive abilities (Zohar et al., 2011; Deselms et al., 2016). Diffuse neuronal loss is generally evident, along with markers of apoptosis (Tweedie et al., 2007; Tashlykov et al., 2009; Deselms 2016). Concussion models can be used in either mouse or rat, and can involve either a single or repeated injury (Kondo et al., 2015). Neuroinflammation is invariably evident (Faden and Loane 2015), as assessed by astrocytic/microglial reactivity, and can be accompanied with or without alterations in BBB and elevations in phospho-tau levels, particularly the selective *cis* phospho-tau form (Kondo et al., 2015) that is evident in chronic traumatic encephalopathy associated with American footballers and other contact sports following multiple concussive and subconcussive injuries (Turner et al., 2013; Gandy et al., 2014). Such animal models, detailed above, are clearly essential for the screening of new therapies for mild concussive and mild to moderate contusion injuries that represent the most frequent types of TBIs, particularly as recent studies suggest that such injuries may be treatable both immediately following and perhaps long after the insult in relation to the neuroinflammation that accompanies them (Faden and Loane 2015).

## METHODOLOGICALLY EVALUATING NEUROINFLAMMATION: WHAT CAN BE MEASURED?

As discussed above, extensive research has been undertaken to define the wide-ranging homeostatic changes that ensue following a TBI as a response to attempt to mitigate damage and initiate reparative processes – numerous of which are centered on inflammatory and anti-inflammatory signaling pathways. The earliest quantitative alterations involve cerebral gene expression changes in response to TBI. Transcriptional changes in the injured brain of rodent TBI models have been widely reported (Kobori et al., 2002; Natale et al., 2003; Israelsson et al., 2008 and 2009) in order to increase our understanding of the molecular responses to TBI. Such studies are optimally performed when changes are evaluated time-dependently consequent to the transient changes that occur across cellular and molecular pathways. As an example, Israelsson et al., (2008) evaluated the transcriptional changes that occurred from 1 hr to 7 days following CCI in mice by evaluating injured neocortex and hippocampus using the quantitative reverse transcriptase–polymerase chain reaction (qRT-PCR) and performing an unbiased genome-wide search for transcripts up and down regulated in injured brain, as compared to uninjured brain samples. Spatial distribution of enhanced expression was then characterized by the use of *in situ* hybridization to evaluate in which cell types (microglia, astrocytes, oligodendrocytes, etc.) transcriptional changes were found. Along with this, injured brains were fixed by perfusion, cryosectioned and subjected to immunohistochemistry in order to detect activated microglial (IB4-positive) cells (Israelsson et al., 2008). Particularly, notable in this study is that over 100 gene transcripts were up regulated 3-fold or more, each in an orchestrated time-dependent manner, and were associated with defined cell types. Over 50% of the evaluated genes up regulated 3 days after injury encoded proteins involved in inflammation, immunity, defense responses, cell migration and adhesion, or the encompassed extracellular matrix. Particularly evident was that chemokines and cytokines were upregulated within hours after injury, some (Ccl3, Ccl12) by log-folds.

Mitochondrial dysfunction contributes to cell death in TBI (Hiebert et al, 2015; Yokobori et al, 2014). Recent research has characterized new roles for mitochondria in the regulation of inflammatory processes. The release of signals from mitochondria in response to stress and infection advances the formation of the inflammatory signaling platform identified as inflammasomes. The activation of inflammasomes by damaged mitochondria results in caspase-1-dependent secretion of inflammatory cytokines IL-1 $\beta$  and IL-18, and triggers an inflammatory form of cell death known as pyroptosis (Gurung et al., 2015). Furthermore, mitochondrial MAVS (mitochondrial antiviral-signaling) recruits NLPR3 (nucleotide-binding oligomerization domain-like receptor family, pyrin domain-containing 3) inflammasome components to the mitochondria and is required for optimal NLPR3 inflammasome activity (Haneklaus and O'Neill, 2015). Thus, evaluation of mitochondria-associated inflammasome activity and of NLPR3 inflammasome components (NLPR3, ASV and Caspase-1) and MAVS, likely will bring a greater understanding of the possible signaling cascades that are triggered by, and then underpin, deficits evident in TBI. Recently, increases in reactive oxygen species (ROS) generation were found to be a key factor to activate NLRP3 inflammasomes (Bauernfeind et al., 2011). ROS, that can readily be

measured in brain by multiple methodologies (Mattiasson 2004; Wojtala et al., 2014; Bar-Or et al., 2015), appear to be at the crossroads of inflammasomes and inflammation, and elevated markers of oxidative stress have been reported in TBI (Table 5).

As described above, measuring microglia M1 and M2 phenotypes can be used to determine inflammatory status and mechanisms. M1 is pro inflammation and M2 is anti-inflammation. Isolated microglia or frozen tissues can be evaluated by RT-PCR or protein analyses methods (ELISA as well as multiplex technologies) to measure expression of markers of **M1**: Marco, IL1 $\beta$ , IL-6 (low IL10), S100A8, 9 and **M2**: Arg1, Ym-1, FIZZ, IL10, IGF1, together with quantification of other key inflammatory markers such as TNF $\alpha$  and nitric oxide. Likewise, from an immunohistochemistry perspective, antibodies to key proteins such as IBA1, CD-68 and MHC-II (OX6) can be utilized to probe the inflammatory status of the brain time-dependently following injury in both mechanism-focused and drug evaluation studies. A recent notable study is that of Kumar et al., (2015) that involved a detailed phenotypic analysis of M1-and M2-like polarized microglia during the acute phase after CCI in mice. Both phenotypes were activated early after TBI, but the classical ensuing M2-like phenotype was replaced by M1-like and mixed transitional (Mtran) phenotypes that expressed high levels of NOX2 at 7 days post-injury. This shift towards M1-like and Mtran phenotypes, creating an imbalance, is associated with increased neurodegeneration. And thus, these studies indicate that notwithstanding activation of both M1-like and M2-like microglia/macrophages responses after TBI, early M2-like responses may become dysfunctional over time, triggering development of pathological M1-like and Mtran phenotypes that time-dependently drive neuroinflammation from an aberrant perspective.

## CONCLUSION

Neuroinflammation in response to TBI involves the activation of glia, release of inflammatory mediators within the brain, and recruitment of peripheral immune cells. Multiple markers of neuroinflammation have been reported to occur across animal models of TBI (Tables 1–5) as well as in the human condition (Woodcock and Morganti-Kossmann, 2013; Di Battista et al., 2015) and, importantly, appear to associate with both patient and animal model outcome measures (Di Battista et al., 2016). Understanding the cellular and molecular mechanisms underpinning neuroinflammation by combining methodologies overviewed herein may beneficially aid the development of new therapies aimed at modulating the inflammatory response acutely post-injury, to mitigate the short- and long-term consequence of TBI.

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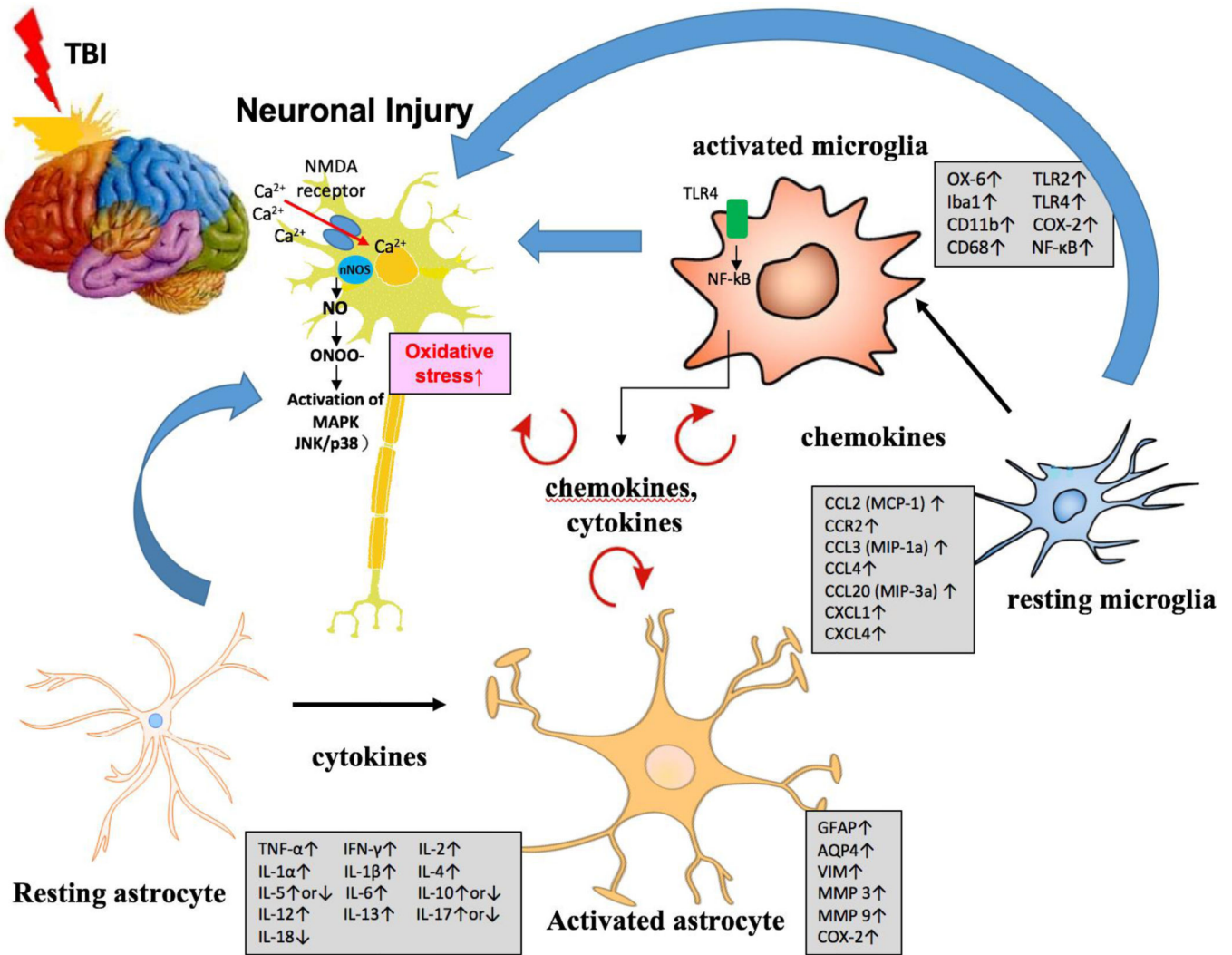
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**Figure 1.** After a TBI event, resting glia of multiple types become rapidly activated in a process identified as “reactive gliosis.” This process involves activated microglia initiating and sustaining astrocytic activation via the generation and release of inflammatory markers/mediators (see Tables 1 and 2) that, in turn, act on surrounding glia and neurons via autocrine and paracrine functions (red arrows). Glial activation causes morphological and functional changes within the cells that impact critical neural–glial and glial–glial interactions. This can cause dysfunction of synaptic connections, imbalances of neurotransmitter homeostasis, potential axonal degeneration and neuronal death. Glial cells, most notably astrocytes and microglia, become activated. Their processes become hypertrophied. They upregulate cell surface immune modulatory proteins, and increase the synthesis and release of pro-inflammatory molecules including cytokines, chemokines (see Tables 3 and 4) and prostanoids.

TABLE 1

Studies showing astrocyte activation in animal models of TBI

Markers	model	Species	Findings	Reference
<b>Increased Expression in Brain Tissue (Homogenate)</b>				
GFAP <sup>a</sup>	CCI, WD, LFP	Rat, Mice	mRNA expression↑ (1 – 30 days) Protein expression↑ (3 – 14 days)	(Fenn et al., 2014; Lagraoui et al., 2012; Liu et al., 2013; Mayeux et al., 2015; Sandhir et al., 2008; Singh et al., 2015; Su et al., 2014; Zhao et al., 2014)
AQP4 <sup>b</sup>	CCI, WD, LFP	Rat, Mice	mRNA expression↑ (1 – 21 days) Protein expression↑ (2 days)	(Lagraoui et al., 2012; Lopez-Rodriguez et al., 2015; Tomura et al., 2011)
VIM <sup>c</sup>	CCI, WD	Mice	mRNA expression↑ (1 – 21 days)	(Lagraoui et al., 2012; Lopez-Rodriguez et al., 2015)
MMP 3 <sup>d</sup>	CCI	Mice	mRNA expression↑ (1 day)	(Lagraoui et al., 2012)
MMP 9	CCI	Mice	Protein expression↑ (1 day)	(Chen et al., 2012)
COX-2 <sup>e</sup>	CCI	Mice	Protein expression↑ (1 day)	(Chen et al., 2012)
<b>Increased Levels in Serum</b>				
GFAP	WD	Mice	Protein expression in Serum	(Yang et al., 2013b)

<sup>a</sup>GFAP: Glial Fibrillary Acidic Protein

<sup>b</sup>AQP4: Aquaporin 4

<sup>c</sup>VIM: Vimentin

<sup>d</sup>MMP 3: Matrix Metalloproteinase-3

<sup>e</sup>COX-2: Cyclooxygenase-2

TABLE 2

Studies showing microglia activation levels in Animal Models of TBI

Markers	model	Species	Findings	Reference
<b>Increased Expression in Brain Tissue (Homogenate)</b>				
OX-6 <sup>a</sup>	CCI	Rat	Protein expression↑ (8 weeks)	(Acosta et al., 2013)
Iba1 <sup>b</sup>	CCI	Rat, Mice	mRNA expression↑ (1 – 28 days) Protein expression↑ (3 – 14 days)	(Sandhir et al., 2008; Turtzo et al., 2014)
CD11b <sup>c</sup>	CCI	Mice	mRNA expression↑ (1 – 28 days)	(Sandhir et al., 2008)
CD68	CCI, LFP	Rat	Protein expression↑ (3 h – 5 days)	(Shojo et al., 2010; Zhang et al., 2012)
TLR2	WD	Rat	mRNA expression↑ (5 days) Protein expression↑ (2 days)	(Chen et al., 2008; Zhang et al., 2012)
TLR4	CCI, WD	Rat, Mice	mRNA expression↑ (1 – 21 days) Protein expression↑ (1 – 21 days)	(Chen et al., 2008; Dong et al., 2011; Wei et al., 2014; Ye et al., 2014; Zhang et al., 2012)
COX-2	CCI	Mice	Protein expression↑ (1 day)	(Chen et al., 2012)
NF-κB <sup>d</sup>	CCI, WD	Rat	mRNA expression↑ (1 day) Protein expression↑ (1 – 5 days)	(Chen et al., 2012; Chen et al., 2008; Dong et al., 2011; Jin et al., 2010; Jin et al., 2008a; Jin et al., 2008b)

<sup>a</sup>OX-6: MHC Class II antibody<sup>b</sup>Iba1: Ionized Calcium Binding Adaptor Molecule 1<sup>c</sup>CD11b: Cluster of Differentiation Molecule 11b<sup>d</sup>NF-κB: Nuclear factor-κB

TABLE 3

Studies showing elevated cytokine levels in brain tissues, CSF and serum in acute stages of TBI in animal models

Markers	model	Species	Findings	Reference
<b>Increased Cytokines Expression in Brain Tissue (Homogenate)</b>				
IL-1 $\beta$	CCI <sup>a</sup> , WD <sup>b</sup> , LFP <sup>c</sup>	Rat, Mice	mRNA expression $\uparrow$ (1 h – 7 days) Protein expression $\uparrow$ (3 h – 24 h)	(Kamm et al., 2006; Lagraoui et al., 2012; Dalgard et al., 2012; Chen et al., 2008)
IL-6	CCI, WD, LFP	Rat, Mice	mRNA expression $\uparrow$ (3 h – 7 days) Protein expression $\uparrow$ (1 – 3 days)	(Lagraoui et al., 2012)
TNF- $\alpha$	CCI, WD, LFP	Rat, Mice	mRNA expression $\uparrow$ (3 h – 5 days) Protein expression $\uparrow$ (1 – 7 days)	(Lagraoui et al., 2012; Dalgard et al., 2012; Chen et al., 2008; Zhao et al., 2014; Mukherjee et al., 2011)
IL-10	CCI, WD, LFP	Rat, Mice	mRNA expression $\uparrow$ (3 h – 7 days) Protein expression $\uparrow$ (1 – 7 days)	(Kamm et al., 2006; Lagraoui et al., 2012; Perez-Polo et al., 2013; Su et al., 2014)
	CCI, WD, LFP	Rat, Mice	mRNA expression $\downarrow$ (1 – 5 days) Protein expression $\downarrow$ (1 – 3 days)	(Lee et al., 2012; Mukherjee et al., 2011; Wang et al., 2011; Zhao et al., 2014)
IL-1 $\alpha$	WD, LFP	Rat	mRNA expression $\uparrow$ (3 h – 7 days)	(Lu et al., 2005a; Lu et al., 2005b; Perez-Polo et al., 2013; Shojo et al., 2010; Su et al., 2014)
IL-4	CCI, LFP	Rat	mRNA expression $\uparrow$ (7 days) Protein expression $\uparrow$ (4 – 1 day)	(Dalgard et al., 2012; Su et al., 2014)
IL-5	CCI, LFP	Rat	mRNA expression $\uparrow$ (7 days) Protein expression $\uparrow$	(Dalgard et al., 2012; Su et al., 2014)
	LFP	Rat	mRNA expression $\downarrow$ (1 day)	(Mukherjee et al., 2011)
IL-2	LFP	Rat	mRNA expression $\uparrow$ (7 days)	(Su et al., 2014)
IL-12	CCI	Mice	Protein expression $\uparrow$ (3 days)	(Lagraoui et al., 2012)
IL-13	CCI	Rat	Protein expression $\uparrow$ (3 days)	(Dalgard et al., 2012)
IL-17	LFP	Rat	mRNA expression $\uparrow$ (7 days)	(Su et al., 2014)
			mRNA expression $\downarrow$ (1 day)	(Mukherjee et al., 2011)
IL-18	LFP	Rat	mRNA expression $\downarrow$ (1 day)	(Mukherjee et al., 2011)
IFN- $\gamma$	CCI, LFP	Rat, Mice	mRNA expression $\uparrow$ (7 days) Protein expression $\uparrow$ (4 – 12 h)	(Dalgard et al., 2012; Lagraoui et al., 2012; Su et al., 2014)
<b>Increased Cytokines levels in CSF</b>				
IL-6	CCI	Rat	Protein expression $\uparrow$ (8 h – 2 days)	(Stover et al., 2000)
TNF- $\alpha$	CCI	Rat	Protein expression (0 h – 2 days)	(Stover et al., 2000)
<b>Increased Cytokines levels in Serum</b>				
IL-6	WD	Rat	Protein expressions levels	(Yang, Gangidine, Pritts, Goodman, & Lentsch, 2013; Yang, Gustafson, et al., 2013)
TNF- $\alpha$	WD	Rat	mRNA expression	(Kamm et al., 2006; Singh et al., 2015)
IL-10	WD	Rat	mRNA expression	(Singh et al., 2015)

<sup>a</sup>CCI: Controlled Cortical Impact;

<sup>b</sup>WD: Weight Drop;

<sup>c</sup>LFP: Lateral Fluid Percussion

TABLE 4

Studies showing elevated chemokine levels in brain tissues, CSF and serum in acute stages of TBI in animal models

Markers	model	Species	Findings	Reference
<b>Increased Chemokine Expression in Brain Tissue (Homogenate)</b>				
CCL2 <sup>a</sup> (MCP-1)	CCI, WD, LFP	Rat, Mice	mRNA expression↑ (4 h–10 days) Protein expression↑ (4–12 h)	(Dalgard et al., 2012; Lagraoui et al., 2012; Liu et al., 2013; Mukherjee et al., 2011; Rau et al., 2014; Rhodes et al., 2009; Semple et al., 2010a; Teng and Molina, 2014)
CCR2	WD	Rat	mRNA expression↑ (10 days)	(Liu et al., 2013)
CCL3 (MIP-1a)	CCI, WD, LFP	Rat, Mice	mRNA expression↑ (1 day) Protein expression↑ (1 day)	(Lagraoui et al., 2012; Mukherjee et al., 2011; Su et al., 2014; Yang et al., 2013a)
CCL4	CCI	Mice	mRNA expression↑ (1–20 days)	(Leonardo et al., 2012)
CCL20 (MIP-3a)	CCI, LFP	Rat	Protein expression↑ (2 days)	(Dalgard et al., 2012; Das et al., 2011)
CXCL1 <sup>b</sup>	CCI	Rat, Mice	Protein expression↑ (4 h)	(Dalgard et al., 2012; Lagraoui et al., 2012)
CXCL4	CCI	Mice	mRNA expression↑ (6 h)	(Lagraoui et al., 2012)
<b>Increased Chemokine Levels in Serum</b>				
CCL2 (MCP-1)	CCI, WD, LFP	Mice	mRNA expressionkine Level	(Probst et al., 2012)
CCL3 (MIP-1a)	WD	Mice	Protein expression12) day)	(Yang, Gangidine, et al., 2013)

<sup>a</sup>CCL2: Chemokine (C-C Motif) Ligand 2

<sup>b</sup>CXCL1: Chemokine (C-X-C motif) Ligand 1



TABLE 5

## Studies Showing Elevated Oxidative Stress markers in Animal Models of TBI

Markers	model	Species	Findings	Reference
<b>Increased Oxidative Stress markers in Brain Homogenate</b>				
SOD	WD	Rat	mRNA expression↓ (1 – 3 days) Protein expression↓ (1 day)	(Ding et al., 2014a; He et al., 2012; Lu et al., 2015; Wang et al., 2011)
NO	WD, LFP	Rat	Protein expression↑ (3h – 1day)	(Ferreira et al., 2013; Wang et al., 2011; Wei et al., 2014)
iNOS	CCI, WD,L FP	Rat	Protein expression↑ (1 – 3 days)	(Gunther et al., 2012; Jafarian-Tehrani et al., 2005; Jung et al., 2014; Wang et al., 2011; Wei et al., 2014)
MDA <sup>a</sup>	WD	Rat	Protein expression↑ (1 – 3 days)	(Ding et al., 2014a; He et al., 2012; Lu et al., 2015; Wang et al., 2011)
MPO <sup>b</sup>	CCI, WD	Rat	Protein expression↑ (1 day)	(Chen et al., 2012; Clark et al., 1994)
GPx <sup>c</sup>	Rat	Rat	Protein expression↓ (1 day)	(Ding et al., 2014b)

<sup>a</sup>MDA: Malondialdehyde

<sup>b</sup>MPO: Myeloperoxidase

<sup>c</sup>GPx: Glutathione Peroxidase