

Old Herborn University Seminar Monograph

26. THE GUT MICROBIOME AND THE NERVOUS SYSTEM

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Old Herborn University

Old Herborn University Seminar

Monograph 26

ISBN 3-923022-38-7

ISSN 1431-6579

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INTEROCEPTION AND THE SENTIENT SELF

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INTRODUCTION

Langley was the first person to describe the autonomic nervous system (ANS) (*Langley, 1903*). Near the end of his report, he noted explicitly that he had omitted a description of the sensory inputs that are required for the ANS to function efficiently; he explained that he had not been able to unequivocally distinguish the necessary elements anatomically. As Cannon later emphasized, the neural processes (autonomic, neuroendocrine and behavioural) that maintain an energy-efficient, physiological balance across conditions in the body, i.e., homeostasis, must receive modality-selective afferent inputs that report the condition of the tissues of the body (*Cannon, 1939*). Finally, Precht and Powley suggested that the missing category of homeostatic afferents could be identical to the anatomically well-defined small, dark B-cells in the mammalian dorsal root ganglia (*Precht and Powley, 1990*); unfortunately, their proposal was rejected by nearly all of the discussants of their publication. Had they been aware of the findings described in the present report, they would have recognized the central continuation of the pathway they had envisioned and the unmistakable confirmation of their proposal.

The sensory pathway that is described in the following sections provides not only the sensory inputs required for organotopic homeostatic control of the body's condition, but also the basis for human feelings from the body, such as cool, warm, pricking pain, burning pain, itch, sensual touch, muscle ache,

bowel distension, urge to urinate, vascular flush, hunger, taste, thirst and "air hunger". These feelings, which are all related to the condition of the body and underlie mood and emotional state, are all associated with strong affective motivations that are the correlates of behavioural responses needed to maintain the health of the body. Thus, these feelings can all be viewed as homeostatic emotions, a concept which emphasizes their essential autonomic role. The anatomical pathways described below underpin the homeostatic nature of these feelings, and conversely, reveal a fundamental relationship with the ANS that explains why the affectively charged feelings from the body all have strong autonomic sequelae. So, pain is accompanied by autonomic changes because it is the perceptual correlate of a behavioural motivation generated in response to a condition which the homeostatic system cannot rectify automatically.

In the conventional view, the well-discriminated feelings of temperature, itch and pain are associated with a somatosensory system that maps the sense of touch to a recognized map of the body (homunculus) in Rolandic cortex (Figure 1). In contrast, the less distinct visceral feelings of vasomotor activity, hunger, thirst and internal sensations are said to be associated with a separate visceral system in more archaic regions. That conceptualization obscures fundamental discrepancies, such as the fact that stimulation of Rolandic somatosensory cortices almost

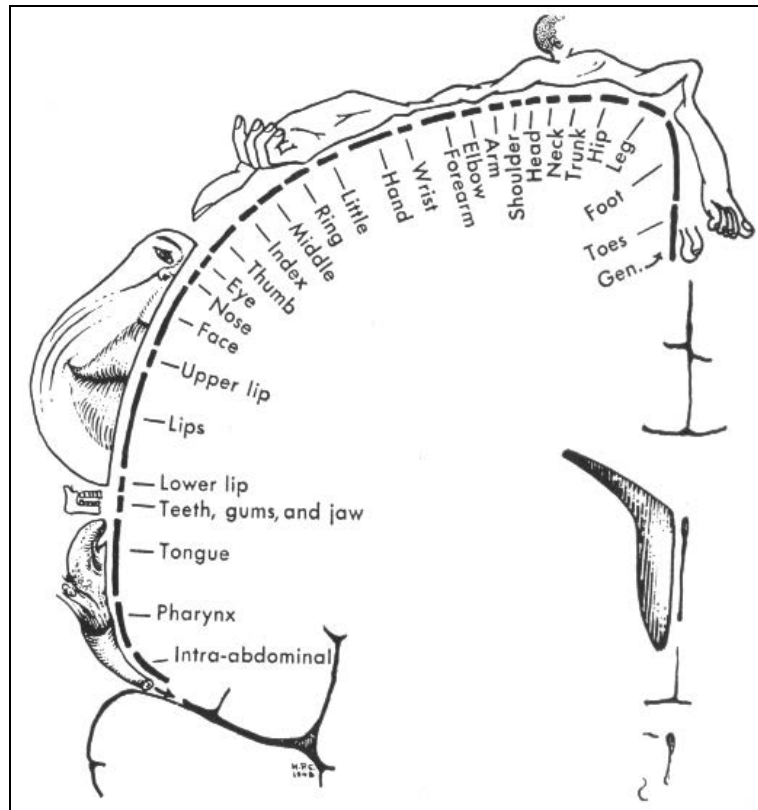


Figure 1: Human homunculus (*Penfield and Rasmussen, 1950*).

never produces feelings of pain or temperature, or that lesions of Rolandic cortex have no effect on temperature or pain sensations. It also leaves unexplained the inherent emotional (affective/motivational) qualities and reflexive autonomic effects that all feelings from the body share, which distinguish them from tactile mechanoreception and from the sense of limb position (proprioception). In the following sections it is shown that all feelings from the body are represented in a phylogenetically new system in primates that evolved from the afferent limb of the evolutionarily ancient, hierarchical homeostatic system that maintains the integrity of the body, that is, the sensory complement of the ANS. These feelings thus represent a sense of the physiological condition of the entire

body, providing a broad redefinition of the term 'interoception'. More importantly, from the clinical perspective, these findings reveal that feelings from the body, such as pain, are inherently linked with autonomic conditions, such as plasma extravasation or cardiac rhythmicity, because they are, respectively, sensory and motor aspects of the same homeostatic system. In humans, further processing builds a meta-representation of primary interoceptive activity, engendered in the anterior insula, which seems to provide the basis for the subjective image of the material self as a feeling (sentient) entity, that is, emotional awareness. More detailed reviews of the evidence for these views are available elsewhere (*Craig, 2002, 2003a, 2009*).

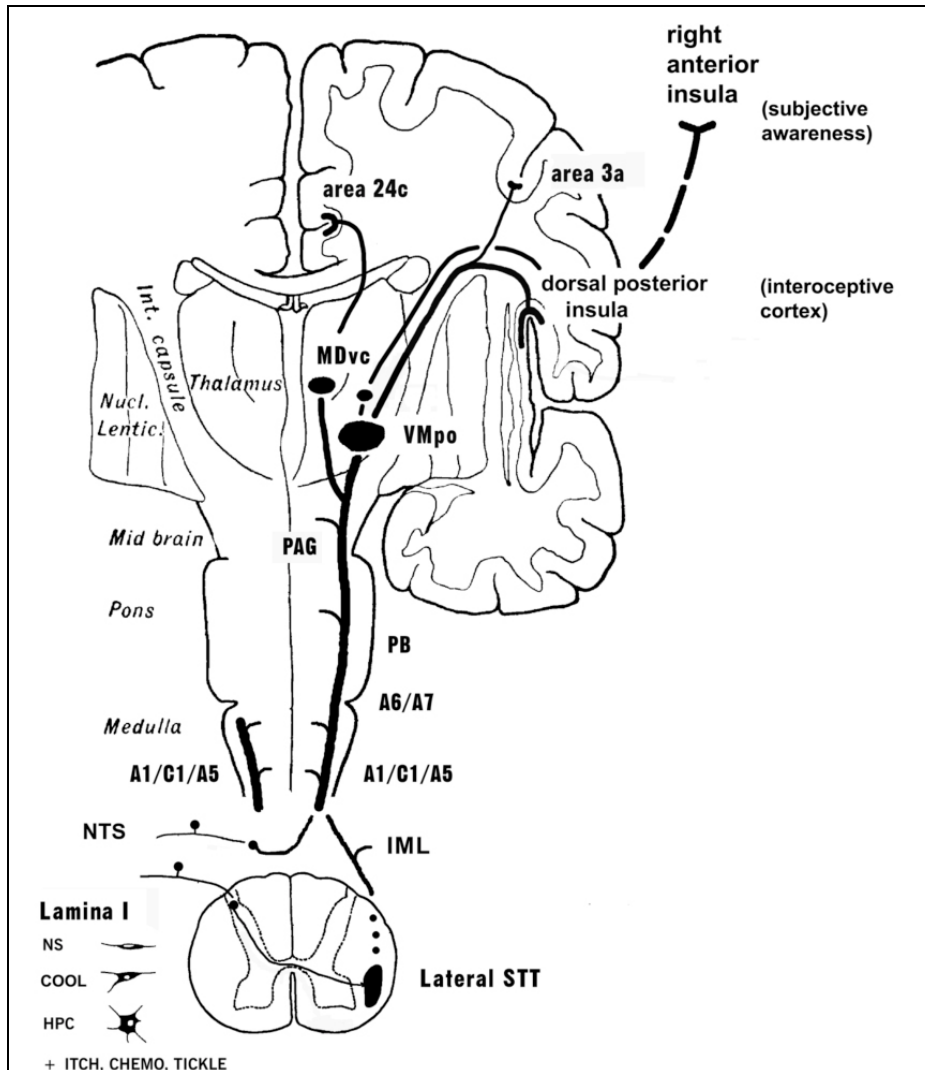


Figure 2: The overall organization of lamina I projections in the primate.

THE ASCENDING PATHWAY AND ITS PRINCIPLES OF ORGANIZATION

Spinal cord

In the periphery, the small-diameter A-delta and C primary afferent fibres that emerge late in development from small dorsal root ganglion cells (small, dark B-cells) innervate every tissue of the body, and they project to the superficial dorsal horn of the spinal cord or

to the medullary nucleus of the solitary tract (NTS). The output neurons from these two regions (i.e., lamina I and the NTS) project to the homeostatic integration sites and pre-autonomic motor regions in the brainstem. Lamina I neurons also project heavily to the spinal autonomic nuclei, where sympathetic

pre-ganglionic neurons are found. Altogether, these substrates provide the sensory and motor components of the hierarchically organized homeostatic (autonomic) nervous system. This conclusion is underscored by the observation that the descending projections from the hypothalamus (which many view as a master autonomic control centre) target exactly these sites. Indeed, the superficial dorsal horn that is part of the homeostatic afferent system is easily distinguishable in myelin-stained transverse sections of the human spinal cord from the deep dorsal horn, where large neurons receive input from large-diameter primary afferents (which emerge early in development from large dorsal root ganglion cells, or A-cells) and project to motoneurons in the ventral horn and to motor control sites centrally. Thus, the terms interoception and exteroception can be redefined (*Craig, 2002*) to differentiate these two systems (i.e., one that controls smooth muscle, as distinct from one that receives large-diameter mechanoreceptive and proprioceptive inputs and controls striate muscle). An important principle of the hierarchical homeostatic system is that it has identifiable sensory and motor components at each level that are tightly interconnected centrally.

Brainstem

Lamina I and NTS neurons project densely and selectively to pre-autonomic sites in the brainstem, thus extending the afferent limb to the next rungs of the homeostatic hierarchy (Figure 2) and generating spino-bulbo-spinal loops for somato-autonomic reflexes (*Sato and Schmidt, 1973; Craig, 1995*). In all mammals, the highest level of this homeostatic hierarchy in the upper brainstem consists of the parabrachial nuclei (PB) and the periaqueductal gray (PAG). These sites can

be viewed as the lowest level of the so-called limbic system that controls emotional behaviour (*Heimer and Van Hoosen, 2006*), because together they organize whole-body behaviours that serve life-supporting functions (cardiorespiratory control, ingestion, elimination, reproduction, etc.), as discovered in studies of chronic decerebrate and decorticate animals at the end of the 1800's (e.g., *Sherrington, 1900*).

More recent experiments that revealed approach/avoidance columns in the PAG with correlative, opposing cardiorespiratory actions (*Bandler et al., 1991*) supply the fundamental pattern for a combined behavioural and autonomic opponent organization that many authors have envisaged in the forebrain of mammals and all vertebrates (*Solomon, 1980; Craig, 2005; Uvnas-Moberg, 2005; Macneilage et al., 2009*). The principle of opponent organization is found throughout physiology, e.g., in colour vision, antagonist muscles, hormones controlling water balance, and cardiac function, probably because it provides an energy-efficient method for precise control. Indeed, opponent interaction is present between the lamina I (i.e., "sympathetic") afferent pathway and the NTS (i.e., vagal, or "parasympathetic") afferent pathway already in the medulla and spinal cord (*Chandler et al., 2002; Potts, 2006*), and a similar behavioural/autonomic opponent organization is present in the medial and lateral portions of the hypothalamus (*Swanson, 2000*). Thus, the PB and PAG can be viewed as identifiable, complementary sensory and motor regions, respectively, that support homeostasis with a coordinate behavioural/autonomic opponent organization.

Forebrain

In mammals other than primates, the ascending pathway from lamina I

and the NTS generates widely scattered projections, and the main homeostatic afferent pathway to their forebrains conveys integrated activity from PB to hypothalamus, amygdala, and, by way of the thalamus, to striatum and insular and cingulate cortices (*Saper, 2002*). Accordingly, multimodal context-dependent responses have been recorded in these regions in the rat. The insular cortex can be viewed as limbic sensory cortex, because it provides descending control of brainstem homeostatic integration in PB, and the cingulate cortex can be viewed as limbic motor cortex, because it projects densely to the behavioural/autonomic columns of the PAG. Lesions at cingulate cortex and PAG disrupt homeostatic behaviour in rodents (*Johansen et al., 2001; Saper, 2002*). The emotional behaviour of non-primate mammals suggests the anthropomorphic inference that they experience feelings from the body in the same way that humans do. However, the neuro-anatomical evidence indicates that they cannot, because the phylogenetically new pathway that underlies feelings from the body in humans is either rudimentary or absent in non-primates (*Craig, 2002*).

In primates, lamina I neurons and NTS neurons extend such pathways by projecting topographically to a pair of relay nuclei in the postero-lateral thalamus, the posterior ventral medial nucleus (VMpo) and the adjoined basal ventral medial nucleus (VMb). The lamina I axons ascend in the lateral spinothalamic tract, precisely where lesions can selectively interrupt the feelings from the body in human patients (*Craig et al., 2002*). The VMpo / VMb is organized antero-posteriorly, orthogonal to the medio-lateral topography of the main somatosensory ventral posterior (VP) nuclei, to which it is connected at the representation of the mouth. The VMb receives direct input

from NTS in addition to the integrated input that it receives from PB in all mammals (*Beckstead et al., 1980*). The VMpo is small in macaque monkeys, but in the human thalamus it is almost half as large as the VP (*Blomqvist et al., 2000*).

The VMpo and VMb project topographically to interoceptive cortex in the dorsal margin of the insula (a cortical 'island' buried within the lateral sulcus that has intimate connections with the ACC, amygdala, hypothalamus, and orbitofrontal cortex). The projections of VMpo and VMb extend over the entire posterior-to-anterior extent of the insula in the macaque monkey (*Beckstead et al., 1980; Craig and Zhang, 2005; Ito and Craig, 2008*), approximately 6-8 mm. However, in humans, the insula extends approx. 50-60 mm antero-posteriorly, and functional imaging studies indicate that lamina I input (e.g., pain, temperature, or itch stimuli) first activates the most posterior 15-20 mm, while vagal and gustatory input (e.g., gastric distension, salty intensity) activates the next 10 mm or so (*Craig, 2009, 2010; Small, 2010*). In other words, primary interoceptive cortex occupies the entire dorsal insula in monkeys, but only the posterior third in humans. This pathway contains modality-selective components that each generate a distinct "feeling" from the body in humans, including first (pricking) pain, second (burning) pain, cool, warm, itch, muscle ache, gastric distension, vasomotor flush, sweet, salty, and so on. PET imaging studies of innocuous cool sensation (*Craig et al., 2000*) showed that activation in the dorsal posterior insula, which is linearly related to objective stimulus intensity, is accompanied by activation of the mid-insula and the anterior insula, where activity correlates much more strongly with subjective feelings of cool. Indeed, activation in the anterior insula is

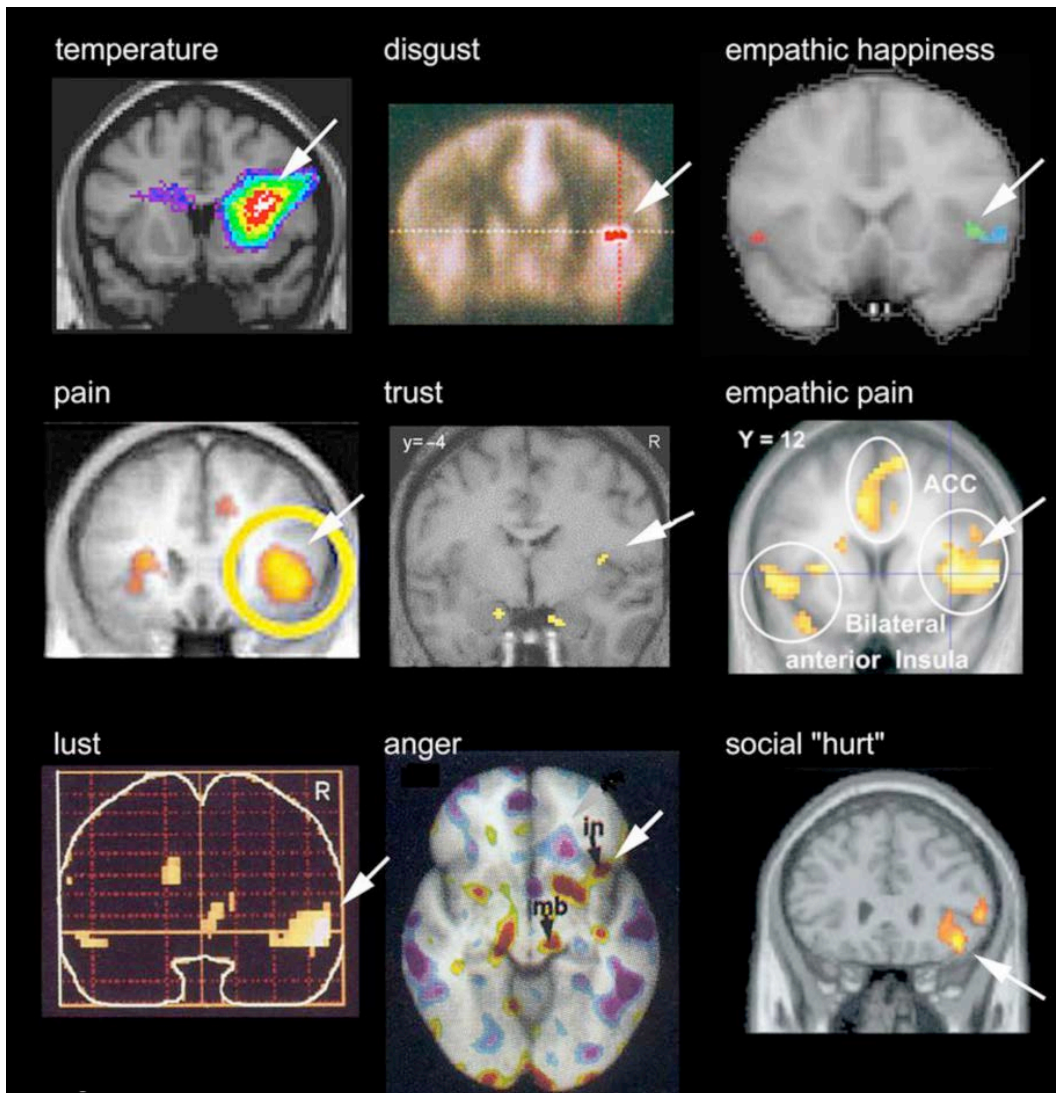


Figure 3: Activation of the right anterior insula by subjective feelings (Craig, 2002).

uniquely associated with subjective feelings of all kinds (Figure 3) (Craig, 2002, 2009). This pattern suggests a posterior-to-anterior processing gradient in the human insular cortex, which fits with considerable evidence (e.g. Schweinhardt et al., 2006) and that subjective feelings are based directly on homeostatic sensory integration, which is consistent with the James-Lange theory of emotion and the “somatic

marker” hypothesis (James, 1890; Damasio, 1993). This pattern also suggests that integration within the insula generates the template for a “feeling”, namely a neural representation of homeostatic sensori-motor conditions that can value or quantify energy utilization, thus providing a metric for amodal computation of homeostatic efficiency (a “common currency”) (Rainville et al., 2006; Duncan and

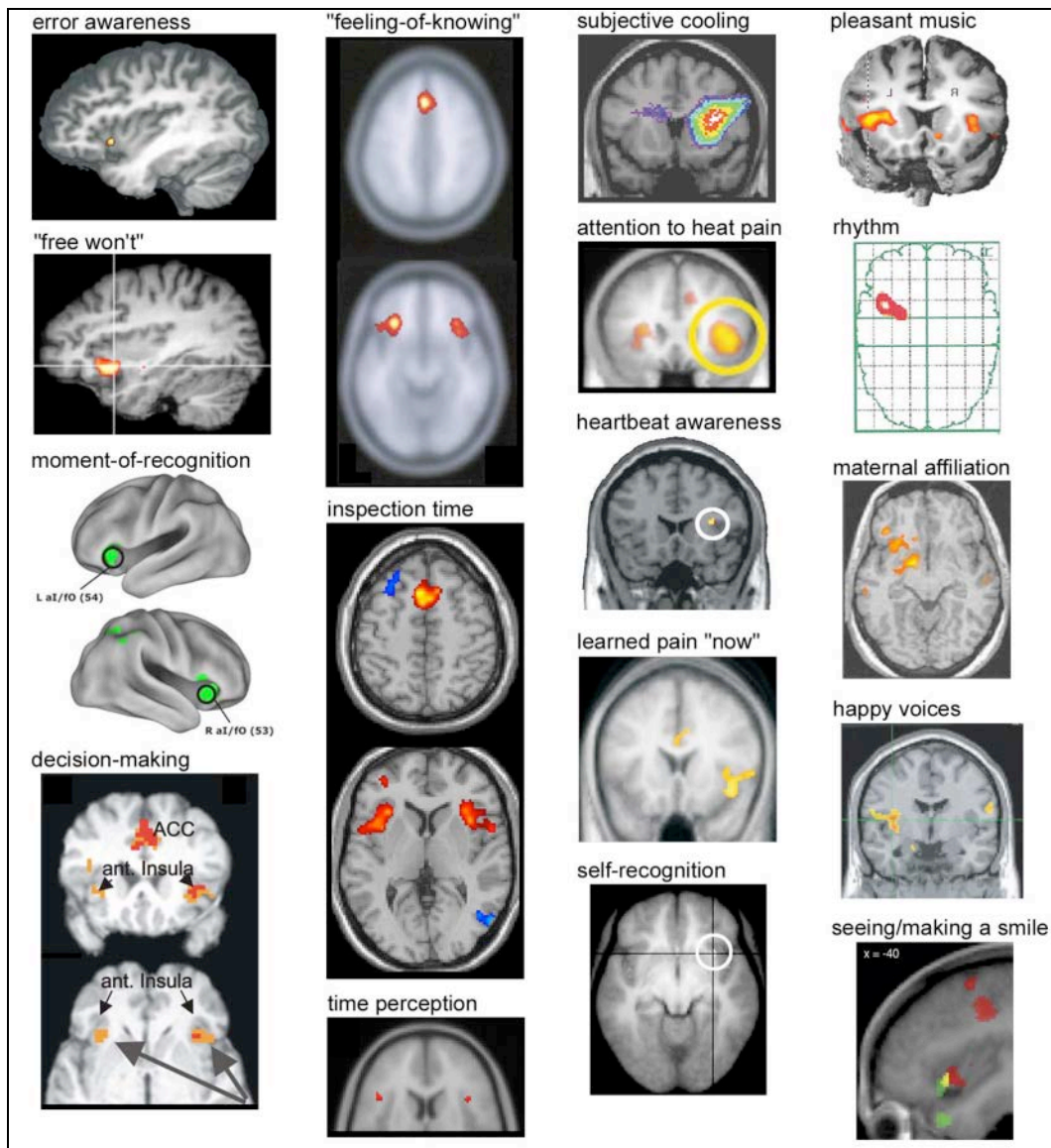


Figure 4: The anterior insula and human awareness (*Craig, 2009*).

Barrett, 2007; Harrison et al., 2010). From an evolutionary perspective, it makes sense that an integrated representation of the activity in all brain networks was needed in order to improve behaviour from the perspective of homeostatic efficiency. The goal of homeostatic efficiency (with respect to both the individual and the species)

provides a plausible explanation of the progressive posterior-to-anterior integration in the insula.

A corollary VMpo projection to area 3a in sensorimotor cortex may relate cutaneous pain to (exteroceptive) somatic motor activity and to cortical control of spinal viscerosomatic reflex activity. In addition, a direct lamina I

pathway to the ACC is also present in primates by way of a topographic projection to the ventral caudal portion of the medial dorsal nucleus (MDvc). In non-primates, in contrast, the ACC (i.e. limbic motor cortex) receives integrated homeostatic information from the PB by way of the medial thalamus, and lamina I activity is relayed instead to ventrolateral orbitofrontal cortex through the submedial nucleus. Physiological and behavioural studies validate the primordial role of the ACC in homeostatic behaviour in rats (*Johansen et al., 2001*) and in the affective/motivational component of human pain by way of the direct lamina I path to MDvc.

The direct activation of both the interoceptive cortex and the ACC by the distinct homeostatic modalities corresponds with the simultaneous generation of both a sensation and a motivation. In humans, an emotion can be defined as a feeling and a motivation; this directly supports the view of these feelings from the body as homeostatic emotions that reflect the survival needs

of the body. Pain, temperature, and itch are homeostatic emotions that drive behaviour, just as hunger and thirst do (*Craig 2002, 2003a, 2009*). Convergent functional imaging data indicates that the anterior insula is associated with subjective feelings from the body and with virtually all human emotions, and so it seems to provide an image of the physical self as a feeling (sentient) entity (Figure 4). The association of the anterior insula with the subjective perception of pain, the anticipation of pain, the subjective reduction of pain (placebo analgesia), and the subjective generation of pain (hypnotic psychogenic pain) underscores the importance of the meta-representation of interoceptive state in the anterior insula for clinical understanding of the effects of emotion and belief on health. Furthermore, the recognition that sensual touch is included in the interoceptive system emphasizes the need to incorporate the neurobiological basis of conspecific human contact in therapies for emotional and physical health (*Björnsdotter et al., 2009*).

PAIN AS AN ASPECT OF HOMEOSTASIS

Pain is a homeostatic feeling. It has characteristics exactly comparable to other physical sensations (feelings) from the body. Pain normally originates with a change in the condition of the tissues of the body, a physiological imbalance that automatic (subconscious) homeostatic systems alone cannot rectify. It comprises a sensation, an affective behavioural drive and autonomic adjustments. Pain generates characteristic reflexive motor patterns, as do itch, hunger and rectal distension. The behavioural motivation of pain is normally correlated with the intensity of the sensory input, but this can vary under different behavioural, autonomic

and emotional conditions, so that pain can become intolerable or it can disappear, similar to any other homeostatic emotions (e.g., hunger). However, unremitting pain that outlasts its homeostatic role is pathological.

Viewing pain as a homeostatic emotion provides a ready explanation of the interactions of pain with other homeostatic conditions (including temperature, blood glucose, blood pressure, level of arousal), because homeostasis is an integrated, dynamic process, and it explains the modulation of pain by homeostatic mechanisms. This conceptual perspective also provides a firm basis for explaining the interac-

tions of pain with emotional status or attention (i.e., the psychological dimension of pain), and it unifies the different conditions that can cause different types of pain from different tissues under a common homeostatic function - the maintenance of the integrity of the body. *Darwin* (1872) recognized that all animals respond with emotional behaviour to stimuli that in humans cause a feeling of pain. The new data reveal that noxious stimuli are represented in an evolutionarily ancient neural pathway that has the primary purpose of driving homeostatic mechanisms at spinal and brainstem levels and generating integrated behavioural motivation at the forebrain level. In primates, novel thalamo-cortical projections have emerged from this basic homeostatic system that provide encephalized cortical mechanisms for highly resolved sensations and motivations. Notably, sub-primates have the sub-cortical mechanisms that drive integrated homeostatic (emotional) behaviour, but they do not have these direct telencephalic pathways, and so they do not have the neuroanatomical capacity to feel pain in the same way that humans do.

The concept that human pain sensa-

tion is underpinned by a distinct and separate pathway for nociceptive-specific lamina I neurons to the primary interoceptive cortex in the dorsal posterior insula contradicts the conventional view that spinal lamina V (“wide dynamic range”) neurons are “necessary and sufficient” for pain (*Price et al.*, 2003). Evidence to the contrary has accumulated for years (*Craig*, 2003b), and recently the conventional view was definitively refuted by evidence that almost all such lamina V neurons convey Group II muscle afferent activity, respond tonically to limb position, and project directly onto ventral horn motoneurons and other motor-related sites. That is, such lamina V neurons are an integral component of the skeletal motor system (*Craig*, 2008). Recent functional imaging results on so-called “windup” (temporal summation of “second pain”; *Staud et al.*, 2008) in fact corroborates strongly the fundamental role of lamina I spino-thalamo-cortical projections in pain. Nevertheless, in light of the fundamental role of the lamina I pathway in homeostasis, it would be more appropriate to call it a homeostatic afferent pathway than simply a “pain pathway” (*Craig*, 2006).

CONCLUSION

It is important to recognize that, contrary to the conventional textbook view, feelings from the body, such as pain or temperature, are neurologically distinct from tactile mechanoreception and proprioception at all levels. Such feelings from the body represent homeostatic afferent activity, that is, the sensory input representing the physiological condition of the body, which drives the central network that controls the ANS. The spinal and brainstem levels of the hierarchical ho-

meostatic network are present in all mammals, but in humans there is a high-resolution representation of the condition of the body in primary interoceptive cortex in the posterior insula, which generates an energy-efficient map of all brain activity in the anterior insula that underpins the subjective “material me.” Thus, there is a fundamental relationship between the physiological condition of the body and subjective feelings of all kinds.

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MICROBIAL ENTERIC NEUROPHYSIOLOGY

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SUMMARY

The myenteric plexus contains a type of neuron that innervates the mucosa, and projects to all other classes of myenteric neurons. This neuron has a specific multipolar morphotype and possesses a characteristic action potential whose firing frequency is moderated a potassium current dependent post-spike slow after-hyperpolarisation. The neuron, termed AH cell, is functionally an intrinsic intestinal primary afferent neuron (IPAN) with chemosensory and mechano-sensory responses to adequate stimuli. With about 80% of sensory neuropeptide containing nerve fibres in the mucosa belonging to IPANs they are ideally positioned to respond to signals from commensal or probiotic gut bacteria. Application of *Lactobacillus rhamnosus* JB-1 or *Bacteroides fragilis* to the mucosal epithelium evokes sensory action potentials in the IPANs within a few seconds of administering the bacteria. In the case of *B. fragilis*, a capsular polysaccharide A is necessary and sufficient to carry the signal from microbe to neuron. This sensory activation leads to a longer-term increase in the intrinsic excitability of the IPAN sensory neuron network caused at least in part by a decrease in a calcium dependent potassium conductance. We have identified a molecular and neuronal target of commensal signalling. The neuron's rapid sensory responses may activate the neuronal circuits that mediate some of the motility and central nervous system effects of ingesting beneficial microorganisms.

INTRODUCTION

It may be time to consider the idea of probiotic or microbial neurophysiology. This notion derives from observations that microbes, especially symbiotic, commensal or probiotic bacteria, can change how the host nervous system functions. The concept has parallels to other constructs such as microbial endocrinology (Lyte, 2010, 2011; Roshchina, 2010) or microbial immunology (Artis, 2008; O'Hara and Shanahan, 2006) that seek to elucidate how the host systems interact with the

microflora. It is tacitly recognised that within the whole animal, or even for individual organs, there must be reciprocal interplay between these systems. A simple example of this is if behavioural stress (nervous system) and increased stress hormones (endocrine system) co-exist to alter the constituents of the microbiome (see Lyte, 2011). Within the enteric nervous system, neuronal behaviour may be changed by luminal microbes, mast cell products or inflammation or paracrine

hormones (Nurgali et al., 2011; Furness and Poole, 2011; Buhner and Schemann, 2012; Sundler et al., 1989; Ahlman and Nilsson, 2001).

The gut microbiome forms a complex ecosystem with its associated “metabolome” producing myriads of metabolites including chemical messengers and foodstuffs. The totality of this microbial organ has profound effects on the host during development and adult life. Such effects include education of the immune system and the normal development of the gut-brain axis. Much of this knowledge has been deduced from work with germ-free animals or alterations of the microbiome using antibiotics (Collins and Bercik, 2009; Bienenstock and Collins, 2010; Hejtz et al., 2011). Such major experimental perturbations cannot unaided explain the remarkable observation that ingesting about 1 billion cells of a single probiotic strain (that may or may not be a commensal) can have a therapeutic effect (Moayyedi et al.,

2010) on an adult who at the same time carries 100 trillion or more gut commensal organisms.

The FDA defines beneficial bacteria that are intended to prevent or help treat disease as drugs (Hoffman, 2008). Homeostatic organ responses to repeated dosing with probiotics may mask the underlying physiological mechanisms responsible for the direct neuronal action of active probiotic derived ligand(s) (Dykstra et al., 2011). In addition, pharmacological tolerance (Koch and Höllt, 2008), sensitisation and priming (Kostrzewa, 1995) are potential additional confounding factors. To clarify the mechanisms of action of beneficial bacteria, quantitative measurements of their acute actions on individual neurons and other target cells should be made. In the same way, the mechanisms of action of opium, antidepressant or anxiolytic plants, or other biologics could not have been deduced solely from their long-term chronic actions.

DO COMMENSALS, PROBIOTICS ACT ON THE NERVOUS SYSTEM?

Even in the absence of overt inflammation, probiotics may influence behaviour or alter brain chemistry. Some of the symptoms of chronic fatigue syndrome have been reported to be decreased by ingestion of a Shirota strain of *Lactobacillus casei* (Rao et al., 2009). Ingestion of a *Lactobacillus rhamnosus* strain (JB-1) had anti-depressive and anti-anxiety effects (Bravo et al., 2011). On the other hand, *Citrobacter rodentium*, when given at a dose that produces no inflammation or increase in plasma inflammatory cytokines, induced anxiety in mice (Lyte et al., 2006). A formulation of *Lactobacillus helveticus* plus *Bifidobacterium longum* reduced anxiety in a rat model and decreased anxiety scores in hu-

mans (Messaoudi et al., 2011).

Probiotics can modulate physiological parameters controlled by the autonomic nervous system. Intra-duodenal injection of *Lactobacillus johnsonii* (La1) has been shown to reduce systemic and renal blood pressure in rats (Yamano et al., 2006; Tanida et al., 2005) within 15 min of injection. Feeding milk fermented with *Lactobacillus helveticus* appeared to decrease ambulatory blood pressure in hypertensive patients (Jauhiainen et al., 2005; Aihara et al., 2005). There is also evidence that certain probiotic strains moderate gut migrating motor complexes (MMCs) (see below).

It is possible that the behavioural and autonomic effects ascribed to pro-

biotic ingestion could be caused by alterations in the immune status of peripheral tissue or the release of circulating hormones (Bansal et al., 2010; Bercik et al., 2012). Another explanation, not mutually exclusive, is that primary afferent neurites are activated within the gut wall and these then transmit synaptically to the higher order autonomic neurons whose processing modulate peripheral autonomic

reflexes or limbic system function centrally. To resolve this question, it will be important to determine if neurons in the intestine are in fact direct or early targets of probiotic application. Early perturbations of primary afferent neuron firing by commensals could also underlie later longer-term effects on immune, endocrine systems (Logan and Katzman, 2005; Lyte, 2011).

SPINAL PRIMARY AFFERENTS

Spinal primary afferent neurons have their soma in the dorsal root ganglia that lie on either side of the spinal cord. Gut spinal primary afferents have sensory terminals that ramify throughout the width of the gastrointestinal wall where they are activated by mechanical or chemical stimuli, generally of a nociceptive nature (Blackshaw et al., 2007).

Some probiotic strains attenuate afferent pain signals. Feeding a non-absorbable antibiotic to decrease colon *Lactobacillus* species has been reported to increase thresholds of pseudo-affective pain responses to colorectal distension (CRD) (Verdu et al., 2006), suggesting a possible role of these species in visceral pain transmission or transduction. In a more strain-specific study, Kamiya et al. (2006) showed that 9 day feeding of JB-1 to rats decreased pain responses to CRD, and that this was paralleled by a reduction of CRD evoked increases in spinal dorsal root single unit firing. It is important to realise that the anti-nociceptive action of JB-1 occurred in the absence of experimentally induced or a detectable peripheral inflammation. Therefore, even if the bacterium exerted anti-inflammatory actions on the host, this

may not explain its pain-suppressing ability. Similarly, feeding *L. acidophilus* (NCFM) reduced pseudo-affective responses to CRD in rats, and this was accompanied by an increase in opioid and cannabinoid receptor expression in mucosal epithelial cells (Rousseaux et al., 2007). It is not clear how such receptors in epithelial cells could alter firing in nociceptive neurons.

Probiotic bacteria may be able to block activity-dependent sensitisation of pain pathways. Afferent pain pathways can be sensitised by repeated painful stimuli (Woolf and Salter, 2000). Such sensitisation represents a form of cellular memory of pain, and is implicated in maintaining pathological pain states (Woolf and Salter, 2000). CRD induces greater than normal substance P expression in rat DRG neurons that persists at least 24 h after the distensions (Lu et al., 2005). Functionally, the substance P overexpression was accompanied by hyper-excitability in the pseudo-affective response to CRD (Ma et al., 2009). It is noteworthy that this type of sensitisation occurred in the absence of histological or chemical markers for inflammation. Prior feeding of JB-1 was able to block this nociceptive sensitisation (Ma et al., 2009).

INTESTINAL PRIMARY AFFERENT NEURONS

The putative intestinal primary afferent neuron (IPAN) is a plausible target for beneficial microbes. IPANs are part of the enteric nervous system, which, long regarded as a part of the parasympathetic division of the autonomic nervous system, is now considered to be a third independent division (*Gershon, 1999*). It has been acknowledged that the gut can perform its motor and secretory roles in the absence of connections with nervous systems extrinsic to the gut. This has led to the proposition (*Furness et al., 1998*) that there are neurons (IPANs), with somata within the wall of the intestine, whose activation by chemo- or mechano-sensory stimuli lead to propulsive reflexes. Patterned on-going activity in networks of IPANs contributes to motor or secreto-motor programs that produce propulsive MMCs, and possibly stationary motor complexes that result in mixing (*Gwynne and Bornstein, 2007; Bornstein et al., 2002, 2004*). Yet, whether IPANs truly exist, or what their identity might be, and if the apparent autonomy of the gut results from axon reflexes of extrinsic primary afferent fibres embedded in the gut wall is still under discussion.

IPANs were first anticipated because of the morphology and physiology of a specific type of myenteric neuron. Such neurons have a large flattened oval soma and multiple long neurites that innervate adjacent myenteric ganglia and the epithelial cell layer of the mucosa (Dogiel Type II morphology). This morphotype led *Dogiel (1899)* to propose that the neurons were sensory in function. David Hirst (*Hirst et al., 1972; Hirst and*

Spence, 1973; Hirst et al., 1974) found that the action potentials of Dogiel type II neurons were broad with a calcium hump on their repolarising phase. Significantly, because of its effects on firing patterns, the action potential was followed by a slow inhibitory after-hyperpolarisation (sAHP) lasting several seconds (*Hirst et al., 1985, 1974*). Such action potential characteristics are very similar to those of unmyelinated spinal DRG neurons (*Hay and Kunze, 1994; Schild et al., 1994*). These putative IPANs, termed "AH cells" by Hirst, did not appear to receive the classical fast (inotropic) synaptic input that characterises ganglionic inter- and motor- or relay-neurons (*Hirst et al., 1974*). The absence of synaptic input from other neurons suggested that the neurons are by default sensory. Hirst argued that if AH cells were not activated by other neurons they must be the first or primary afferent neuron whose activation arises from sensory stimuli (*Hirst et al., 1974*). Interneurons or motoneurons would necessarily receive synaptic input from sensory or other interneurons. Later, *Kirchgessner et al. (1992)* blocked nicotinic transmission in the submucosal plexus and then mechanically stimulated the mucosa. They reported enhanced c-fos expression in some neurons, even under nicotinic receptor blockade. Lack of nicotinic synaptic input has been taken as proof that some submucosal neurons are primary afferent by *Furness (2006a)*. Against this, there remained the possibility of non-nicotinic synaptic transmission in the submucosal plexus.

SENSORY RESPONSES TO CHEMICAL LUMINAL AND MECHANICAL STIMULI

The "classic schema" has been that luminal chemicals and bacterial products are detected by the immune system which then signals via the release of mediators to the enteric nervous system (Cooke, 1994). Experimental data, however, suggest that myenteric AH cells can respond directly to luminal chemicals with varying degrees of involvement enteroendocrine cells (EECs) playing the role of "taste cells" (Bertrand, 2009). Orthodromic action potentials can be recorded from guinea pig myenteric AH cells in response to applying brief puffs of HCl to the mucosal epithelium (Kunze et al., 1995). "Orthodromic" means travelling in the "right" or normal direction; for a peripheral sensory neuron action potential this is from the receptive field towards the soma and, in the case an AH cell, from the mucosal epithelium to the myenteric plexus. AH cells were shown to be IPANs when the response to HCl persisted even if all synaptic transmission was blocked by removing extracellular calcium and raising extracellular magnesium tenfold (Kunze et al., 1995). Since the response could not have come from other neurons, it either must have been generated by sensory transduction occurring in the neuronal endings near the lumen or in closely associated mucosal entero-endocrine "taste" cells (Bertrand, 2003, 2009). Sensory responses have also been recorded in myenteric AH cells in response to epithelial applications of short chain fatty acids for mouse small intestine (Mao et al., 2006) and rat colon (Kunze et al., 2009).

AH cells are additionally mechano-sensitive neurons responding to tension. Generator and action potentials have been recorded from myenteric AH cells when their processes within the

ganglia are distorted. In contrast, compression of the soma inhibits firing (Kunze et al., 2000). Such responses were recorded during total synaptic blockade establishing their primary afferent nature. Active muscle contraction was required for these responses to occur, and passive stretch with paralysed muscle could not evoke them (Kunze et al., 1998). Thus, tensions sensitive mechano-sensitive IPANs are also Dogiel type II AH cells (Kunze et al., 1999, 2000). Sub-modalities and multimodal properties have been ascribed to IPANs (Mayer, 2011); so far, experimental evidence for this is lacking.

Mechano-sensory responses have also been recorded from significant proportions of myenteric S cells (so named because they receive prominent fast synaptic input) (Schemann and Mazzuoli, 2010; Mazzuoli and Schemann, 2009; Spencer and Smith, 2004), which have been previously assumed to be inter- or motor-neurons within the enteric circuits (Nurgali et al., 2004; Furness et al., 1998, 2004; Kunze et al., 1999). These responses occurred even when the muscle was paralysed with nicardipine, suggesting that these S cells are stretch rather than tension receptors. Since MMCs require active muscle contraction for their initiation (Lüderitz, 1891) it is not easy to know what might be the functional role of these mechano-sensory S cells.

The promiscuous proliferation in the literature of putative intrinsic gut primary afferent neurons has not gone without criticism (see: Wood, 2008). It is argued that intramural vagal or spinal axon reflexes are sufficient to account for the functional independence of the gut (Christofi and Wood, 1993; Wood, 2008). Peristaltic reflexes that persist in

ex vivo gut segments are proposed to be mediated by the severed stumps of extrinsic sensory fibres that remain in the organ wall. Also, the idea that the enteric nervous system contains its own primary afferent neurons has been rejected on principles of evolutionary parsimony (Christofi and Wood, 1993; Wood, 2008). It is suggested that extrinsic vagal and spinal primary afferents would suffice for all the sensory innervation of the gut. However, the idea that in biology evolution designs the simplest system for a particular function (ontological parsimony) has been refuted many times (for a discussion of the general issue and a distinc-

tion between ontological and methodological parsimony see for example: Crisci, 1982). Occam's razor (in the form of ontological parsimony) cannot reasonably be used as an argument against the existence of IPANs. Finally, Wood (2008) has argued that since chemosensitive AH cells appear to require sensory transduction from specialised entero-endocrine cells, they cannot be primary afferent neurons. If this argument is granted, then the lingual nerve, for example, which appears to require type 4 taste cells for some of its responses would not be primary afferent.

RESPONSES TO LUMINAL PROBIOTIC OR COMMENSAL BACTERIA

A key function of chemosensory IPANs may be to monitor and respond to the microbiome and its metabolome. There are 500 million enteric neurons in humans and 500,000 in mice. Dogiel Type II/AH cells make up 15 to 20% of the total neurons (Kunze et al., 1999; Furness et al., 1998). An important teleological question arises; why would the gut have so many chemosensory neurons all of which innervate the mucosa (Song et al., 1994)? The total numbers of cells contributing to the microbiome is not known with certainty, but the concentrations of dominant commensal genera can reach 8 log cfu/ml in the small, and 11 log cfu/ml in the large intestine (Tappenden and Deutsch, 2007; Reuter, 2001). By far the richest innervation (compared to spinal or vagal afferents) for mucosal epithelial layer cells derives from the myenteric plexus, which provides in excess of 90% of sensory neuropeptide containing fibres to the mucosal layer (Ekblad et al., 1987; Keast et al., 1984). Each enteric AH neuron innervates 80-120 villi (Kunze et al., 1999) and there

are about 500,000 neuropeptide (calcitonin gene related peptide, CGRP) containing AH cells in the mouse (Furness, 2006b). Therefore, IPANs are ideally positioned to sample signals from the microbiome and ingested beneficial bacteria; possibly having evolved just so, to monitor this large source of metabolites and foreign DNA.

There is experimental evidence that probiotics influence myenteric IPANs. Using a modified Trendelenburg *ex vivo* gut segment preparation to record intraluminal pressure, MMCs were reduced 50% in amplitude 9-16 min after 7.7 log cfu/ml (Wang et al., 2010a) were introduced into the lumen. Nine day ingestion 9 log cfu JB-1 similarly reduced MMC amplitudes (Wang et al., 2010b). Since the MMC were blocked by the neuron sodium channel blocker tetrodotoxin (TTX) (Wang et al., 2010a, 2010b), these results suggest that the probiotic acted on enteric neurons. Slow wave related contractions persisted when all neural activity was blocked with tetrodotoxin (Wang et al.,

2010a, 2010b) were not altered by JB-1. Kamm and colleagues fed $7.3 \log$ cfu/g of *Saccharomyces boulardii* per day to pigs for 9 days, after which jejunal myenteric neurons were assayed histochemically for chemical markers known to correlate with major functional subpopulations within the enteric nervous system (ENS) (Kamm et al., 2004). The authors reported decreased expression of the vitamin D dependent calcium binding protein, calbindin, in myenteric Dogiel Type II neurons (Kamm et al., 2004; Jungbauer et al., 2006). They also assayed for choline acetyltransferase, substance P, calcitonin gene-related peptide, vasoactive intestinal polypeptide, nitric oxide synthase and the calcium binding protein calretinin. These chemicals identify AH cell/Dogiel Type II neurons or each of the major classes of inhibitory and excitatory motor neurons or interneurons (S cells). For none of these chemicals (except for calbindin) was there a change in the amount expressed in the ENS, demonstrating what appears to be a high functional selectivity in perturbation of the ENS by the fungus. (Kamm et al., 2004; Jungbauer et al., 2006). Nine day feeding of $9 \log$ cfu per day of JB-1 increased the intrinsic excitability (decreased firing thresholds and increased number of action potentials fired during a standard stimulus current pulse) of rat colon myenteric IPANs. S cell (inter- and motor-neuron) excitability was unaffected (Kunze et al., 2009). Since myenteric IPAN/Dogiel Type II cells,

but not S cells, innervate the mucosa (Furness et al., 1998; Bertrand, 2004; Song et al., 1994) it is likely that for each ingestion, IPANs are the first type of neuron to be activated (Furness et al., 1999; Kunze et al., 1995). Then, the increase in IPAN firing is transmitted to S cells by metabotropic synaptic transmission (Kunze et al., 1993). Such daily activation of IPANs would cause them to evoke transient slow postsynaptic potentials and firing in their target S cells (Kunze et al., 1993). IPANs (Clerc et al., 1999) but not S cells (Alex et al., 2002) have a form of activity dependent long-lasting memory that is entrained by their repeated, frequency dependent, excitation. This may be why only IPANs were found to have heightened intrinsic excitability after 9 day feeding with JB-1. That is, inter- or motor-neurons may have been activated during and after presentation of the bacteria to the mucosal epithelial surface but this effect would have waned when the intestine was excised for subsequently electrophysiological analysis. IPANs have the ability to induce long-term potentiation of their excitability many hours beyond the duration of their sensory stimulation (Clerc et al., 1999). How long such potentiation could ultimately last, and what are the optimal intervals between probiotic ingestion periods, are questions that require further research and may well be specific for individual probiotic strains and host species and gut regionalisation.

IPAN ION CHANNEL TARGETS FOR PROBIOTIC ACTION

IPANs excitability and discharge properties are determined by a complex interaction of membrane ion channel currents. In general, and with the exception of the pig, myenteric AH cells

have electrophysiological properties that are well conserved from mouse to man (Mao et al., 2006). The action potential upstroke, which is generated by transient and persisting Na^+ (Zholos et

al., 2002; *Rugiero et al.*, 2002, 2003), and N (and R) -type Ca^{2+} currents (*Rugiero et al.*, 2002; *Bian et al.*, 2004), is followed by a fast (fAHP) and then a slow (sAHP) after-hyperpolarisation. The fAHP is generated by a mixture of voltage sensitive K^+ currents including the delayed rectifier, an A current (*Starodub and Wood*, 2000) and a Ca^{2+} dependent large conductance K^+ conductance (*Kunze et al.*, 2000; *Vogalis et al.*, 2002). The sAHP is produced by the generation an intermediate conductance Ca^{2+} dependent K^+ (IK_{Ca}) current and is opposed by a coincident hyperpolarisation activated cationic current (I_{h}) (*Mao et al.*, 2006). The duration and frequency of action potential firing are determined by the sAHP and fAHP, I_{h} and the inactivation characteristics of the Na^+ currents. Action potential firing thresholds depend on the activation characteristics of Na^+ currents and on the total plasmalemma leak conductance. The resting membrane potential is determined by various background or leak conductances, which include I_{h} , IK_{Ca} current, Na^+ window currents and at least one type of tandem pore K^+ channel current (*Matsuyama et al.*, 2008).

The IK_{Ca} current underlying sAHP

in IPANs is at present the most plausible target for JB-1 although other bacteria might act on any other or combination of other IPAN ion channels. The reduction in MMC amplitude by JB-1 (see above) was reproduced within 5-15 min (see for example Figure 4 in *Wang et al.*, 2010a and Figure 3 in *Wang et al.*, 2010b) of adding the specific intermediate conductance Ca^{2+} dependent K^+ (IK_{Ca}) channel blocker TRAM-34 to the Krebs buffer superfusing segments of rat colon or mouse small intestine (*Wang et al.*, 2010b). In the absence of overt inflammation, only IPANs (AH cells) but not inter- or motor-neurons (S cells) express functional IK_{Ca} channels. We deduce that the probiotic altered motility by altering IPAN function, probably by decreasing the IK_{Ca} dependent inhibitory slow after-hyperpolarisation current (*Wang et al.*, 2010a, 2010b). It is important to note that a similar effect on MMCs was produced for rat colon after log 9 cfu JB-1 was fed to the animals daily for 9 days (*Wang et al.*, 2010b), suggesting IK_{Ca} may be a probiotic target for both acute and repeated probiotic applications and for more than one host species.

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MICROBIOTA, STRESS AND THE BRAIN

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SUMMARY

Bacterial colonisation of the intestine has a major role in the post-natal development and maturation of the immune and endocrine systems. These processes are key factors underpinning central nervous system (CNS) signalling. Regulation of the microbiota-gut-brain axis is essential for maintaining homeostasis, including that of the CNS. Moreover, there is now expanding evidence for the view that commensal organisms within the gut play a role in early programming and later responsiveness of the stress system. Research has focused on how the microbiota communicates with the central nervous system (CNS) and thereby influences brain function. The routes of this communication are not fully elucidated but include neural, humoral, immune and metabolic pathways. This view is underpinned by studies in germ-free animals and in animals exposed to pathogenic bacterial infections, probiotic agents or antibiotic agents which indicate a role for the gut microbiota in the regulation of mood, cognition, pain and obesity. Thus the concept of a microbiota-gut brain axis is emerging which suggests that modulation of the gut microflora may be a tractable strategy for developing novel therapeutics for complex stress-related CNS disorders where there is a huge unmet medical need.

INTRODUCTION

The fields of microbiology and neuroscience in modern medicine have largely developed in distinct trajectories, with the exception of studies focused on the direct impact of infectious agents on brain function, which include early investigations of syphilis to more recent studies of neuroAIDS. In addition to the direct effect of bacteria on CNS function, the field of psychoneuroimmunology has emerged to provide a framework as to how pathogenic bacterial agents can alter brain function. Thus, the role of the CNS in mediating the behavioural responses to infections ranging from “sickness behav-

our” to septic encephalopathy has been advanced significantly. More recently, a new concept has emerged which indicates that commensal bacteria can also affect brain function in both health and disease. In this review we discuss the evidence to date and delineate how harnessing such pathways may provide for a novel approach to treat a variety of disorders of the brain-gut axis.

It is increasingly recognized that the brain-gut axis provides a bi-directional homeostatic route of communication which, if dysfunctional, can have important pathophysiological consequences (Mayer, 2011). This axis is

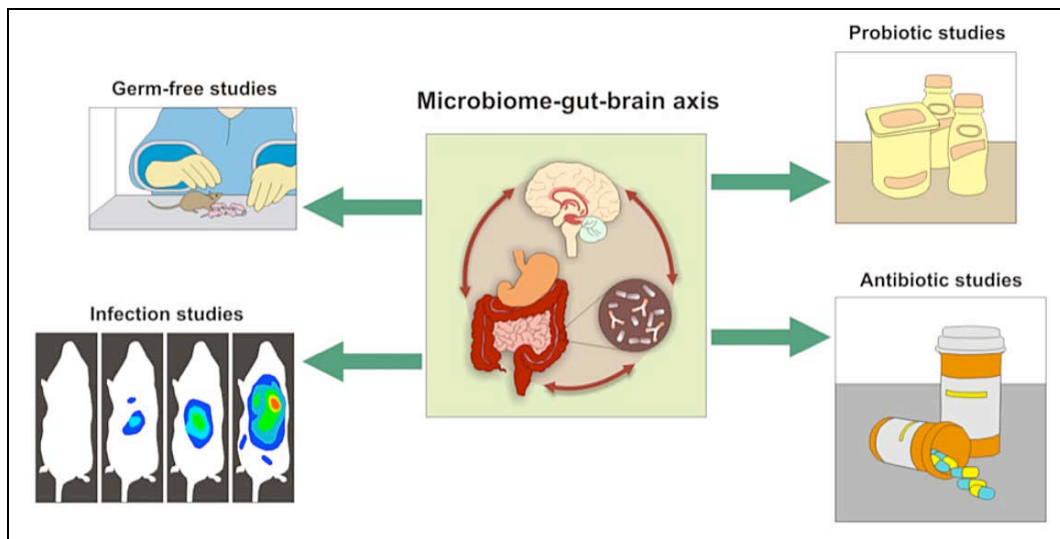


Figure 1: Strategies used to investigate the role of the microbiome gut brain axis in health and disease

regulated at neural, hormonal and immunological levels and alterations in brain-gut interactions are associated with gut inflammation, chronic abdominal pain syndromes and eating disorders (Mayer, 2011). Indeed, modulation of brain-gut axis function is associated with specific alterations in the stress-response and overall behaviour (Rhee et al., 2009). The high comorbidity between stress-related psychiatric symptoms such as anxiety with gastrointestinal disorders including irritable bowel syndrome (IBS) and inflammatory bowel disorder (IBD)

(Reber, 2012) is further evidence of the importance of this axis. Thus modulation of the brain-gut axis is being seen as an attractive target for the development of novel treatments for a wide variety of disorders ranging from obesity, mood and anxiety disorders to GI disorders such as IBS (Mayer, 2011). In addition, increasing evidence also suggests that the enteric microbiome can greatly influence all aspects of physiology (Clemente et al., 2012; Sekirov et al., 2010) not least of which is its ability to impact on gut-brain communication.

THE MICROBIOTA

The human gastrointestinal tract (GIT) is inhabited with 10^{13} - 10^{14} microorganisms, which is >10 times that of the number of human cells in our bodies and 150 times as many genes as our genome (Gill et al., 2006; Qin et al., 2010), and thus often referred to as the “forgotten organ” (O’Hara et al., 2006). Our appreciation of the relation-

ship between the microbiome and host is changing rapidly and it now can be viewed as being mutualistic (with both partners experiencing increased fitness) (Backhed et al., 2005), playing a crucial role in the development and functionality of the innate and adaptive immune responses (Olszak et al., 2012; Round et al., 2010) regulating gut mo-

tility, intestinal barrier homeostasis, nutrient absorption and fat distribution (Backhed et al., 2004; Bercik et al., 2012). Over the past 5 years significant advances have been made in the technology for assessing microbiota com-

position at the genetic level (Fraher et al., 2012; Qin et al., 2010) that is also having an immense impact on increasing our understanding of host-microbe interactions.

THE MICROBIOTA-GUT BRAIN AXIS AND BEHAVIOUR

Taken together, it is thus perhaps not surprising that there is a growing body of literature focused on assessing the impact of enteric microbiota on brain and behaviour and the concept of the microbiome-gut-brain axis is emerging. The general building blocks of this axis include the CNS, the neuroendocrine and neuro-immune systems, the sympathetic and parasympathetic arms of the autonomic nervous system (ANS) and the enteric nervous system (ENS) along with the intestinal microbiota, which is being increasingly viewed as the cornerstone. These components converge to form a complex reflex network with

afferents that project to integrative CNS structures and efferents to smooth muscle (Mayer, 2011). Crucially, this axis functions bi-directionally (Mayer, 2011). Approaches used to parse the role of gut microbiota on brain function (see Figure 1) include using germ-free animals, assessing the impact of probiotic agents, antibiotic-induced dysbiosis and pathogenic infections (Cryan and O'Mahony, 2011). In addition, accumulating studies have also shown that manipulations known to impact brain function (e.g. stress) also impacts microbiota composition (Dinan et al., 2012).

GERM-FREE ANIMALS

The use of germ-free (GF) animals enables the direct assessment of the role of the microbiota on all aspects of physiology. In these animals surgical delivery replaces the normal birthing process, thus eliminating the opportunity for post-natal colonization of the GIT and allows for direct comparison with their conventionally colonized counterparts. In a landmark study, Sudo and colleagues (Sudo et al., 2004) provided direct evidence that intestinal microbiota plays a key role in the development of the hypothalamic-pituitary-adrenal (HPA) axis. In GF mice a mild restraint stress induced an exaggerated release of corticosterone and adrenocorticotrophin hormone compared to the specific pathogen free controls. The stress re-

sponse in the GF mice was partially reversed by colonization with faecal matter from control animals and fully reversed by mono-association with *Bifidobacterium infantis* in a time dependent manner (Sudo et al., 2004). These data clearly demonstrated that the microbial content of the GIT is critical to the development of an appropriate stress response later in life and also that there is a critical window in early life where colonization must occur to ensure normal development of the HPA axis. From a neuronal point of view, a decrease in brain derived neurotrophic factor (BDNF), a key neurotrophin involved in neuronal growth and survival, and decreased expression of the N-methyl-D-asparaginezuur (NMDA)

receptor subunit 2a (NR2a) in the cortex and hippocampus of GF animals compared to controls was also observed. However, it took a further seven years for these findings to be followed up at a behavioural level. Three independent groups have now shown that GF animals (from different strains and genders) have reduced anxiety in the elevated plus maze or light dark box (Clarke et al., 2012a; Heijtz et al., 2011; Neufeld et al., 2010), but see (Gareau et al., 2011) The mentioned tests are widely used to assess anxiety related behaviour (Cryan and Sweeney, 2011). These findings are somewhat puzzling as it is opposite to what one would have been predicted based on the exaggerated HPA axis. Interestingly, Neufeld and colleagues (Neufeld et al., 2010) also reported changes in BDNF, NR_{2B} and 5-HT_{1A} receptor mRNA expression in GF mice. However, it is worth noting that the direction of such changes is not in agreement with data reported by Sudo et al. (2004) From a cognitive point of view GF mice displayed deficits in simple non-spatial and working memory tasks (novel object recognition and spontaneous alternation in the T-maze). Future studies should focus on enhancing the repertoire of behavioural cognitive assays employed. However, maintaining

animals GF and conducting complex behavioural studies is not a trivial logistical hurdle.

More recently, we have shown that GF animals have a significant elevation in the hippocampal concentration of 5-HT and 5-HIAA, its main metabolite, compared with conventionally colonised control animals (Clarke et al., 2012a). Concentrations of tryptophan, the precursor of serotonin, are also increased in the plasma of GF animals, suggesting a humoral route through which the microbiota can influence CNS serotonergic neurotransmission. Interestingly, colonisation of the germ-free animals post-weaning is insufficient to reverse the CNS neurochemical consequences in adulthood of an absent microbiota in early-life despite the peripheral availability of tryptophan being restored to baseline values. Gender may play a role in such effects. Indeed, we have recently shown that many of the neurochemical but not endocrine or immune effects of growing up in a germ-free environment are only evident in male animals (Clarke et al., 2012a). Further behavioural studies, including the use of other species such as germ-free rats will greatly expand our knowledge of the role of microbiota in stress-related disorders.

PROBIOTICS

Probiotics are live organisms that, when ingested in adequate quantities, exert a health benefit on the host (Gareau et al., 2010; Quigley, 2008). Probiotics are reported to have a wide variety of effects in both human and animal studies (Gareau et al., 2010; Quigley, 2008). Increasing evidence points to beneficial effects of various probiotics in the treatment of the gastrointestinal symptoms of disorders

such as IBS (Clarke et al., 2012b). Moreover, there is some clinical evidence to support the role of probiotic intervention in reducing the anxiety and stress response as well as improving mood in IBS patients and those with chronic fatigue (Logan et al., 2005; et al., 2009). Recently, a study assessing the effect of a combination of *Lactobacillus helveticus* and *B. longum* on both human subjects and rats

demonstrated the ability of this probiotic cocktail to reduce anxiety in animals and had beneficial psychological effects with a decrease in serum cortisol in patients (Messaoudi et al., 2011). While the mechanism of action is not known it has been postulated that probiotic-induced effects on pro-inflammatory cytokines, oxidative stress and in nutritional status may contribute to such effects (Cryan and O'Mahony, 2011; Logan et al., 2005).

Recently we have shown that a bacterium of the *Lactobacillus* species *L. rhamnosus* (JB1), decreases anxiety and despair-like behaviour as well as reducing the stress-induced increase of corticosterone in mice (Bravo et al., 2011). Moreover, this potential probiotic alters the mRNA expression of both GABA_A and GABA_B receptors in the CNS. Alterations in these receptors are associated with anxious and depressive-like behaviours in animal models. Interestingly, these effects are vagus-dependent as vagotomy prevented the anxiolytic and antidepressant effects of this bacterium as well as the effects on the central GABA receptors. This suggests that parasympathetic innervation is necessary for *L. rhamnosus* to participate in the microbiota-brain interaction. Whilst there have been studies showing that potential probiotics can reverse the effects of colitis, infection or stress these data are the first to our knowledge to show beneficial effects in animal assays used to assess anxiolytic or antidepressant activity (Cryan and Sweeney, 2011).

Indeed, previous studies have shown that the probiotic *B. longum* NCC3001 but not *L. rhamnosus* NCC4007 reversed colitis-induced anxiety and alterations in hippocampal BDNF without impacting gut inflammation or circulating cytokines (Bercik et al., 2010; Bercik et al., 2011a). The anxiolytic effect of *B. longum* NCC3001 was absent in mice with vagotomy, suggesting a neural mechanism, which was confirmed by *ex vivo* electrophysiological studies, in enteric neurons (Bercik et al., 2011b). We have also shown that probiotic agents such as *B. infantis* can modulate antidepressant-like behaviour in a maternal separation model (Desbonnet et al., 2010) and modulate peripheral pro-inflammatory cytokine and tryptophan concentrations both of which have been implicated in depression. Finally, exciting studies are emerging showing that brain fatty acid concentrations (including stearic acid, arachidonic acid, and DHA) can be elevated in mice whose diets were supplemented with *B. breve* NCIMB 702258 (Wall et al., 2012). Interestingly, this effect was bacterial strain dependent as it was not induced by another *B. breve* strain DPC 6330. Taken together, certain probiotic strains can modulate various aspects of the microbiome-gut-brain axis some of which are vagus dependent. However, it is clear that caution needs to be exercised when generalising such effects from one bacterial strain to another and efforts need to be directed at identifying the mechanism of how each strain induces their effects.

PAIN

Some of the most convincing data on the microbiome-gut-brain axis emerges from the pain field. Visceral pain is a pronounced and, at times, dominant feature of a variety of gastrointestinal

disorders, including IBS. Recurrent, episodic but often unpredictable painful events can exert a disabling impact on daily life and result in impairment of several domains of quality of life. Vis-

ceral pain perception is regulated by complex mechanisms. These include peripheral sensitization of sensory nerves whereas the central processing of visceral nociception is mediated at both cortical and subcortical levels by pathways also involved in the processing of psychological stress. Specifically, the prefrontal cortex has been shown to play an integral role in these processes, with imaging studies in humans (Mayer et al., 2008; Mertz et al., 2000) and animal (Gibney et al., 2010; O'Mahony et al., 2010; Wang et al., 2008) showing activation of the anterior cingulate, pre-limbic and infra-limbic cortices in response to painful and stressful stimuli. Growing evidence suggests that both central and peripheral mechanisms could be affected by intestinal microbiota. In animal studies, probiotics (mostly *Lactobacilli* and *Bifidobacteria*) have been shown to alleviate visceral pain in stress models (Ait-Belgnaoui et al., 2006; Gareau et al., 2007; Johnson et al., 2011; McKernan et al., 2010; Rousseaux et al., 2007; Verdu et al., 2006). This has also been also the case clinically with

many different probiotics showing beneficial effects in abdominal pain (Bercik et al., 2012; Clarke et al., 2012b). The mechanisms of action of such effects remain unclear currently and as in animal studies may involve a combination of effects on neural, immune and endocrine effects. We have recently demonstrated that *B. infantis* 35624 is effective at increasing the pain threshold in rats and reducing the number of pain behaviours following CRD in both a normo-sensitive and a hypersensitive rat strain (McKernan et al., 2010). Recently, it has been shown that *Lactobacillus acidophilus* reduces visceral hypersensitivity in rats by inducing cannabinoid (CB2) and opioid receptor (MOR1) expression in the colonic epithelium (Rousseaux et al., 2007). Furthermore, in a number of recent studies, *Lactobacilli* have been shown to affect the excitability of enteric neurons and nerves innervating the gut, which in turn has been shown to have effects on colonic motility (Kunze et al., 2009; Ma et al., 2009; Wang et al., 2010).

MICROBIOTA AND STRESS

It is long known that stress and the HPA axis can influence the composition of gut microbiome (Tannock et al., 1974). However, the functional consequences of such changes are now only being unravelled (Dinan et al., 2012). Maternal separation, an early life stressor which can result in long-term HPA axis changes (O'Mahony et al., 2011), has been shown to cause a significant decrease in faecal lactobacilli on day 3 post separation, which returns to baseline by day seven as assessed by enumeration of total and Gram-negative aerobic and facultative anaerobic bacterial species (Bailey et al., 1999).

However, we have more recently shown that early life stress can also have long-term effects on the microbiome. Analysis of the 16S rRNA diversity in adult rats exposed to maternal separation for three hours per day from post natal days 2-12 revealed a significantly altered faecal microbiome when compared to the non-separated control animals (O'Mahony et al., 2009). A study using deep sequencing methods demonstrated that the community structure of microbiota from mice exposed to chronic restraint stressor was significantly different to that in non-stressed control mice (Bailey et al., 2011). More

recently chronic psychosocial stress decreased the relative abundance of *Bacteroides*, while increasing the relative abundance of bacteria in the genus *Clostridium* in the caecum. The stressor also increased circulating levels of IL-6 and MCP-1, which were significantly

correlated with stressor-induced changes to three bacterial genera (i.e., *Coprococcus*, *Pseudobutyrvibrio*, and *Dorea*). These data show that exposure to repeated stress affects gut bacterial populations in a cytokine dependent manner (Bailey et al., 2011).

CONCLUSIONS AND PERSPECTIVE

A growing body of experimental data and clinical observations support the existence of the microbiome-gut-brain axis and suggest that it is poised to control canonical aspects of brain and behaviour in health and disease. Future research should focus on deconvoluting the relative contributions of immune, neural, and metabolic pathways to this axis. A better understanding of these relationships will inform our understanding of a host of GI and extra-GI disorders including neuropsychiatric diseases such as depression and anxiety. Much work is needed to tease apart the various constructs at play in this complex communication network. It is not clear how the various microbial strains can differentially affect CNS functioning but metabolite production, polysaccharide actions, structural effects and direct and indirect activation of the immune system are likely factors at play. Indeed, the bacterial metabolism of dietary fibre to short-chain fatty acids is a significant energy source for humans and these metabolites are of importance for gut motility, have a trophic effect on epithelial cells, impact

on immune system development and modulate entero-endocrine hormone secretion (Grenham et al., 2011). Certain microorganisms including *Lactobacilli* are able to convert nitrate to nitric oxide, a potent regulator of both the immune and nervous systems whilst others can produce neuroactive amino acids such as GABA (Forsythe et al., 2010). Elucidating the mechanisms underlying such effects will be crucially important for the development of any microbiota-based therapeutic strategies for CNS diseases.

It is clear that the clinical translation of any animal data especially those in complex areas of anxiety, depression and cognition is now warranted and that this should be done with the same rigour as pharmaceutical drug development. Overall, research to date clearly shows that behaviours, physiology, and neurochemistry can be affected in many ways by modulation of gut microbiota. Whether this translates to microbial-based CNS therapeutics remains a tempting possibility and one that is worthy of much further investigation.

ACKNOWLEDGEMENTS

The author thanks Dr. Marcela Julio-Pieper at Imágenes Ciencia for assistance with the figure. The Alimentary Pharmabiotic Centre is a research centre funded by Science Foundation Ireland (SFI), through the Irish Government's National Development Plan. The author and his work were supported by SFI (grant numbers 02/CE/B124 and 07/CE/B1368).

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GUT BACTERIA, THE VAGUS NERVE AND THE BRAIN

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SUMMARY

There is now strong evidence from animal studies that gut microorganisms can activate the vagus nerve and that such activation plays a critical role in mediating effects on the brain and behaviour. The vagus can differentiate between commensal and potentially pathogenic bacteria even in the absence of overt inflammation and vagal afferent signals can induce both anxiogenic and anxiolytic effects depending on the nature of the stimulus. In addition to direct afferent signalling to the brain circuitry associated with stress and anxiety there are well described anti-inflammatory efferent responses that may contribute to behavioural effects of vagal stimulation in certain circumstances. Advances in our understanding of the microbiome-gut-brain axis will come from studies of how distinct microbial stimuli activate the vagus and the nature of the signals transmitted to the brain that lead to differential neurochemical changes that subsequently drive distinct behavioural changes.

THE VAGUS NERVE

The vagus (10th cranial nerve) innervates the pharynx, larynx and visceral organs. It contains more afferent than efferent nerve fibres and projects from the medulla oblongata in the brain stem to the colon. Indeed, the vagus nerve is the main afferent pathway from the abdominal cavity to the brain. Information from the heart, lungs, pancreas, liver, stomach and intestines are delivered tonically to the brain via sensory fibres in the vagus nerve (*Browning and Mendelowitz, 2003*). Sensory vagal inputs arrive in the nucleus of the solitary tract (NTS), and are thence transmitted to widespread areas of the CNS, including the cerebral cortex and medulla oblongata. Neurones of the rostral ventrolateral medulla oblongata (RVLM) provide one of two major sources of afferent inputs to the locus coeruleus (*Aston-Jones et al., 1986*),

which in turn projects to areas of the cortex that are associated with stress-related behaviour and affective disorders. The locus coeruleus is also considered a major site for integrating stress-responses (*Aston-Jones et al., 1996*). Following repeated activations, a feed-forward system between noradrenergic locus coeruleus neurones and areas of the forebrain that produce corticotropin-releasing factor (CRF) can lead to altered behavioural responses (*Ziegler et al., 1999*). Chronic activation of this system induces changes in neuronal activity that underlies anxiety, panic disorders and depression (*Arborelius et al., 1999*). The concept of interoception and experimental data suggesting that changes in visceral sensation can affect the perception and interpretation of external inputs (*Crucian et al., 2000*) has

lead to the suggestion that altered sensory vagal inputs can influence our attitude to the outside world and that pathological changes in sensory vagal inputs may increase the risk of affective behavioural disorders. It has been proposed that chronic sensory vagal

inputs could act as 'natural' breaks for augmentation of stress-related behavioural responses via tonic modulation of the neuronal activity in the locus coeruleus and in turn the forebrain (Zagon, 2001).

THE VAGUS AND SICKNESS BEHAVIOUR

Some of the earliest indication of the role of the vagus in modulating behaviour came from studies of animals exposed to endotoxin. Sickness behaviour is a term used to describe the drastic changes in behaviour that occur in physically ill patients and animals, and is a motivational state responsible for re-organizing perceptions and actions to enable ill individuals to cope better with infection (Dantzer et al., 2000). The associated behaviours include lethargy, depression, anxiety, and loss of appetite, sleepiness, hyperalgesia, and reduction in grooming. These behavioural changes are mediated by pro-inflammatory cytokines particularly IL-1 β and TNF (Dantzer et al., 2000).

The role of vagal afferents in the induction of sickness behaviour following intraperitoneal administration of the cytokine inducer lipopolysaccharide

(LPS) or IL-1 β has been assessed in laboratory animals that have been submitted to subdiaphragmic vagotomy (Luheshi et al., 2000; Konsman et al., 2000). In these experiments carried out in rats and mice, sickness behaviour was measured by decreased social exploration and by depressed operant responding for a food reward in mice that had been trained to repeatedly poke their noses into a hole for getting a food pellet. After recovery from surgery, a dose of LPS or IL-1 β that induced consistent sickness behaviour in sham-operated animals was no longer able to decrease social exploration in rats and mice (Laye et al., 1995; Bluthe et al., 1994). In the same manner, vagotomy blocked the depressing effects of LPS on food-motivated behaviour in mice (Bret-Dibat et al., 1995).

VAGAL STIMULATION AS AN ANTI-DEPRESSANT

While vagal activation by cytokines has been associated with sickness and depressive type behaviour it is also emerging that stimulating the vagus can lead to a reduction in anxiety and depression associated behaviours. In one study, rats were administered 30 minutes per day of continuous vagus nerve stimulation for 4 days, and were then subjected to the forced swim test, a well validated assessment of antidepressant activity. Vagus nerve stimulation significantly reduced immobility

time compared to unstimulated controls, reflective of antidepressant effects (Krahl et al., 2004). Interestingly, vagal nerve stimulation-induced decreases in immobility were associated with increased swimming behaviour, which has been linked to a predominantly serotonergic mechanism of action (Cryan et al., 2005). In a subsequent controlled trial, rats received desipramine or vagal nerve stimulation for 2 h at three time points over a 24 hour period, prior to undergoing the

forced swim test and both treatments resulted in reduced immobility compared to saline control (Cunningham et al., 2008). However, chronic vagal nerve stimulation for 1 month failed to show any behavioural alterations in rats subjected to the forced swim test or the elevated plus maze test, in contrast to treatment with another classical antidepressant, imipramine (Biggio et al., 2009). Vagal stimulation is an FDA accepted alternative treatment for intractable depression and has also been

used successfully in the treatment of refractory epilepsy, demonstrating clear behavioural effects of modulating vagal afferent signals (Walsh and Kling, 2004). While this treatment is controversial, largely due to a lack of positive sham treatment controlled clinical trials, there have been reports that vagal nerve stimulation is beneficial in at least some patients with depression and may be particularly effective with chronic treatment (Rizvi et al., 2011; Martin and Martin-Sanchez, 2012).

VAGAL INFLAMMATORY REFLEX

The vagus innervates tissues known to participate in immune functions and/or contain important immune elements, such as thymus, lung, liver, and gastrointestinal tract. Furthermore, trunks or branches of the vagus are often associated with lymph nodes that drain regions in which immune activation occurs. It has recently been identified that the vagus plays a critical role in a neural circuit that controls the inflammatory response in a reflex-like manner. The vagus nerve senses inflammation sending afferent signals to the brain that then activates an efferent response, releasing mediators including acetylcholine that, through an interaction with immune cells, attenuates inflammation.

Tracey and colleagues first highlighted the anti-inflammatory role of the vagus demonstrating that direct electrical stimulation of the peripheral vagus nerve in vivo during lethal endotoxaemia in rats prevented the development of shock through the inhibition of TNF synthesis (Borovikova et al., 2000). The vagus nerve also plays a counter-inflammatory role in the experimental colitis (Ghia et al., 2006). Macrophages have been identified as the major source of TNF during endotoxae-

mia, and are suggested to be the main target of the anti-inflammatory function of the vagus nerve in a murine model of inflammatory bowel disease (Ghia et al., 2006).

In addition to suppressive effects on macrophages the vagus nerve also acts to regulate T cell function. O'Mahony et al. (2009) demonstrated that transfer of CD4⁺ T cells from vagotomised donors into non-vagotomised with DSS induced colitis reduced the number of splenic Foxp3⁺ regulatory T cells in recipient animals, and was associated with aggravated disease symptoms mimicking the effects of vagotomy on colitis. Subdiaphragmatic vagotomy leads to a dramatic increase in T cell proliferation and production of inflammatory cytokines when compared to cells from sham-operated animals (Karimi et al., 2010). The effect of vagotomy is not limited to the spleen as lymphocytes isolated from the mesenteric lymph nodes also demonstrated a significant increase in inflammatory cytokine production. Overall this data suggests that CD4⁺ T cells are also under tonic inhibitory control from the vagus. This anti-inflammatory efferent response may, in certain circumstances play a

role in mediating the anti-depressive effects of vagal nerve stimulation.

Immune system dysfunction has also been linked to depression (*Connor and Leonard, 1998; Miller et al., 2009; Li et al., 2011*). Approximately one-third of people with depression, without co-morbid disease, have higher levels of inflammatory markers compared with the normal, non-depressed population. Furthermore, inflammatory illnesses are associated with greater rates of major depression while patients treated with cytokines for various illnesses are at increased risk of

developing major depressive illness. Conversely, successful treatment with an antidepressant decreases levels of pro-inflammatory cytokines such as IL-6 and TNF (*Capuron and Dantzer, 2003; O'Brien et al., 2007; Hernandez et al., 2008*). While it is as yet unclear whether neurostimulation therapies for depression affect immune function, there is evidence in vagal nerve stimulation treated epilepsy patients that pro-inflammatory cytokine levels were reduced with successful treatment (*De Heerdt et al., 2009; Majoie et al., 2011*).

VAGUS AND THE GUT

Vagal primary afferents innervate the muscular and mucosal layers of the gut. They are 30,000 to 80,000 vagal afferent nerves (and as many spinal afferents) that supply the intestine with the ratio of afferent to efferent fibres in peripheral nerve bundles being 9:1 (*Mei, 1983; Blackshaw et al., 2007*). Vagal afferents innervate all of gut with the coeliac branch supplying the intestine from proximal duodenum to the distal part of the descending colon (*Wang and Powley, 2007*). Vagal innervation is densest proximally but still substantial for the colon. Histological and electrophysiological data reveal that visceral afferent chemosensitive endings are free endings (*Mei, 1983*) that express a large mixture of chemical and mechanosensitive receptors (*Blackshaw et al., 2007*).

Chemosensitive receptors are the targets of gut hormones and regulatory peptides such as ghrelin, CCK, GLP-1 and PYY(3–36) that activate vagal afferent neurons, whose terminals lie in the mucosa that can powerfully influence the control of food intake and regulation of energy balance (*Black-*

shaw et al., 2007). Labelling experiments have identified vagal afferent fibres in the lamina propria of duodenal and jejunal villi and crypts of Lieberkühn, but they do not cross the basal membrane to innervate the epithelial layer (*Wang and Powley, 2007*). Thus, vagal afferents are not in a position to sense luminal nutrients directly, but are in close anatomical apposition to the basal membrane of entero-endocrine cells (*Li, 2007*).

Intraganglionic laminar vagal afferent endings (IGLEs) are located in the connective tissue capsule of myenteric plexus ganglia, between the longitudinal (outer) and circular (inner) muscle layers. These fibres respond to muscle tension generated by both passive stretch and active contraction of the muscle layers (*Berthoud et al., 2001*). This type of vagal afferent ending is found in large numbers throughout the oesophagus and gastrointestinal tract and is thought to be important for generating vagal afferent tone for balanced interoceptive awareness and emotional well-being.

THE VAGUS IN THE MICROBIOTA-GUT BRAIN AXIS

Thus, given the key role of the vagus in communicating visceral signals to brain and particularly to neural circuitry associated with mood and anxiety it is perhaps not surprising that many investigations of communication between gut bacteria and the CNS have examined the role of the vagus. There is now strong evidence from animal studies that gut microorganisms can activate the vagus nerve and that such activation plays a critical role in mediating effects on the brain and subsequently, behaviour.

Such evidence came early from the study of animals infected with pathogens. Subdiaphragmatic vagotomy attenuated c-fos expression in the PVN of rats inoculated with *Salmonella typhimurium* (Wang et al., 2002). Although *S. typhimurium* infection was accompanied by intestinal inflammation subsequent studies have indicated that microorganisms in the gastrointestinal tract can directly activate neural pathways even in the absence of an identified immune response (Goehler et al., 2005). The anxiogenic effect of orally administered subclinical doses of *Campylobacter jejuni*, in mice was associated with a significant increase in c-Fos expression in neurons bilaterally in the vagal ganglia and activated visceral sensory nuclei in the brainstem. The areas of brainstem activation, the NTS and lateral parabrachial nucleus, participate in neural information processing that ultimately leads to autonomic neuroendocrine and behavioural responses (Goehler et al., 2005).

Non-pathogenic bacteria also activate vagal signalling from gut to brain. Tanida et al. (2005) demonstrated that intraduodenal injection of the bacterial strain *Lactobacillus johnsonii* La1 reduced renal sympathetic nerve activity and blood pressure while enhancing

gastric vagal nerve activity. All of these effects could be abolished by pre-treatment with a histaminergic H3-receptor antagonist. Similarly the effects were absent in animals that had bilateral lesions of the hypothalamic suprachiasmatic nucleus, a major regulator of circadian rhythm. These findings suggest that the influence of the bacteria on autonomic neurotransmission and subsequently blood pressure is mediated centrally, likely through histaminergic nerves and the suprachiasmatic nucleus (Tanida et al., 2005).

Consequently, infradiaphragmatic denervation of vagal nerve fibres surrounding the oesophagus eliminated the ability of *L. johnsonii* La1 to reduce renal sympathetic nerve activity and blood pressure indicating that at least some of the effects of this bacterium on autonomic nerve responses were elicited by interaction with afferent vagal nerve fibres (Tanida et al., 2005).

Recently it was demonstrated that oral administration of a *L. rhamnosus* strain (JB1) could alter the normal behaviour of adult balb/c mice (Bravo et al., 2011). Chronic treatment with the bacteria reduced anxiety-like behaviour as assessed in an elevated plus maze and decreased the time spent immobile in a forced swim test. In addition, stress-induced plasma corticosterone levels were lower in treated mice a similar effect to subchronic or chronic treatment with antidepressants that can prevent forced swim stress-induced increases in plasma corticosterone in both mice and rats. Overall, changes induced with *L. rhamnosus* were indicative of reduced anxiety, and decreased depression-like behaviour. Assessment of neural correlates to behavioural changes determined that mice receiving *L. rhamno-*

sus had alterations in central GABA receptor subunit mRNA expression. *L. rhamnosus* administration decreased expression of GABA type B (GABAB) subunit 1 isoform b (GABAB1b) mRNA in the amygdala and hippocampus, while increasing expression in cortical areas. Expression of GABAA α 2 receptor mRNA was reduced in the amygdala and cortical areas, whereas levels were increased in the hippocampus (Bravo et al., 2011). It is difficult to attribute a causal relationship between behavioural effects observed and neural correlates. However, reduced expression of GABAB1b mRNA, in the amygdala, hippocampus, and locus ceruleus is consistent with the antidepressant-like effect of GABAB receptor antagonists (Cryan and Slattery, 2010) and with studies of GABAB1b-deficient animals, indicating an important role for this subunit in the development of cognitive processes, including those relevant to fear (Jacob-

son et al., 2007a, 23007b). It is also interesting to note that in a recent study of transcriptomes from the mucosa of the proximal small intestines of healthy human subjects following treatment with different lactobacillus species, there was a strong correspondence between *in vivo* transcriptional networks altered after consumption of one of the strains, *Lactobacillus casei*, and the response of human cells to the anxiolytic GABA A receptor modulator, Tracazolate (van Baarlen et al., 2011).

Subdiaphragmatic vagotomy blocked the anxiolytic and antidepressant effects of chronic *L. rhamnosus* ingestion in normal adult Balb/c mice while also preventing the associated alterations in GABAA α 2 mRNA expression in the amygdala (Bravo et al., 2011). Similarly, the ability of *B. longum* to attenuate DSS colitis induced anxiety was abolished by vagotomy (Bercik et al., 2011a).

CONCLUSION AND FUTURE DIRECTIONS

Overall, studies indicate that vagal pathways mediate signals that can induce both anxiogenic and anxiolytic effects depending on the nature of the stimulus and, interestingly, the vagus appears to differentiate between non-pathogenic and potentially pathogenic bacteria even in the absence of overt inflammation.

It is therefore clear that the involvement of the vagus in microbiota-gut-brain communication is not straightforward or simply dependent on "activation". Assuming that an increase in c-fos expression always uniquely reflects an increase in neuronal firing rates, a dubious assumption, existing anatomical data cannot answer the question why in some cases vagal activation causes depression and in others, for example, electrical stimulation of

the vagus, eases depression. What is currently lacking is relevant data on the electrophysiology of the system. In spite of our obvious lack of understanding of how probiotics encode vagal neural discharge, very little work has been published on a probiotic neural code. Tanida et al. (2005) showed that injecting *L. johnsonii* into rat duodenum increased gastric vagal multiunit firing rate by about 10% within 15 minutes, and this slowly grew to a 90% increase over the baseline 1 h after the injection was delivered. Clearly, much more work of this sort needs to be done and should be compared with vagal responses to anxiogenic and anxiolytic peripheral stimuli.

Electrophysiology may also be utilized to determine the nature of the peripheral signal acting to stimulate the

vagus nerve in the gut following exposure to specific bacteria. Single chemosensitive vagal afferent units supplying the gut are normally silent or have a low resting discharge of 0-3 Hz (*Blackshaw and Grundy, 1993*). They respond to most luminal molecules by increasing their firing rate. Response latencies vary according to the chemical nature of the stimulus. The short chain fatty acid butyrate had a response onset latency of 2-3 ms (*Lal et al., 2001*), the long chain fatty acid sodium oleate had a latency of 15 ms (*Lal et al., 2001*), amino acids evoked responses within about 9 ms (*Mei, 1983*) the response to casein acid hydrolysate has a latency and of 19 ms (*Eastwood et al., 1998*), and glucose takes 20 ms (*Hardcastle et al., 1978*). *Salmonella typhimurium* lipopolysaccharide evoked an increase in the mesenteric nerve discharge with 30 min (*Liu et al., 2009*) while LPS from a commensal *E. coli* had no effect (*Liu et al., 2009*). Mesenteric vagal afferents are mainly unmyelinated fibres with conduction speeds of 0.7 m/s (*Cervero and Sharkey, 1988*), so the conduction from mucosa to the mesenteric recording electrode (less than 10 mm distance) would be ≤ 7 ms. Thus most of the response times could be attributed to mucosal endocrine cells sensing and transduction, transmission to adjacent vagal endings and generation of a supra-threshold neurite receptor potential.

Certainly, important advances in our understanding of the microbiome-gut-brain axis will come from studies

of how distinct microbial stimuli activate the vagus and the nature of the signals transmitted to the brain that lead to differential changes in the neurochemistry of the brain and behaviour. However, while it appears that the vagus is critical to mediating gut-brain communication by specific bacteria in some model systems, it is by no means the only potential signalling method. Indeed, largely due to technical difficulties, few studies have investigated the role of spinal afferents in mediating bacteria induced changes in behaviour and brain chemistry. It is certainly possible that the observed changes in brain chemistry behaviour induced by gut bacteria require parallel input from both the vagal and spinal afferents. Furthermore, behavioural changes induced through disruption of the microbiota by antibiotic treatment have been demonstrated to be independent of vagal signalling (*Bercik et al., 2011b*) with some additional evidence that neither sympathetic afferents nor immune modulation is required. This clearly suggests that the bacteria in the gut can communicate to the brain through multiple pathways. A potential means of communication, that has been somewhat neglected in existing studies, involves direct hormonal signalling to the brain. Nevertheless understanding the induction and transmission of anxiolytic signals in the vagus nerve may have important implications for the development of microbial-based therapeutic strategies for mood disorders.

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MAPPING THE CONSEQUENCES OF METABOLIC INTERACTIONS BETWEEN HOST AND MICROBIOME ON THE BRAIN

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INTRODUCTION

The gut microbiome, defined by Joshua Lederberg as the sum of the bacterial genomes and their environmental interactions (*Lederberg, 2001*), acts as an extra organ in the mammalian host with a vast capacity for metabolism of chemicals deriving from endogenous mammalian metabolism, nutrients and other xenobiotics. This surrogate organ not only functions to shape the immune system and harvest energy, but is also capable of direct chemical communication and contributes to a wide range of signalling pathways that connect various organs and tissues throughout the body (*Cryan and O'Mahony, 2011; Nicholson et al., 2012*). The communication between the gut and the brain, the so called 'gut-brain axis' is a critical factor in many physiological and

pathological processes. In addition to direct interaction between the brain and enteric nervous system in the gut via the vagus nerve, a great deal of chemical communication occurs and many of the chemicals produced by the gut microbiota are potentially neuroactive including γ -amino butyric acid (GABA), 5-hydroxytryptophan and indoxyl compounds (*Wikoff et al., 2009; Barrett et al., 2012*). Conversely the brain can modulate the behaviour of the microbiota via mechanisms such as stimulation of the endochromaffin cells. This review addresses the influence of the gut microbiota on the brain and central nervous system (CNS) and explores their consequent impact on metabolism under various physiological and pathological conditions.

METABOLIC SIGNATURE OF AUTISM: CONTRIBUTIONS FROM THE MICROBIOME

Autism spectrum disorder (ASD) represents a group of developmental conditions characterised by dysfunction in verbal and non-verbal communication and social interactions and is associated with repetitive behaviour and difficulty in imaginative play in children. First described by Kanner in 1943, autism typically manifests during the first three years of life and is part of the Pervasive Developmental Disorders (PDD) family. It is diagnosed according to the Diagnostic and Statistical

Manual of Mental Disorders (DSM-IV) and there are several clinical scoring scales used for establishing the severity and type of autism (*Faras et al., 2010*). A recent review reports that whilst the conservative estimate of autistic spectrum disorder prevalence is 27.5 per 10,000 individuals, the real prevalence estimate based on newer surveys is 60 per 10,000 individuals, with a 4:1 male-to-female ratio (*Faras et al., 2010*), thus autism is a growing clinical, social and financial concern.

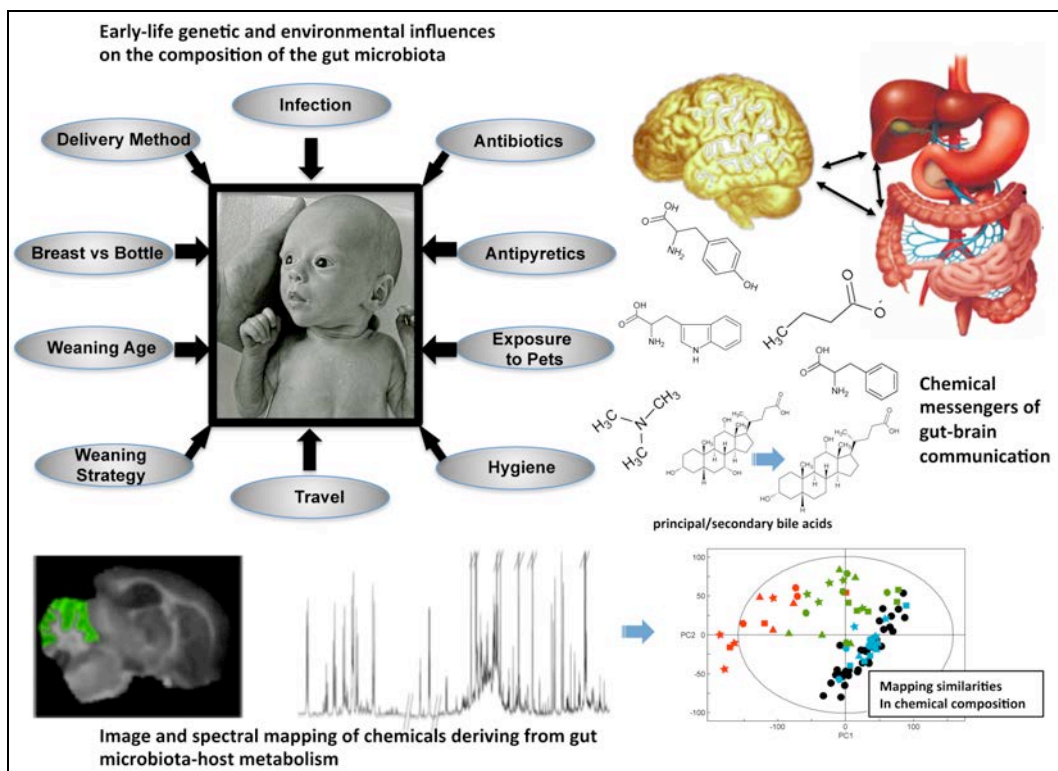


Figure 1: The early life environment influences the composition of the gut microbiota with consequent risk or protection for later-life disease. One of the ways in which the brain and gut are inextricably linked is through chemical dialogue between the gut microbiota and the brain in the form of small molecule messengers such as bile acids, biogenic amines, products of choline degradation and short chain fatty acids. These molecules can be detected in the NMR and MS profiles of urine, plasma, cerebrospinal fluid and other biofluids. The distribution of these chemicals can also be mapped in the brain in order to ascertain their topographical distribution. Computational modelling can be used to efficiently extract and visualise information relating to gut-brain communication and to unravel the profound dependence of humans on their microbiota.

Clinicians, scientists and parents of autistic children have proposed multiple theories regarding the causes of autism. However, only limited clinical data are available and in some cases the data are contradictory and/or inconclusive. Numerous aetiological hypotheses have been postulated including: *In utero* exposure to chemicals such as pesticides, genetic causes (particular association with the X chromosome), oxidative stress, measles, mumps and rubella (MMR) vaccination or its thiomersal carrier, advanced maternal age, planned caesarean section, low Apgar

scores, hyperbilirubinaemia and birth defects (*Duchan et al., 2012; Guinchat et al., 2012*). Inflammation has also been associated with autism and could be mediated by a defective placenta, immature blood-brain barrier, the immune response of the mother to infection while pregnant, a premature birth, encephalitis in the child after birth, or a toxic environment either *in utero* or in the first few months of life (*Faras et al., 2010*). Although some of the theories on the causes of autism, such as the MMR vaccine, have been largely discredited, it is evident that ASD repre-

sents a complex set of interrelated conditions and is likely to originate from a highly multifactorial aetiology. This is further supported by the vast array of co-morbidities that typically accompany autism, in particular gastrointestinal dysfunction. Understanding the role of the gut microbiota in autism would undoubtedly offer new therapeutic avenues, regardless of whether the intestinal dysfunction is causal or merely co-incident.

The compositional landscape and functionality of the gut microbiota are determined by a sequence of factors beginning at or before birth. The first large-scale exposure to bacteria occurs during the birth process and continues to be modulated by subsequent exposure to the external environment, feeding method and early life infections. Whilst the early microbial composition is dynamic, this plasticity diminishes over time to form a relatively stable microbiome that persists throughout adulthood. However, it is thought that these early influences on the microbiota can persist and influence disease risk later in life. For example preterm infants have a higher risk of cardiovascular disease, pulmonary disease, metabolic diseases and several psychological and neurodevelopmental conditions including autism (Rogers and Veltan, 2011). Metabolic profiling of biofluids and tissues can detect changes in microbial activity via profiling or imaging of microbial products such as cresols, biogenic amines, short chain fatty acids etc. (Figure 1), and represents one means of understanding the relationship between the gut and the brain.

Gastrointestinal (GI) dysfunction is reported in a high percentage of children diagnosed with autism with reported symptoms ranging from diarrhoea to constipation and abdominal bloating and pain. In one study, intesti-

nal permeability was found to be higher in individuals with ASD (36.7%) in comparison with healthy controls (4.8%), whereas ASD participants on a casein free diet did not show this increase in intestinal permeability (de Magistris et al., 2012). Interestingly, family members of autistic children also showed increased intestinal permeability. Given the prevalence of GI dysfunction in children with ASD, there has been growing interest in the role of the gut microbiota, specifically bacterial populations such as the Clostridia, which are known to produce toxins and often flourish in a perturbed gut ecosystem. However, as yet the literature contains few examples of studies in which the microbiome of autistic individuals has been systematically characterised and those that have been reported suffer from a low sample size and poor comparison between autistic children with and without GI dysfunction (Critchfield et al., 2011). Williams and colleagues showed in a study of the mucosal biopsies of 22 children with autism that disaccharidases and hexose transporters were deficient and that this deficiency correlated with the intestinal transcription factor caudal type homeobox 2 (CDX2) that regulates transporters of glucose and other sugars (Williams et al., 2011). This change in transcription factors was correlated with the bacterial profiles of the mucosal samples that showed an increase in the *Firmicute:Bacteroidete* ratio and increased numbers of Betaproteobacteria.

A series of relatively small scale studies have demonstrated that autistic individuals harbour a distinctive faecal microflora compared with that of healthy children (Parracho et al., 2005; Finegold et al., 2010), with autistic children carrying greater numbers of bacteria of the *Clostridium histolyticum* group (Parracho et al., 2005) and *Desulfovibrio* (Finegold et al., 2010)

and manifesting a shift at the phylum level towards an increased *Bacteroidetes:Firmicute* ratio (Finegold et al., 2010). Other bacteria found in high concentrations in the epithelial mucosa of children with ASD associated GI symptoms are the *Sutterella* genus, predominantly *Sutterella wadsworthensis* and *Sutterella stercoricanis* (Williams et al., 2012).

Metabolic profiling studies have also generated indirect evidence of a shift in clostridial species. Urinary excretion of 4-cresyl sulphate is increased in autistic children, and to a lesser extent their siblings (Yap et al., 2010). 4-Cresol is a gut microbial metabolite that can be synthesized by several bacteria including *Clostridium difficile* and *Clostridium scatologens*, and which subsequently undergoes phase II metabolism to the sulphate conjugate with minor amounts of the glucuronide conjugate formed. Children with ASD have also been found to have higher urinary levels of another clostridial metabolite, 3-(3-hydroxyphenyl)-3-hydroxypropionic acid (HPPHA), which is thought to be a metabolite of the tyrosine analogue 3-hydroxyphenylalanine (Shaw, 2010). This metabolite was also found in high levels in the urine of an adult that had experienced repeated *C. difficile* infections (Shaw, 2010).

Other metabolites that characterize the urine of autistic children include bacterial products of choline degradation such as methylamine and dimethylamine, hippurate, phenylacetylglutamine, reinforcing the possible involvement of the microbiota in autism. In contrast, Lis and colleagues reported lower urinary levels of hippurate and 4-hydroxyhippurate in autistic children compared to age matched controls, as measured by ion exchange chromatography (Lis et al., 1976). Thus the relationship between autism and the gut microbiota is not straightforward, like

most other aspects of ASD.

As with the role of the gut microbiota, the involvement of oxidative stress in the aetiology of ASD is similarly ambiguous. Both oxidized glutathione and the ratio of oxidized to reduced glutathione are increased in autism (Ghanizadeh et al., 2012; Frustaci et al., 2012), whilst blood levels of reduced glutathione, glutathione peroxidase and sulphur-containing amino acids cysteine and methionine were found to be reduced in a meta analysis of ASD (Frustaci et al., 2012). There is some evidence that dietary supplementation with glutathione may improve the levels of trans-sulphuration metabolites (Kern et al., 2011).

Low levels of reduced plasma glutathione and sulphur-containing amino acids are consistent with the observation that autistic children are deficient in sulphation capacity (Alberti et al., 1999), thus any intervention that challenges the already impaired capacity for sulphation has the potential to compound the expression of ASD. Acetaminophen use in children has been suggested as a trigger for autism via activation of the endocannabinoid system, which is known to be capable of modulating brain function during development (Schultz, 2010). The primary route of acetaminophen excretion in children is sulphation. In autistic children that are already sulphur deficient, acetaminophen could further deplete already low sulphur pools with subsequent impact on the glutathione pathway. Interestingly the metabolic fate of acetaminophen can be predicted from pre-dose urinary profiles and the most predictive metabolite for high acetaminophen sulphate excretion is 4-cresyl sulphate (Clayton et al., 2009), the synthesis of which has been largely attributed to *Clostridium difficile* and *C. scatologens*. Thus it is possible that the gut microbiota contribute to the deple-

tion of sulphate pools in autistic children by generating phenols and other chemicals that undergo sulphation prior to excretion.

In conclusion, the role of the gut microbiota in ASD is far from clear. Various studies show differential microbial profiles between autistic and healthy children, and the presence of various GI-related co-morbidities points to an association between the microbiome and ASD. The fact that children with ASD tend towards food sensitivity and are typically on numerous therapeutic regimes including con-

trolled diets, chelation agents and a cocktail of drugs such as aripiprazole, altrexone, buspirone, divalproex sodium, lamotrigine, levetiracetam, memantine, mirtazapine, riluzole, pioglitazone, and topiramate (Doyle and McDougale, 2012) confounds the picture as these agents may in themselves induce a change in the gut microbiota. This underscores the requirement for high quality, systematic and controlled studies to be carried out in order to ascertain the true relationship between the gut microbiota and ASD.

INFECTION-INDUCED DISRUPTION OF THE GUT MICROBIOTA-HOST METABOLIC INTERFACE

Both chronic and acute infections have been shown to have profound impact on the gut microbiome. Reduced cognitive function in children in developing countries has been correlated with repeated incidences of infection causing diarrhoea (Oria et al., 2009). Evidence of both direct and indirect influence of the microbiota on the central nervous system (CNS) can be found in the literature. For example, increased anxiety, brought about through viscerosensory signalling from the gastrointestinal tract, can be induced in mice by experimental infection with *Campylobacter jejuni* (Goehler et al., 2007).

The hygiene hypothesis has led to the association of certain autoimmune diseases with infection and bacteria. The onset of these diseases has been linked to bacterially driven immune responses. In an animal model of multiple sclerosis, it has been shown that commensal gut microbiota are necessary for initiating immune responses that result in myelin-specific CD4(+) T cells attacking the CNS (Berer et al., 2011).

Examples in both the insect and in the human world provide evidence that

parasitic infection can alter behaviour. Parasitic hairworms manipulate their cricket host by inducing suicide behaviour, causing the insect to leap into water, where the parasite continues its life cycle (Ponton et al., 2011). Epidemiological studies have found associations between certain helminths, including *Schistosoma mansoni*, *Ascaris lumbricoides* and *Trichuris trichiura*, and cognitive impairment in school age children (Jardim-Botelho et al., 2008; Shang and Tang, 2010) but the mechanism is unknown. Direct contact of a parasite with the CNS can result in overt histological and biochemical changes. Most prominent examples are cerebral manifestations of malaria, due to malaria toxin excretion, excess cytokine secretion and billharziosis-induced granuloma formation caused by sequestration of Schistosome erythrocytes. Serendipitous ectopic worm manifestations in the brain by cestodes, trematodes and protozoa have also been reported to cause lesions and haemorrhages (Walker et al., 2005). However, for most host-parasite interactions involving neurological damage or altered behaviour, the molecular mechanisms

are not well understood.

There is some suggestion that certain changes in brain biochemistry following helminth infection may be associated with dysregulation of the microbiota. The parasitology literature contains several examples of infection-induced disturbances of the microbiota (Wang et al., 2010; Li et al., 2012). Many parasites ranging from *Giardia* to hookworm are associated with gastrointestinal disturbances. It is unsurprising that parasites that reside in the gut should impact upon the microbiota, since they share the same physical environment. However, studies in animal models have shown that several parasites, some of which reside in the blood or in non-gastrointestinal tissues, can modulate the excretion of gut microbial metabolites.

Parasite infections have been shown to perturb several metabolites of the gut microbiota in various animal models and in humans (Wang et al., 2004, 2010). Metabolic profiling studies in humans and animal models have shown modulation of urinary gut microbial metabolites including hippurate, 4-cresyl sulphate and glucuronide, phenylacetyl glycine / glutamine, 4-hy-

droxyphenylacetic acid and 4-hydroxy-3-methy-phenylpropionate acid (Wang et al, 2004, Wang et al, 2010; Balog et al, 2011). In a study investigating the metabolic effects of a foodborne trematode, *Fasciola hepatica*, in a rat model, clear evidence of altered gut microbial metabolism was found in both the urine (decreased hippurate levels and modified bacterial products of choline degradation) and faecal metabolite profiles and, more interestingly, these changes correlated with altered brain biochemistry following infection. Significant perturbations of the nucleotide balance in the brain suggested a shift toward modulation of immune reactions, which could serve to prolong the camouflage of the parasite within the host via minimization of inflammatory damage (Saric et al., 2010).

Thus, it seems that there is a complex tripartite interaction between host, parasite and microbiota mediated by both immunoregulatory mechanisms and direct chemical communication between microbe and host. Moreover, this three-way relationship has system-wide impact, including neurological consequences and warrants deeper interrogation.

METABOLIC EFFECTS OF THE GUT MICROBIOTA IN RELATION TO IMPACT ON MOOD AND BEHAVIOUR

There is a growing body of evidence associating depression and other psychiatric disorders with perturbed gut microbiota. The cytokine hypothesis of depression suggests that increased translocation of LPS from Gram-negative bacteria and inflammation are causally associated with clinical depression and neurodegeneration (Qin et al., 2007; Maes, 2008). In another stress-induced rat model of depression associated with leaky gut, the administration of *Lactobacillus farciminis*

was shown to reverse the stress-induced hyperpermeability and behavioural changes (Ait-Belgnaoui et al., 2012) In addition to producing LPS and other neurotoxic chemicals, the gut bacteria can synthesize metabolites such as pyrogallol and urolithins from dietary polyphenols that are neuroprotective and can counteract the effects of diabetes-induced neurodegeneration (Verzelli et al., 2011).

Gut microbial metabolites found in urine and other biofluids in animal and

human studies of depression also point to the involvement of the gut bacteria in behaviour. An LC-MS profiling study of a rat model of depression found elevated urinary levels of kynurenic acid, hippurate, phenylacetyl glycine and xanthurenic acid with lower levels of tryptophan, indoxyl sulphate, indole-3-acetate and tricarboxylic acid cycle intermediates in rats challenged by chronic unpredictable mild stress suggesting that gut microbial metabolism and modulation of the TCA cycle were key components of this model of depression (Zheng et al., 2009). Interferon- α administration has been associated with depressive disorders in cancer or hepatitis-C patients treated with interferon- α (Raison et al., 2006). Interferon- α induced activation of the tryptophan degrading enzyme indoleamine 2,3-dioxygenase results in the generation of quinolinic acid and other neuroactive metabolites, which are thought to relate to depression. In a bacterially-induced animal model of depression, induced by inoculation with *Bacillus Calmette-Guérin* (BCG), administration of indoleamine 2,3-dioxygenase resulted in increased plasma concentrations of the kynurenine:tryptophan ratio (O'Connor et al., 2009).

Examples of the effect of microbiota on cognition are scattered throughout the literature. As previously mentioned, repeated diarrhoeal infections have been associated with detrimental effects on cognition in children. Similarly cirrhotic patients with encephalopathy show poor cognition, which is correlated with *Veillonellaceae* in faecal material (Bajaj et al., 2012). Higher faecal levels of *Enterobacteriaceae*, *Alcaligenaceae* and *Fusobacteriaceae* with lower levels of *Ruminococcaceae* and *Lachnospiraceae* were also found in cirrhotic patients.

There is increasing acceptance of the fact that surgery *per se* can impose

short-term or long-term consequences on mood, behaviour and cognition. Several analyses of patients undergoing coronary artery bypass graft surgery (CABG) have indicated that neurological complications can include stroke, depression or mild cognitive decline reflected by short-term memory loss or psychomotor slowing (Hawkes et al., 2006). The cause of these neurological effects is not well understood but surgical trauma, genetic susceptibility, inter-operative or post-operative ischaemia and body temperature during surgery have all been proposed as causal factors (Hawkes et al., 2006). Probiotics and synbiotics (a combination of pre- and probiotics) have been used to reduce the incidence of post-operative sepsis after elective surgery and to counteract the effect of antibiotics, typically administered as part of surgical procedures (Kinross et al., 2012). Prebiotics have also been shown to influence anxiety and mood. For example, Silk and colleagues showed that administration of a trans-galacto-oligosaccharide enhanced faecal bifidobacteria and improved anxiety and depression symptoms in patients with irritable bowel syndrome (Silk et al., 2009). Similarly probiotics such as lactobacilli have been reported to regulate emotional behaviour in mice through vagus nerve stimulated modulation of GABA receptor expression (Bravo et al., 2011).

Obesity has been associated with poor cognitive function, particularly in executive function (Lokken et al., 2010). There is controversy regarding the effect of weight loss surgery (bariatric surgery) on cognition and memory with some suggestion that bariatric surgery can cause memory impairment and depression. An animal model of gastric restriction was able to show structural alterations in the hippocampus (Sonoda et al., 2011). The mecha-

nisms of bariatric surgery-induced weight loss are known to involve alteration of gastrointestinal hormones, which are important in appetite regulation. Several gastrointestinal hormones can contribute to obesity by modulating the activity of the gut-brain axis. Recently we have characterized the metabolic response of rats undergoing RYGB surgery using high resolution spectroscopic profiling and integrated

the response with the post surgical change in the microbiome and shown a dramatic shift towards the gamma-proteobacteria. The surgery also resulted in a modulation of gut microbial metabolites, some of which were neuroactive. Increased urinary cresols, phenylacetyl glycine and indoxylsulfate occurred post surgery together with increased production of γ -aminobutyric acid (GABA) (Li et al., 2011).

CONCLUDING REMARKS

The manner in which the gut bacteria influence the CNS largely remains elusive and merits systematic study. The gut and brain use several communication axes involving nerve stimulation, immunological correspondence and direct metabolic interactions in order to maintain homeostasis. The gut microbiota contribute to the communication highway between the gut and the brain and there is enough evidence to implicate the microbiota in various neurodegenerative diseases, behavioural disorders, neurodevelopmental conditions

and cognition. The partnership between culture independent sequencing of the microbiome, the human genome and metabolic profiling of the microbial components of biofluids should help to elucidate the complex interactions of host and microbe and to place this interaction in terms of regulation/dysregulation of the CNS. Understanding this partnership will open new avenues for therapeutic intervention and opportunities for improving disease risk by modulation of the microbiota early in life or even prenatally.

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MICROBIAL “OLD FRIENDS”, IMMUNOREGULATION AND PSYCHIATRIC DISORDERS

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SUMMARY

Many diseases are increasing in prevalence in urban communities in developed countries. Immigrants are also at increased disease risk, particularly if they move from a poor to a wealthy country during infancy. Moreover, the prevalence of many of these conditions increases further in second-generation immigrants, suggesting that exposure (or lack of exposure) to critical influences during pregnancy and infancy may play an important role in conferring risk for many chronic diseases common in the modern world. The diversity of diseases involved is remarkable. They include chronic inflammatory disorders (autoimmunity, allergy and inflammatory bowel disease), many cancers, (such as prostate, colorectal and various childhood cancers) and a range of psychiatric disorders including depression, disorders precipitated by psychosocial stressors or low socioeconomic status, and disorders with a developmental component such as schizophrenia and autism. Here we explore important parallels among the increases in these diverse types of disease. We merge the immunological explanation (hygiene, or “Old Friends” hypothesis) with psychosocial explanations, and suggest that there are underlying mechanisms, many involving the gut microbiota, that are relevant to *all* these disorders and that transcend the boundaries between traditional medical disciplines.

INTRODUCTION

Many diseases are increasing in incidence in developed countries. These increases tend to be greatest in urban communities. Immigrants are also especially vulnerable to these diseases, particularly if they move from a poor to a wealthy country during infancy, suggesting that infancy provides a critical window for the influence of factors that are protective in poor countries, or det-

rimental in rich ones. Remarkably, the incidence of many of these conditions increases further in second-generation immigrants, suggesting that exposure (or lack of exposure) to critical influences during pregnancy may play an important role in conferring risk for many diseases common in the modern world. The most remarkable aspect of this problem is the diversity of diseases

involved. These include chronic inflammatory disorders (such as autoimmunity, allergy and inflammatory bowel disease), many cancers, (such as prostate, colorectal and various childhood cancers [Hodgkin's lymphoma, acute lymphatic leukaemia]) and, still more unexpectedly, a range of psychiatric disorders including depression and disorders with a developmental component such as schizophrenia and autism. Medicine tends to be strictly compartmentalized, so the hypotheses put forward to explain the increases in, for example, psychiatric disorders do not usually overlap with the hypotheses put forward to explain parallel increases in cancer or inflammatory diseases, despite the similar epidemiology and the very obvious tendency for all three types of disorder to occur in the same individuals. An immigrant from a developing country arriving in a modern developed city is confronted with psychosocial changes and stressors, a

new diet, and a totally different microbiological environment. Psychiatrists and psychologists interpret increased incidences of psychiatric diseases in terms of the changed psychosocial environment, while immunologists naturally try to interpret the increases in the diseases that fall within their domain in terms of the changing microbial environment, and immunological inputs. The aim of this paper is to explore the parallels between the increases in these diverse types of disease in developed countries and to suggest that there are underlying mechanisms, relevant to them *all* that transcend the boundaries between traditional medical disciplines. The keys to this discussion are the profound effects that psychosocial stressors exert on the immune system and vice versa, so that the two types of influence end up operating through similar pathways, often involving the intestinal microbiota.

INFLAMMATION AND PSYCHIATRIC DISORDERS

It is increasingly apparent that inflammation is involved not only in chronic inflammatory disorders such as allergies, autoimmunity and inflammatory bowel disease (IBD) but also in many psychiatric disorders. We have pointed out elsewhere that inflammation and immunoregulation are important in depression (*Raison et al., 2010; Rook and Lowry, 2008*). A large subset of depressed individuals has persistently raised levels of pro-inflammatory cytokines and other downstream inflammatory markers (*Maes et al., 1992; Miller et al., 2009a*), together with a relative deficit in anti-inflammatory mediators and regulatory T cells (fully referenced in *Raison et al., 2010*). When cytokines such as interferon-alpha (IFN- α) are used therapeutically

(to treat viral hepatitis or some cancers) they can cause depression-like symptoms that can be treated with standard anti-depressants, such as selective serotonin reuptake inhibitors (SSRI) (*Miller et al., 2009a; Musselman et al., 2001*).

It is also clear that inflammatory events during pregnancy, often triggered by infections, can lead to the central nervous system (CNS) developmental abnormalities that underlie the subsequent appearance of autism and schizophrenia (extensively reviewed and referenced in *Meyer et al., 2011*) (*Crespi and Thiselton, 2011; Schwarz et al., 2011; Zerbo et al., 2012*). Indeed autism is very clearly associated with a family history of other chronic inflammatory disorders

such as autoimmunity and allergies, and it is accompanied by abnormal microbiota (*Finegold et al., 2010*) (of which the immunoregulatory role is discussed more below and in other chapters in this volume) and by incontrovertible evidence of background inflammatory activity (*Becker, 2007; Onore et al., 2012*). This concept is powerfully supported by animal models (rodents and monkeys) showing that inflammation in the mother during pregnancy induced by injecting lipopolysaccharide (LPS) or poly I:C, or by direct injection of IL-6, will cause changes in the grey and white matter of

the foetuses and behavioural changes that are reminiscent of autism and schizophrenia (*Brown and Derkits, 2010; Smith et al., 2007; Willette et al., 2011*). Thus immunoregulatory deficits during pregnancy or adult life could play a role in these conditions.

Finally, as discussed at greater length later, inflammation is also involved in the detrimental health consequences of low socio-economic status (SES), both in humans (*Hemingway et al., 2003; Miller et al., 2009b*) and in captive colonies of rhesus macaques (*Tung et al., 2012*).

EPIDEMIOLOGICAL PARALLELS

The parallels between the epidemiology of chronic inflammatory disorders and the epidemiology of psychiatric disorders highlight factors that expose the individual simultaneously to a changing psychosocial environment, and to changing immunological input. In the text that follows we use as examples the psychiatric disorders outlined in the previous section, and several particularly prevalent chronic inflammatory disorders; allergies, IBD and two autoimmune disorders (multiple sclerosis [MS] and Type 1 diabetes [T1D]).

Urban versus rural

A feature shared by most of the disorders discussed here is a higher prevalence in urban communities, compared to rural ones. For example a meta-analysis of high quality studies performed in high-income countries since 1985 found that the prevalence of depression in urban areas was 39% higher than in rural areas. Similarly, the prevalence of anxiety disorders was 21% higher in urban than in rural areas (*Peen et al., 2010*), though a small mi-

nority of studies fails to find this urban-rural difference (*Kovess-Masfety et al., 2005*). Peen and colleagues also noted an increased urban prevalence of psychiatric disorders in general (38% more in urban communities) (*Peen et al., 2010*). This agrees well with another large meta-analysis which found a significantly raised prevalence of schizophrenia in urban communities (*McGrath et al., 2004*). Similarly, a study of all children born in Denmark between 1 January 1984 and 31 December 1998 found that the degree of urbanisation of place of birth was very significantly correlated to risk of autism ($p < 0.0001$) (*Lauritsen et al., 2005*).

It has been suggested that mentally healthy people move away from socially deprived inner cities while vulnerable mentally ill people tend to gravitate towards these areas where deviant behaviour might be more easily tolerated (*Freeman and Alpert, 1986; Moorin et al., 2006*). However available data suggest that it is the *urban upbringing* rather than a selective migration into cities that lies behind the repeated associations of exposure to the

urban environment and an increased risk of psychiatric disturbance (Blazer et al., 1985; Verheij, 1996). This view is strongly supported by the other epidemiological parallels discussed below.

The urban-rural phenomenon is also well established for chronic inflammatory disorders, where the aetiology is known to involve dysregulation of the immune system. This has been explored in some detail in the allergic disorders. Contact with the farming environment, whether postnatal (Riedler et al., 2001) or prenatal (Ege et al., 2008; Schaub et al., 2009) protects against allergic disorders, whereas the prevalence of these conditions increases with increasing urbanization (Nicolaou et al., 2005). The same is true for inflammatory bowel diseases (Hou et al., 2009), and for autoimmune diseases such as multiple sclerosis (MS) (Antonovsky et al., 1965; Beebe et al., 1967; discussed in Lowis, 1990). Interestingly, Type 1 diabetes (T1D, caused by autoimmune destruction of the pancreatic β cells) is more common in urban than in rural areas in some countries (Greece, southern Italy, Lithuania) (Cherubini et al., 1999; Dacou-Voutetakis et al., 1995; Pundziute-Lycka et al., 2003), but not in others (Finland, New Zealand or the UK) (Miller et al., 2011). This pattern of findings might imply that the effect is seen when the comparison is made in poorly developed countries where rural life is “traditional”, with multiple exposures to animals, farm buildings, and soil.

The urban-rural comparison therefore suggests either that something beneficial is absent from the urban environment, or that something detrimental is present, and these possibilities are as relevant for chronic inflammatory disorders as they are for psychiatric conditions. However, these findings do not allow us to determine

the relative importance of psychosocial factors versus immunological inputs for either group of diseases, despite the copious literature implicating the former for the psychiatric diseases, and the latter for the chronic inflammatory ones.

Immigrants

Another striking parallel between chronic inflammatory diseases and psychiatric disorders concerns the effects of immigration on these conditions. All the diseases discussed here, whether chronic inflammatory (Ahlgren et al., 2011; Hou et al., 2009; Rottem et al., 2005; Söderström et al., 2012) or psychiatric (Breslau et al., 2011; Dealberto, 2010; Keen et al., 2010), tend to be more common in immigrants than in the birth population from which the immigrant was derived, at least when the migration is from a developing to a developed country. Other relevant variables include the age of the individual at the time of immigration, and whether the prevalence increases in second generation immigrants, born in the adopted country. A study of these parameters provides some insight into whether the relevant influences, be they psychosocial or immunological, need to occur before birth, or in early childhood, or whether they can still exert their effects on adults.

Age at immigration, 2nd generation immigrants and psychiatric disorders

Depression is particularly interesting in this respect (Breslau et al., 2009; Vega et al., 2004). Mexicans, Cubans and African/Caribbean peoples have a 2-3-fold increase in the prevalence of depression if immigration to the USA occurred when the individual was less than 13 years old, or was born in the USA, compared to the prevalence in those who migrated after the age of 13

(Breslau et al., 2009). But this is not likely due to psychosocial stress related to skin colour, because white Eastern European immigrants show the same effect. In sharp contrast, the effect is not seen in immigrants from Western Europe, or from Puerto Rico, which is closely associated with the USA. (These last two populations already have a high prevalence of depression that is not increased by immigrating to, or being born in, the USA) (Breslau et al., 2009). These findings imply that influences important for depression occur perinatally, or in the early years of life.

The same is true for psychotic disorders (Coid et al., 2008). A large Danish study noted that immigration into Denmark when less than 4 years old was associated with a strikingly increased risk for psychotic disorders, whereas the increased risk gradually decreased with older age at migration and disappeared in those immigrating when more than 29 years old (Veling et al., 2011). Similarly a large meta-analysis confirmed that schizophrenia was increased amongst 1st generation immigrants, and further increased amongst 2nd generation immigrants, particularly when the country of origin was a developing one (Cantor-Graae and Selten, 2005). Again, early events seem crucial.

Age at immigration is irrelevant to an early onset condition such as autism, but autism is strikingly (as much as 10-fold) increased in 2nd generation Caribbean or African immigrants born in the UK, compared to children of white UK-born mothers, as discussed below (Keen et al., 2010).

These findings implicate crucial early events in the perinatal period or early childhood as risk factors for depression, schizophrenia and autism. Do these more specific findings, usually attributed to the psychosocial chal-

lenges of immigrant status, differentiate these psychiatric disorders from the chronic inflammatory disorders? The answer to this question is again no, as explained in the next section.

Age at immigration, 2nd generation immigrants and chronic inflammatory disorders

Migration has clear effects on the prevalence of MS, and the crucial events that confer increased risk for the disease occur very early in life, as is true for the psychiatric disorders (reviewed and referenced in Gale and Martyn, 1995; Milo and Kahana, 2010). Iranians who migrate to Sweden have twice the prevalence of MS seen in their birth country (Ahlgren et al., 2011). Interestingly, if the 2nd (or later) generation immigrants return to their developing country of origin, they retain their increased susceptibility to MS, which remains higher than in the local population that was not born abroad (Cabre, 2009). A similar phenomenon was seen when people born in the United Kingdom (UK: a high MS country) migrated to South Africa (SA: a low MS country). Migration from the UK to SA was protective when the migrant was a child, whereas adult migrants retained their high UK prevalence of MS (Dean, 1967). Analysis of this and other studies suggests that the environmental factors that protect from or predispose to MS act during the first two decades of life (Gale and Martyn, 1995; Milo and Kahana, 2010). The same is true for T1D. Here the crucial factor is to have been *born* in the receiving developed country, again suggesting that relevant environmental factors act very early, or even in the prenatal period (Söderström et al., 2012).

The role of migration in conferring risk for allergic disorders has been intensively examined. A study of chil-

dren adopted into Sweden from developing countries showed that the prevalences of asthma, hay fever and eczema were highest in those adopted when less than 2 yrs. old (*Hjern et al., 1999*). Similarly, for Mexican immigrants to the USA, the prevalence of asthma was highest for those born in the USA, while in those not born in the USA, the prevalence of asthma decreased as the age at immigration increased (*Eldeirawi et al., 2009*). This effect of age at the time of childhood immigration was also seen in immigrants to Israel from the former Soviet Union or Ethiopia who were assessed when 17 years old (*Pereg et al., 2008*). These observations suggest the importance of early environmental influences for allergy/asthma risk, a conclusion that is powerfully supported by evidence that prenatal exposure (i.e. of the pregnant mother) to the farming environment protects the infant against some allergic manifestations (*Ege et al., 2008; Schaub et al., 2009*). This is discussed later in another context.

Finally, a definitive study of all first- and second-generation immigrants in Sweden between January 1, 1964, and December 31, 2007 showed that some 1st generation immigrants remain partially protected from both ulcerative colitis (UC) and Crohn's disease (CD), presumably by environmental factors encountered in their countries of origin, but the diseases increased in prevalence in 2nd generation immigrants, relative to 1st generation immigrants (*Li et al., 2011*). Similarly, the prevalence of UC in South Asian immigrants to Leicester in the UK was higher in 2nd than in 1st generation immigrants (*Carr and Mayberry, 1999*). This again implicates perinatal factors as potentially causative of this migration effect.

Thus the influence of immigration, acting via factors that occur perinatally

or very early in life, is equally consistent and highly apparent for both psychiatric and chronic inflammatory disorders.

Birth order

The study of disease prevalence in relation to birth order focuses rather specifically on perinatal factors. It was the observation that having multiple older siblings, especially male ones, provided some protection against hay fever that led to the first use of the term "Hygiene Hypothesis", highlighting the notion that grubby older brothers provided an expanded and protective microbiological environment (*Strachan, 1989*). However, subsequent studies of the effects of birth order on other inflammatory conditions have painted a less consistent picture. For example, where IBD is concerned birth order effects are sometimes significant, but the direction of the association is inconsistent (*Hampe et al., 2003; Van Kruiningen et al., 2007*). Results are also often contradictory in MS (*Zilber et al., 1988*). Similarly variation was seen in a meta-analysis of data from studies of childhood onset T1D, but overall, there does appear to be increased prevalence in firstborn children (*Cardwell et al., 2011*).

What about the psychiatric disorders? Again the picture is rather variable. For depression an association with birth order is sometimes reported, but the relationship is inconsistent (*Bergeron et al., 2007; Schmidt and Tolle, 1977; Wells et al., 1985*). The effect may be more pronounced for autism and schizophrenia. A comprehensive Finnish study of families with at least two children, one of whom was schizophrenic, found that being the first-born was a significant risk factor for schizophrenia, but the protective effect of older siblings was complex and depended on how much older they

were (*Haukka et al., 2004*). The relevance of birth order to autism has been reviewed in detail elsewhere (*Becker, 2007*). Briefly, the risk of autism has been shown to fall as the number of older siblings rises in studies in the United States, Western Australia and England, though not every study shows

this (*Becker, 2007*). In view of the significant epidemiological association with familial allergic disorder, where the birth order effect is clear, as mentioned earlier, this is of great interest (discussed in *Meyer et al., 2011; Onore et al., 2012*).

THE OLD FRIENDS HYPOTHESIS AND IMMUNOREGULATION

These epidemiological findings, when applied to the chronic inflammatory disorders, are usually explained by the Hygiene Hypothesis or by the variant of that hypothesis that we prefer, the “Old Friends” hypothesis (plus a few additional recent factors discussed later). The Old Friends hypothesis states that mammals co-evolved with an array of organisms and conditions that, because they needed to be tolerated, took on a role as inducers of immunoregulatory circuits (*Rook, 2010; von Hertzen et al., 2011a*). Such organisms and conditions include various microbiotas and commensals (gut, skin, lung etc.), chronic infections picked up at birth, helminths that persist for life, and environmental organisms from animals, mud and untreated water with which we were in daily contact. For example, helminthic parasites need to be tolerated because although not always harmless, once they are established in the host any effort by the immune system to eliminate them is futile, and merely causes tissue damage (*Babu et al., 2006*). Contact with the “Old Friends” rapidly diminishes when industrialization occurs, and we start to inhabit a plastic and concrete environment, to consume washed food and chlorine-treated water, and to minimize our contact with mud, animals and faeces. This withdrawal of the organisms that drive immunoregulatory circuits results in defective immunoregulation

that, depending on the genetic background of any given individual, can manifest as a variety of chronic inflammatory disorders, including allergies, IBD and autoimmunity. In contradistinction to early articulations of the hygiene hypothesis that focused more exclusively on allergic conditions, we now know that a failure of immunoregulatory mechanisms really can lead to simultaneous increases in diverse types of pathology. For example, genetic defects of the gene encoding the transcription factor *Foxp3* lead to the X-linked autoimmunity–allergic dysregulation syndrome (XLAAD) that includes aspects of allergy, autoimmunity and enteropathy (*Wildin et al., 2002*).

The crucial underlying points are these. First, the chronic inflammatory disorders all show evidence of failed immunoregulation (*Rook, 2009*). Secondly, “Old Friends” (such as helminths, non-pathogenic environmental bacteria [pseudo-commensals] or certain gut commensals, probiotics) can be shown to drive immunoregulation, and to block or treat models of *all* of these chronic inflammatory conditions (*Karimi et al., 2009; Osada and Kanazawa, 2010; Round and Mazmanian, 2009*). Thirdly, some Old Friends, or molecules that they secrete, can be shown to specifically expand Treg populations (*Atarashi et al., 2011; Grainger et al., 2010; Karimi et al.,*

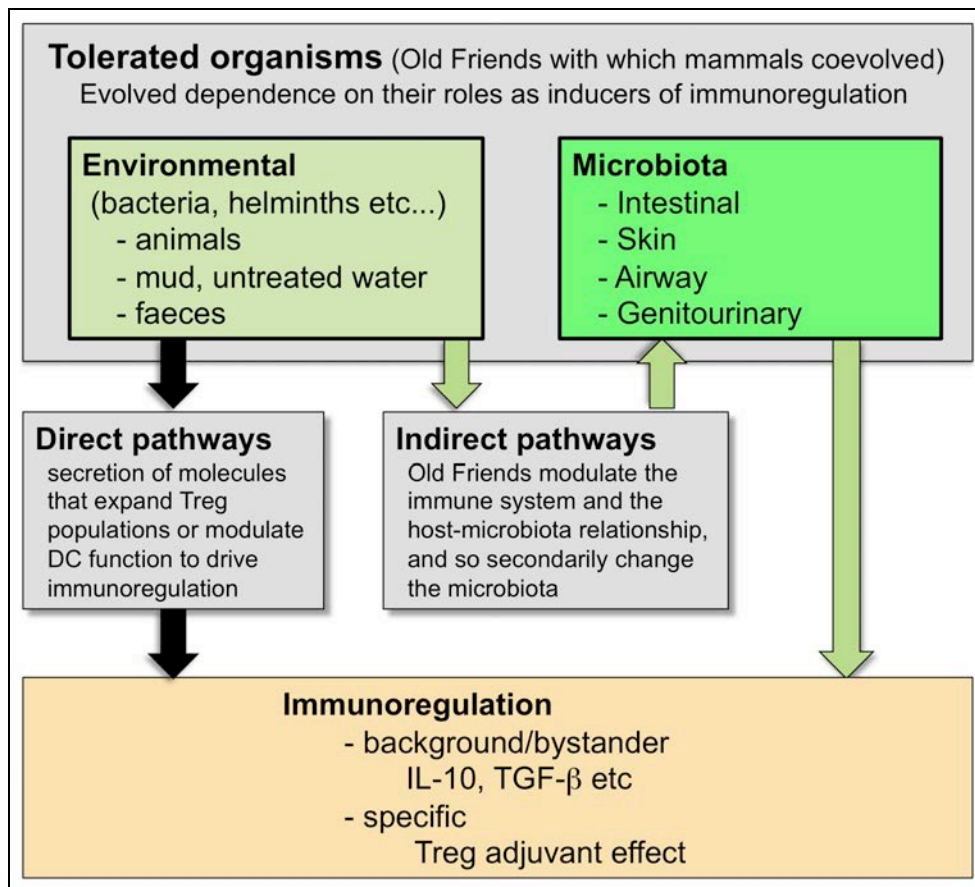


Figure 1: Microorganisms with which mammals co-evolved (“Old Friends”), and that had to be tolerated, have been entrusted with roles in the induction of immunoregulation. These include direct effects on the immune system (for example, driving expansion of Treg, and of regulatory DC), and indirect effects secondary to changes in the host-microbiota relationship. The latter causes changes in the composition of the microbiota that then secondarily modify immune function.

2009; Round et al., 2011), or to cause dendritic cells (DC) to switch to regulatory DC that preferentially drive immunoregulation (Smits et al., 2005). Finally, when MS patients become infected with helminths, the disease stops progressing, and circulating myelin-recognising regulatory T cells (Treg) appear in the peripheral blood (Correale and Farez, 2007; Correale and Farez, 2011), indicating that the helminths act as Treg adjuvants. This is an exciting observation that has led to formal clinical trials (Fleming et al., 2011).

Old Friends Hypothesis and the gut Microbiota

We emphasise that many “Old Friends” are (or were, until changed or depleted) gut microbiota, or gut parasites (Atarashi et al., 2011; Grainger et al., 2010; Round et al., 2011). Others were environmental saprophytes in mud and untreated water that inevitably passed through the gut in large numbers every day (Le Bert et al., 2011). Moreover new data show that other microbiota such as those of the skin or oral mucosa can also be relevant to immunoregulation (Friberg et al., 2010;

Hanski et al., 2012; Singhal et al., 2011). But one of the most important discoveries in recent years is the fact that manipulations of the immune system may act *indirectly* via changes in the gut microbiota. For example, Wen and colleagues showed that specific pathogen free (SPF) non-obese diabetic (NOD) mice that spontaneously develop a condition resembling T1D, are protected from the disease following knockout of the gene encoding MyD88 (an adaptor for multiple Toll-like receptors) (Wen et al., 2008). However this did not mean that MyD88 was directly involved in the autoimmune response to β cells in the pancreas. Rather it emerged that the modification of the immune system resulting from knocking out MyD88 caused profound changes in the interactions between the immune system and the microbiota, leading to changes in the composition of the latter. It was these changes in the composition of the microbiota that were responsible for the immunoregulatory effect that blocked the autoimmune process. Thus changes in the microbiota, which is profoundly different in Europeans than in people living in a traditional rural African village (De Filippo et al., 2010), must be regarded as part of the Old Friends hypothesis, whether these changes are attributable to diet (Cani and Delzenne, 2011) or to diminished exposures. In either case altered exposure to “Old Friends” will simultaneously exert direct effects on the immune system, and indirect effects via secondarily induced changes in the microbiota (Figure 1).

The Old Friends hypothesis and genetics

In parts of the world where there was a heavy load of organisms causing immunoregulation (such as helminths), there has been selection for single nu-

cleotide polymorphisms (SNP) or other variants to partially compensate for this immunoregulation, or to combat new infections such as malaria that spread from gorilla to man about 10,000 years ago (Liu et al., 2010; Sotgiu et al., 2008). This is seen for several pro-inflammatory cytokines (Fumagalli et al., 2009), IgE (Barnes et al., 2005) and STAT6, a transcription factor involved in Th2 responses (Moller et al., 2007). There is also an increased frequency of a truncated form of the serotonin transporter promoter that also has a marked pro-inflammatory effect (Fredericks et al., 2010). The problem here is clear (Figure 2). As soon as the immunoregulation-inducing organisms are withdrawn by the modern lifestyle, these genetic variants lead to excessive inflammation, and become risk factors for chronic inflammatory disorders (Barnes et al., 2005; Fredericks et al., 2010; Fumagalli et al., 2009; Moller et al., 2007). This constitutes a second layer of evolved dependence on the continuing presence of the “Old Friends” (Figure 2).

This is important because work that identifies proximate “causes” for diseases that were rare or non-existent before the Second Epidemiological Transition may merely be unravelling a problem that would be irrelevant if the microbial status of the modern world could be returned to that seen in the paleolithic. For instance, the recent claim to have discovered that the “cause” of Crohn’s disease is a genetically determined defect in the homing of neutrophils (Smith et al., 2009) is difficult to reconcile with the fact that 100 years ago the disease barely existed. But recent environmental changes could conceivably have caused this phenotype to become a risk factor (Figure 2).

It is clear how the Old Friends hypothesis can provide an explanation for

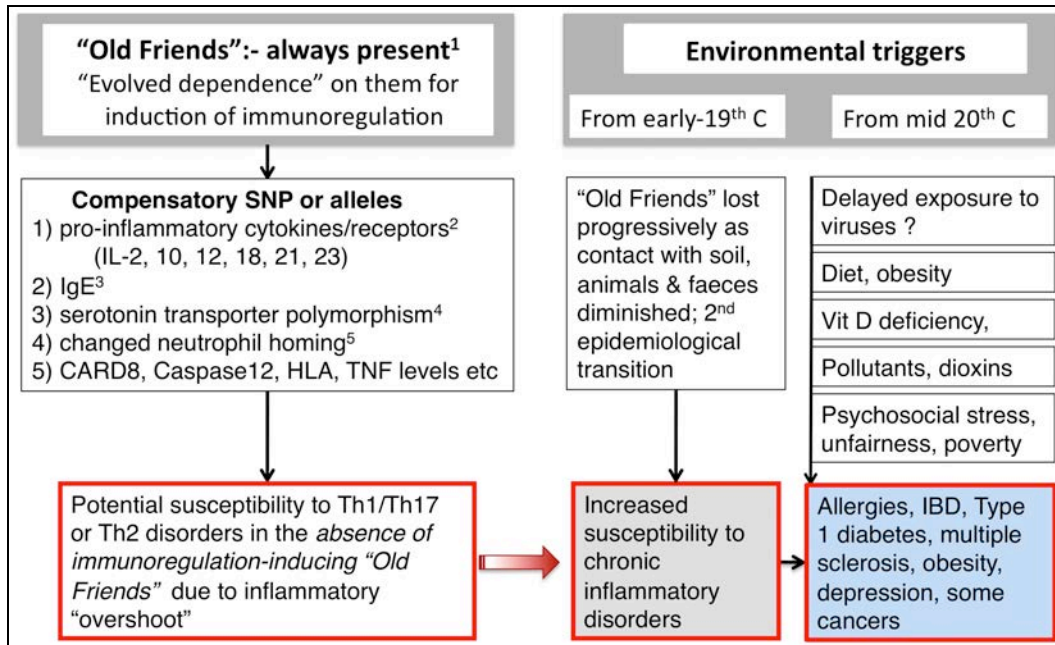


Figure 2: Interaction of genetics and loss of the “Old Friends”. The Old Friends had to be tolerated and so co-evolved roles as triggers of immunoregulatory pathways. In areas with very high loads of these and other organisms, particularly helminths, compensatory genetic variants accumulated, to partially restore inflammatory responses. In the absence of the Old Friends, not only is immunoregulation inadequately primed, but also these genetic variants cause excessive inflammation and become risk factors for chronic inflammatory disorders. Genetic variants that were advantageous, and did not cause disease in the past, start to do so when the Old Friends are lost after the 2nd epidemiological transition (referenced in main text). More recently several aspects of modern life are exacerbating the effects of the lack of “Old Friends” at the level of immunoregulation. Obesity is associated with altered gut microbiota and excessive release of pro-inflammatory cytokines. Stress also alters gut microbiota, and drives corticotropin-releasing hormone (CRH) that increases permeability of the gut mucosa. Increased absorption of lipopolysaccharide (LPS) and other microbial components drives further release of pro-inflammatory cytokines. Lack of vitamin D exacerbates immunodysregulation, as does the triggering of Th17 cells by dioxins. Meanwhile the changes in the gut are also likely to impact on Th17 development. Viruses that used to be encountered harmlessly in early infancy (under cover perhaps of maternal antibody) can trigger autoimmunity if encountered for the first time later in life. Psychosocial stressors exacerbate these problems, as outlined in the main text.

rural-urban differences in the prevalence of chronic inflammatory diseases, and for the consequences of immigration from poor to rich countries. The rural environment and above all the farming environment, provide a microbiological input that is closer to that

with which we evolved, so more likely to prime appropriate immunoregulation. Similarly, the developing country lifestyle exposes us to more diverse and numerous Old Friends than does the rich Western lifestyle.

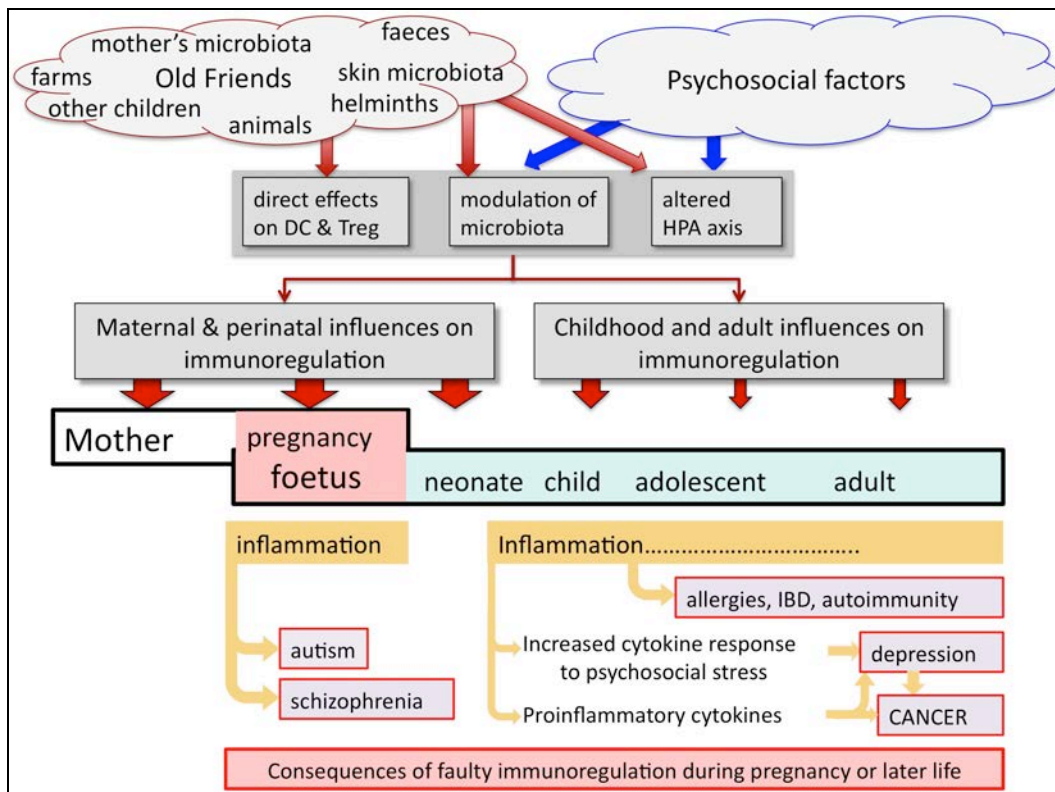


Figure 3: Immunoregulatory influences throughout life, and the consequences of their failure. The immunoregulatory Old Friends and psychosocial factors influence immunoregulation, and converge strikingly on the microbiota and HPA axis in the perinatal period. Withdrawal of Old Friends, and/or perinatal psychosocial stressors predispose to inflammatory disorders. During pregnancy this can predispose to neurodevelopmental problems such as autism and schizophrenia. In adolescence or adult life poor immunoregulation can predispose to chronic inflammatory disorders or to depression or to both together. A late consequence, exacerbated by depression, is inflammation-associated oncogenesis, and promotion of cancer growth and spread.

OLD FRIENDS AND PSYCHOSOCIAL STRESSORS IN THE PERINATAL PERIOD

The previous sections have used three psychiatric disorders to point out that aspects of their epidemiology that are usually interpreted as indicating a crucial role for exposure to psychosocial stressors, are not significantly different from the findings that emerge from the epidemiology of chronic inflammatory disorders such as allergies, IBD and autoimmunity. In the context of the latter disorders these findings are usu-

ally explained by the “Old Friends” hypothesis. Does this mean that we should be changing our view of the role of the psychosocial stressors in psychiatric disease, or should be blaming psychosocial stressors for these chronic inflammatory disorders? The answer, we suggest, is both. Psychosocial stressors and inflammation are closely linked, as discussed below.

Perinatal psychosocial stress and immunoregulation

Although immigrants certainly meet a changed microbial environment, it is equally certain that they face a barrage of psychosocial stressors. Indeed we know that prenatal psychosocial stress (i.e. experienced by the pregnant mother) or early postnatal stress can cause long-term changes in neurogenesis (reviewed in Korosi et al., 2012), in cognition, memory (Entringer et al., 2009a) and in hypothalamic-pituitary-adrenal (HPA) axis function (Entringer et al., 2009b). These dilemmas are partly resolved when one considers the close links between psychosocial stressors and the immune system. We suggest below that psychosocial stressors will exacerbate the immunoregulatory dysfunction caused by the lack of “Old Friends”, while the lack of “Old Friends” will exacerbate the inflammatory effects of psychosocial stressors (Figure 3). There are clear synergistic pathways to the simultaneous development of a mixture of psychiatric and chronic inflammatory problems. The crucial point is that perinatal stress also has long-term modulatory effects on immune system function. This issue is the topic of the following sections.

Perinatal stress and long-term changes to immune function

Many studies in animals and humans have shown that a variety of stressors, including psychosocial ones, during pregnancy activate inflammation (Haroon et al., 2012; Howerton and Bale, 2012). For example, prenatal maternal stress during otherwise normal human pregnancies was associated with raised circulating levels of the pro-inflammatory cytokines IL-6 and tumour necrosis factor- α (TNF- α), raised C-reactive protein (CRP) and low levels of the anti-inflammatory cytokine IL-10 (Coussons-Read et al.,

2005). Similarly overall stress levels during pregnancy correlated with increased release of IL-1 β and IL-6 by lymphocytes stimulated *in vitro* during the 3rd trimester (Coussons-Read et al., 2007).

However, the important point here is that perinatal stress results in adults who themselves show exaggerated inflammatory responses to stress (Carpenter et al., 2010; Danese et al., 2007, 2008). For example, peripheral blood mononuclear cells from healthy young women whose mothers had experienced major negative life events during pregnancy showed altered responses to phytohaemagglutinin compared to cells from a control group. There was a bias towards production of T-helper 2 (Th2) cytokines and both IL-6 and IL-10 were also significantly elevated (Entringer et al., 2008). Similarly maltreated children develop higher levels of IL-6 in response to a standardized social stressor (the Trier Social Stress Test; TSST) when tested as adults in comparison to a non-maltreated control group (Carpenter et al., 2010; Pace et al., 2006), and maltreated children tend to have higher levels of CRP 20 years later (Danese et al., 2007). Low early life social class (socio-economic status; SES) is similarly associated in adult life (aged 25-40) with increased production of IL-6 in cultures of peripheral blood leukocytes stimulated with ligands for toll-like receptor 3 (TLR3) or TLR5 (Miller et al., 2009b). These findings all imply that perinatal stress itself leads to long-lasting problems with immunoregulation (Carpenter et al., 2010; Danese et al., 2007, 2008). Interestingly, negative life events during the first years of life, whether they affect the child directly, or indirectly via traumatic experiences of the mother, predispose to the autoimmune disease T1D (reviewed in Peng and Hagopian, 2006; Sepa et al.,

2005; Vlahjinac et al., 2006). It is likely that this reflects an influence of perinatal negative life events on subsequent immunoregulation.

Many mechanisms are involved in the relationship between perinatal stress and immune activation (Haroon et al., 2012; Howerton and Bale, 2012). We consider two particularly relevant and important mechanisms below; the HPA axis and the microbiota.

Perinatal stress and long-term changes to the HPA axis

In monkeys, exposure to high levels of maternal stress hormones (whether induced by stressing the mother, or by injecting dexamethasone or adrenocorticotropic hormone [ACTH] during pregnancy) causes prolonged changes in the reactivity of the infant's lymphocytes *in vitro* (Coe et al., 1996, 1999). Numerous animal models have demonstrated associations between prenatal stress and long-term alterations in HPA axis function (Kapoor et al., 2006; Weinstock, 2005).

Healthy young human adults who had been exposed to "prenatal stress", because their mothers had experienced severe negative life events such as the death of someone close during pregnancy, responded differently to a standardized social stressor (TSST) when compared to an age-matched comparison group of healthy young women who had not been exposed to prenatal stress. The prenatal stress group had lower cortisol levels ($p=0.007$) before the TSST, and a larger increase in response to the TSST ($p=0.03$) (Entringer et al., 2009b). Similar changes have been associated with severe stress in early childhood (Heim et al., 2000). Moreover adults with PTSD symptoms who were abused as children show increased NF κ B and decreased glucocorticoid sensitivity and these two findings are highly correlated

(Pace et al., 2012). This is consistent with the idea that HPA axis changes as a result of early abuse or neglect contribute to increased inflammatory drive.

Interestingly, a transcriptional profiling of adults whose childhood background had been of low or high socioeconomic status (SES) revealed that those from a low childhood SES background had up-regulation of genes bearing response elements for the cAMP response element binding (CREB)/activating transcription factors (ATF) family of transcription factors involved in signalling to leukocytes, heightened expression of transcripts bearing response elements for nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B), and down-regulation of genes with response elements for the glucocorticoid receptor (GR) involved in anti-inflammatory function (Miller et al., 2009b). A similar pro-inflammatory bias in gene expression emerged from a comparison of asthmatic children from low or high SES backgrounds (Chen et al., 2009). In conclusion, perinatal and early neonatal stressors are likely to induce long-term changes in HPA axis function (Figure 3), with obvious consequences for immune function.

Although perhaps beyond the scope of this discussion document, it is worth noting briefly that the persistence into adult life of HPA axis effects triggered in the perinatal period might be explained by epigenetic changes, such as altered DNA methylation patterns (Guo et al., 2011; Miller et al., 2008; Weaver et al., 2004), or by shortened telomere length, and reduced telomerase activity (Choi et al., 2008; Entringer et al., 2011; Jacobs et al., 2011; Ornish et al., 2008). Reduced telomere length is associated with inflammation and autoimmunity as well as with premature immunosenescence (Carrero et al., 2008; Fitzpatrick et al., 2007; Hohen-

sinner et al., 2011), though whether as cause or consequence is not certain.

Perinatal stress and long-term changes to the intestinal microbiota

It has been known for some time that stress alters the microbiota of experimental animals (Kiliaan et al., 1998), and the same is true of the microbiota of severely stressed critically ill humans, where the changes are rapid and prolonged (Hayakawa et al., 2011). Crucially important in the current context is the observation that the stress of maternal separation for 3 hours per day from post-natal days 2-12 has long-term effects on the subsequent 16S rRNA diversity of the microbiota that is still apparent when the pups become adult rats, compared to control adults that had not been exposed to maternal separation as pups (O'Mahony et al., 2009). Similarly, prenatal stressors have been shown to alter the microbiome in rhesus monkeys by reducing the overall numbers of bifidobacteria and lactobacilli during adulthood (Bailey et al., 2004).

This might be an important mechanism because the nature of the microbiota during the first weeks of life has a profound effect on development of the CNS and the HPA axis. For example, germ-free mice have increased motor activity, reduced anxiety, altered gene expression in several brain areas, and increased turnover of noradrenaline, dopamine and 5-HT in the striatum (Heijtz et al., 2011). These abnormalities persist into adulthood, and cannot be corrected by reconstitution of the microbiota of adult animals (Heijtz et al., 2011). Moreover, the nature of the microbiota is crucial. In another study it was noted that germ-free mice had abnormal responses to restraint stress, specifically increased ACTH and corticosterone responses, together with reduced expression of brain-derived neu-

rotrophic factor (BDNF) in cortex and hippocampus, reduced glucocorticoid receptors (GR) in the cortex, and raised corticotrophin-releasing hormone (CRH) in the hypothalamus (Sudo et al., 2004). Oral reconstitution with a normal microbiota normalised the HPA axis function if done at 6 weeks, but not if done later. Early mono-association with *Bifidobacterium infantis* also normalized HPA axis function, but mono-association with enteropathogenic *E. coli* made the abnormalities more severe. Thus not only is the microbiota modified by stress, but it is also involved in development of the CNS, so given these observations it is possible that perinatal stress might exert physiological effects on the brain in adulthood at least in part via its impact on the microbiota

Consequences of changes to the intestinal microbiota

The nature of the microbiota is likely to modulate both the subsequent response to psychosocial stressors and the functions of the immune system. When mice are stressed by being housed with an aggressive dominant male, they develop altered microbiota, and raised circulating levels of IL-6, TNF and IFN- γ . However, if the microbiota is depleted by an antibiotic cocktail, the same social stressor fails to cause increased pro-inflammatory cytokine levels (Bailey et al., 2011). It seems that increased permeability in the gut caused by stress, results in increased intake of LPS and other pro-inflammatory molecules, which exert a positive feedback on the stress-induced inflammatory response. Stress-induced increases in gut permeability might be partly due to release of CRH by T cells, and by cells within the submucosa and muscle layers of the gut, myenteric neurons, serotonin-containing enterochromaffin cells, and lamina propria

cells of the mucosa in stomach and colon (*Stengel and Tache, 2009*). CRH is not only a regulator of intestinal permeability (*Gareau et al., 2008; Teitelbaum et al., 2008*), but also a potent pro-inflammatory cytokine in its own right in the periphery of the body (*Calcagni and Elenkov, 2006*). These changes may help explain the finding that depressed patients have raised levels of antibody to a range of intestinal bacteria (*Maes et al., 2008*).

Alterations in the microbiota will also impact immunoregulation (Figure

3). The fundamental role of the microbiota in immunoregulation has been reviewed extensively elsewhere (*Round and Mazmanian, 2009*). The organisms that comprise the microbiota can be thought of as one component of the “Old Friends”. Recent observations suggested that, as in animals, in humans fluctuations in the microbiota early after surgery (bone marrow transplantation) may lead to an increased risk of immunoregulatory failure, manifested in this study as graft-versus-host disease (*Jenq et al., 2012*).

SYNERGY BETWEEN THE OLD FRIENDS MECHANISM AND STRESS

The previous section makes clear that perinatal stress can cause long-term dysregulation of the immune response, both via changes to the HPA axis and changes to the microbiota. (No doubt there are other changes too, e.g., changes to the sympathetic and parasympathetic systems, but these are beyond the scope of this paper). However we have also pointed out that in the modern urban environment a second mechanism is also reducing the efficiency of immunoregulatory mechanisms: depletion of immunoregulation-inducing “Old Friends”. In this section we explore the hypothesis that these two mechanisms interact to modulate those psychiatric disorders where inflammation is known to play a role. As outlined in the section immediately after the introduction, inflammation is implicated in depression (*Raison et al., 2010*), and in driving the developmental abnormalities that underlie many cases of schizophrenia and autism (*Meyer et al., 2011*) and in the health consequences of low socio-economic status (*Hemingway et al., 2003; Miller et al., 2009b; Tung et al., 2012*). There are several ways in which the psychosocial and microbial pathways might

work together via immunoregulation to alter patterns of psychiatric disease.

Urban versus rural upbringing, and response to an experimental stressor

A recent functional magnetic resonance imaging (fMRI) study compared the effects of an experimental social stressor on individuals brought up in urban or rural environments. Urban versus rural upbringing correlated with significant differences in activation of the perigenual anterior cingulate cortex, a region involved in regulation of negative affect and the physiological stress response (*Lederbogen et al., 2011*). The authors attributed their findings to putatively different levels of social stressors in individuals with an urban versus rural upbringing. But would social stressors in children differ significantly in the two environments in a wealthy European country (Germany)? It is equally likely that the findings were due to the “Old Friends” mechanism, leading to diminished regulation of pro-inflammatory mediators in those subjects who had an urban upbringing. Indeed the protective effects of the German farming environment against allergies and early onset in-

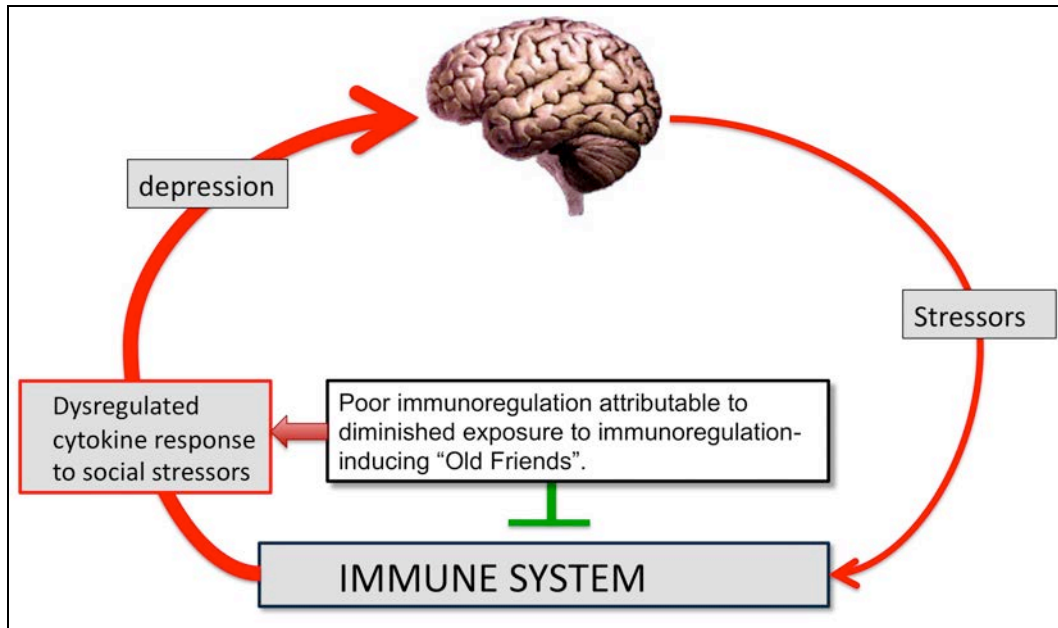


Figure 4: Exaggerated cytokine release in response to a psychosocial stressor leading to depression. Populations that have undergone the 2nd epidemiological transition have minimal exposure to immunoregulation-inducing “Old Friends” such as helminths. The consequent diminished efficiency of immunoregulation is manifested as rising prevalences of chronic inflammatory disorders such as allergies, autoimmunity and inflammatory bowel disease (IBD). Poor immunoregulation will also leave the individual susceptible to excessive and prolonged cytokine release in response to psychosocial stressors, which may result in inappropriate triggering of depressive episodes.

inflammatory bowel disease are well documented and require that a child be exposed to the farming environment during the first 2.5 years of life...a rural upbringing (Radon et al., 2007; Riedler et al., 2001). The authors of the fMRI study did not measure the stress-induced levels of circulating pro-inflammatory cytokines in the two populations. The “Old Friends” view of the data would postulate higher levels in the subjects who had urban upbringings.

Depression

Exposure to psychosocial stressors in later life would be expected to cause greater increases in circulating pro-inflammatory cytokines in individuals with poor immunoregulation as a consequence of lack of exposure to Old

Friends. Thus people living in rich developed countries should have a greater likelihood of becoming depressed when confronted with a given level of psychosocial stress, compared to the citizens of a developing country environment rich in immunoregulation-inducing “Old Friends” (Figure 4). We know that depressed individuals with histories of early life trauma or neglect release more IL-6 in response to the TSST (Pace et al., 2006). To put it another way, it might be that depression is increasing in the USA (Compton et al., 2006) not because our lives are becoming more stressful, but rather because in developed countries our immune systems release more depression-inducing pro-inflammatory cytokines in response to any given level of psychosocial stressor. This would imply

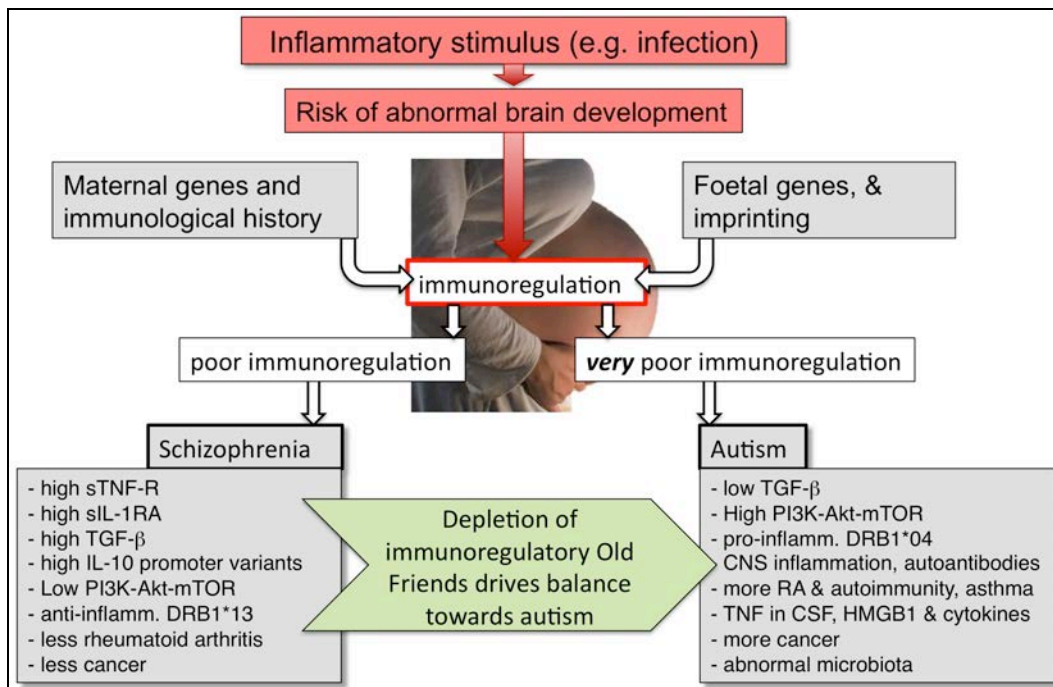


Figure 5: Reduced efficiency of immunoregulation during pregnancy, due to loss of the immunoregulation-inducing Old Friends could explain the reduction in schizophrenia and the increase in autism that are suggested in the recent literature (see main text). Both disorders are associated with inflammatory episodes during pregnancy that lead to neurodevelopmental abnormalities. But the severity of the failure of immunoregulation is much greater in autism, and persists into adulthood. The immunological points listed in the boxes at lower left and right are taken from, and fully explained within, the references discussed in the main text.

that the prevalence of depression should be greater in developed countries than in developing ones. Comparative studies are difficult to do but this is indeed what is indicated by data gathered by the World Health Organization (Ustun et al., 2004).

Schizophrenia and autism

In developed countries pregnant women will themselves have poor immunoregulation as a result of reduced contact with immunoregulation-inducing Old Friends. This will mean that they have reduced ability to shut off or modulate inflammatory episodes during pregnancy (Figure 5), such as those involved in driving the developmental abnormalities that lead to many cases

of autism or schizophrenia (Meyer et al., 2011), (see Figure 3). Because the inflammatory component of autism is much greater than that seen in schizophrenia, one likely consequence of failing immunoregulation would be a reduction in the prevalence of schizophrenia, and an increase in autism. There is evidence that autism is becoming more common (Williams et al., 2006) while schizophrenia may be showing the opposite trend (Der et al., 1990; Woogh, 2001). It is of particular interest to note that genetic studies have revealed that some maternal genes, such as HLA DR4, are involved in modulating the risk of these disorders even when not inherited by the foetus (Johnson et al., 2009). It will be

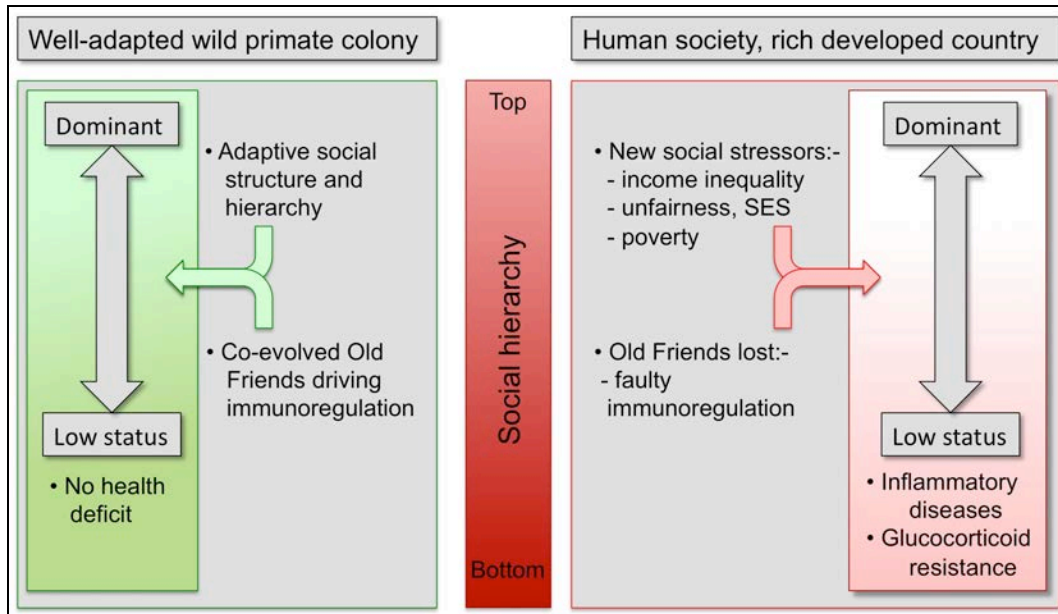


Figure 6: The consequences for long-term health of socioeconomic status and dominance hierarchies. It is often assumed that low position in a dominance hierarchy automatically leads to health deficits, particularly chronic inflammatory problems and cardiovascular disease. This seems maladaptive in a Darwinian sense because low status individuals may later become leaders and breeders. Some recent studies have revealed that in monkeys and primates low status can be compatible with health (i.e. no evidence of stress or raised glucocorticoids). This is likely to be the evolutionarily adaptive state, prevalent in the wild, when habitat is undisturbed and unrestricted, and human observers are absent. We suggest that the health penalty of low socioeconomic status (SES) in modern human communities is attributable to failing immunoregulation (loss of Old Friends) superimposed on the social stress of poverty and perceived “unfairness” (income inequality etc.).

interesting to ask whether many of these genes, like HLA DR4 (*Johnson et al., 2009*), have a role in the control of inflammation.

Health deficits of low socioeconomic status

In the Whitehall study of UK civil servants, circulating levels of CRP and IL-6 were inversely correlated with employment grade, implying an inverse relationship between socioeconomic status (SES) and background inflammation (*Hemingway et al., 2003*). This and other studies show that this gradient is associated with a health deficit that is measurable at every rank below the top of the gradient, despite the fact

that at these upper levels diet and nutrition and healthcare access are not significantly different (*Marmot, 2006; Sapolsky, 2004*). A similar phenomenon has been seen in rhesus macaques. In this species there is a linear dominance hierarchy. It has emerged that the lower the position of a given animal within this hierarchy in a captive colony, the higher the expression in the peripheral blood of genes involved in inflammatory responses (*Tung et al., 2012*). There are also links with chronic inflammatory disorders (*Chen et al., 2009*), and low SES in early life leads to decreased glucocorticoid sensitivity and increased pro-inflammatory signalling in adulthood when cells are

stimulated with various ligands *in vitro* (Miller et al., 2009b).

While these findings are often thought to indicate that psychosocial stress increases as one's position in a hierarchy decreases, it may well be that disruptions in our relationship with Old Friend organisms may contribute to the association between status and health and inflammation. This possibility is highlighted by the fact that the Old Friends mechanism also impacts serum CRP levels (McDade et al., 2010). CRP is lower in adults who experienced greater microbial exposures in childhood (McDade et al., 2010). Moreover when CRP levels were followed in the same individuals over several months it emerged that in a developing country the baseline CRP is very low (i.e. fully shut off), with intermittent peaks when inflammation is needed to cope with infection. Thus the prevalence of "high risk" CRP (>3 mg/l) is greater in a remote Amazonian population with high rates of infectious disease than in the USA (Gurven et al., 2008), but these are *transient peaks* triggered by infection (McDade et al., 2012). In contrast, in the USA CRP is often not fully turned off despite lack of a valid requirement for inflammation (McDade et al., 2012). There is chronic persistent low-level inflammation indicating poor immunoregulation (McDade et al., 2012), and it is this uncontrolled chronic inflammation that can predispose to chronic inflammatory disorders, including the psychiatric effects outlined above.

A simple hypothesis therefore would be that the health deficit driven by low SES is exaggerated in individuals deprived of immunoregulation-inducing Old Friends (Figure 6). If we could compare the health gradients of SES hierarchies in developing and rich countries, an Old Friends perspective would predict that we would find less

health deficit at the bottom end of the social gradient in developing countries (assuming that we could eliminate confounders such as unequal access to health care, etc.) than in a developed ones.

But there is also the possibility of a much stronger version of this hypothesis. Perhaps the health deficit of low SES does not occur at all unless immunoregulation is compromised. The notion that any position below the top of a dominance or SES hierarchy is associated with long-term inflammation-mediated damage to health is anti-intuitive and incompatible with Darwinian medicine. Subordinate individuals may later become dominant and play crucial roles as the main leaders and breeders (reviewed in Sapolsky, 2004). It is maladaptive for such future breeding stock to receive permanent damage (for instance to the cardiovascular system) earlier in life. Most observations of stress and/or inflammation in subordinate animals have been made in populations that were captive (so partly depleted of Old Friends), and/or undergoing social disruption as a result of human observers and interventions and perimeter fencing. For example in many troops of macaques or baboons subordinate animals have high basal glucocorticoid levels, but in other troops of the same species this effect is not seen (reviewed in Sapolsky, 2004). The latter, more difficult to observe and record, is likely to be the adaptive situation, and the norm in thriving undisturbed communities. We tentatively suggest that in human communities, when confounders such as access to nutrition and health care have been eliminated, it will be found that the SES-linked health deficit is a Western artefact of modern social stressors (poverty, unfairness, income disparity) driving inflammation in the context of a dysregulated immune system (Figure 6).

FINAL REMARKS

The purpose of this paper is to explore the relationship between the Hygiene or “Old Friends” hypothesis and the psychosocial stressor hypothesis. The “bottom line” is found in Figures 4, 5 and 6 where we illustrate diagrammatically the ways in which we suggest that these two mechanisms, both equally valid and proven, interact and contribute to the changing patterns of disease in the modern world. These consequences are relevant both to psychiatric disorders and to chronic inflammatory disorders.

This paper is not intended to be a comprehensive review. We did not include the role of immunoregulation and inflammation in cancer apart from a brief comment in the introduction, because this topic was extensively reviewed elsewhere (*Rook and Dalgleish, 2011; von Hertzen et al., 2011b*). Similarly, we do not include discussion of all the factors known to be relevant to associations between environmental conditions, immune function and physical and mental health (though some of these are listed in Figure 2). For example diet is a major factor that has been omitted. Diet has profound effects on the microbiota, and therefore indirectly on immunoregulation (*Maslowski and Mackay, 2011*). Another important factor is delayed exposure to viruses caused by hygienic modern living conditions. Many viruses are harmless when met by neonates, perhaps because of the presence of maternal antibodies, but when en-

countered later such viruses may trigger inflammatory disorders such as allergies and autoimmunity (*Filippi and von Herrath, 2008; Harrison et al., 2008; Serreze et al., 2000*). Lack of vitamin D is also a feature of modern western lifestyles that has a major impact on immunoregulation and has been implicated in schizophrenia (*McGrath et al., 2010*) as well as in several chronic inflammatory disorders (*Hewison, 2010; Poon et al., 2004; VanAmerongen et al., 2004*), and exposure to modern pollutants such as dioxins might drive pro-inflammatory Th17 cells via the aryl hydrocarbon receptor (*Veldhoen et al., 2008*).

Similarly, had space permitted there are other psychiatric conditions that could have been included in the discussion because of evidence for inflammatory components (attention deficit hyperactivity disorder [ADHD], and post-traumatic stress disorder [PTSD]) (*Oades, 2011; Sommershof et al., 2009*).

In conclusion, we suggest here that the pathways controlling brain development, stress responses and mood are so closely related to those controlling immunoregulation that they all need to be considered together. Breaking down the interdisciplinary barriers might focus more attention on the relevance of psychosocial stressors in inflammatory disorders, and more attention on the potential for anti-inflammatory and immunomodulatory treatments for psychiatric ones.

ACKNOWLEDGEMENTS

The authors are grateful to Dr. Christopher Badcock for reading and commenting on a draft of this paper.

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THE EFFECT OF INFECTION AND ANTIBIOTICS ON GUT AND BRAIN

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A growing body of evidence now supports the view that the gut and the brain can communicate and influence each other's function. There are multiple pathways involved in this bi-directional communication, including neural and humoral mechanisms (*Bercik et al., 2012*). The afferent neural pathways include the vagus nerve, spinal afferents and the enteric nervous system (ENS). The gut can influence brain's function by the release of multiple regulatory peptides and pro-inflammatory cytokines, while the brain modulates gastrointestinal function through the autonomic nervous system, hormonal and immune pathways.

Gastrointestinal infection and subsequent inflammation can markedly affect behaviour and central nervous system (CNS) function. Acute inflammation induces a complex of symptoms, termed cytokine-induced sickness behaviour, which include both a neurovegetative and a psychological component (*Dantzer and Kelley, 2007*). Neurovegetative symptoms include loss of appetite, sleepiness, fatigue and fever, while psychological symptoms comprise depression, anxiety and cognitive dysfunction. Chronic exposure to pro-inflammatory cytokines results in changes in behaviour and CNS function, as evidenced during experimental cytokine cancer therapy (*Denicoff et al., 1987*). Psychiatric symptoms are also a frequent side effect of interferon treatment for chronic hepatitis C (*Renault et al., 1987; Keefe, 2007*).

Most of the evidence that gastroin-

testinal infections affect brain function comes from experimental animal studies. *Lyte et al. (1998)* demonstrated that mice infected with *C. jejuni* display anxiety-like behaviour, even during the early stage of the infection, when a systemic immune response was undetectable. This suggests that non-immune factors are also involved in gut-brain communication. The same group has shown that the abnormal behaviour in infected mice was present as early as 4 hours post-infection, and this was associated with increased neural activation pattern in vagal and central autonomic pathways, suggesting that the vagus plays a crucial role in the early detection of pathogens (*Gaykema et al., 2004; Goehler et al., 2005*). We have shown that chronic infection with *H. pylori* induces changes in the gastric cholinergic nerve function, as well as up-regulation of substance P and CGRP within spinal afferents (*Bercik et al., 2002*). This was accompanied by increased sensitivity to gastric distension and altered gastric emptying (*Bercik et al., 2009*). The chronically infected mice also displayed an abnormal feeding pattern, eating more frequently but smaller amounts of food per feeding bout, which is similar to eating habits in patients with functional dyspepsia, whose principle complaint is early satiety and abdominal fullness. When examining the brain chemistry of these mice, we found that chronic infection altered expression of pro-opiomelanocortin (POMC) in the arcuate nucleus, one of the brain centres

involved in food control, as well increased expression of tumour necrosis factor alpha (TNF- α) in the median eminence, one of the circumventricular organs (Bercik et al., 2009). Interestingly, some of these abnormalities did not fully normalize even 2 months after successful *H. pylori* eradication, suggesting that chronic infection may alter permanently the neural and gut function. The infected mice also displayed a trend for anxiety-like behaviour, when assessed by the light preference test, and this abnormal behaviour became more prominent during repeated testing. On closer examination it became clear that the control mice learned and adapted their behaviour in time becoming less anxious, while the infected mice maintained the abnormal behavioural pattern. The results suggest that chronic gastrointestinal infection may affect cognition and memory.

To further explore the effect of chronic infection and inflammation on behaviour, we have used model of chronic non-invasive parasite *Trichuris muris*, which in susceptible mice leads to mild-to-moderate colitis. We have found that mice chronically infected with *T. muris* have anxiety-like phenotype compared to control healthy mice (Bercik et al., 2010). This abnormal behaviour was accompanied by decreased expression of brain-derived neurotrophic factor (BDNF) in the hippocampus, which is one of the main brain centres involved in the regulation of mood and memory (Deng et al., 2010). BDNF is an important neurotrophin that regulates neural plasticity, and its lower levels were associated with anxiety and depression (Duman and Monteggia, 2006; Martinowich et al., 2007). The infected mice had modestly, but statistically significantly increased serum concentration of the pro-inflammatory cytokines TNF- α and IFN- γ . Both of these cytokines have

been shown to alter tryptophan/serotonin metabolism with increasing production of kynurenine, which is able to induce anxiety/depression-like behaviour in a dose dependent fashion (O'Connor et al., 2009a,b). Indeed, we found that mice with *T. muris* infection had increased levels of kynurenine, which normalized together with mouse behaviour, after treatment with anti TNF- α agent etanercept (Bercik et al., 2010). These data suggest that chronic gut inflammation triggers alterations in the function and biochemistry of the CNS through immune mediated pathways.

It is possible that changes in gut microbiota induced by administration of antibiotics are associated with immune activation in the gut and subsequently with changes in behaviour. We have shown in a murine model, that a one-week oral treatment with non-absorbable antimicrobials induced significant alteration in gut microbiota composition, as well as mild acute inflammation (Verdú et al., 2006). This was associated with increased sensitivity to colorectal distension and up-regulation of substance P in the intestine. Interestingly, treatment with probiotic *L. paracasei* ameliorated visceral sensitivity and normalized expression of substance P.

In a recent study using a different mouse strain and lower concentration of the same antimicrobials, we were able to induce a significant intestinal dysbiosis, but which was not associated with over inflammation or changes in neurotransmitter content in the gut (Bercik et al., 2011). Interestingly, the mice treated with antimicrobials increased their exploratory behaviour and became more active. This was associated with an increase in BDNF content in the hippocampus and decreased BDNF in the amygdala. This is consistent with the role of hippocampus and amygdala in mood modulation, as

over-activation of the amygdala has been implicated in depression and anxiety (Drevets, 2000). Since intraperitoneal administration of antimicrobials did not alter the mouse behaviour and germ-free mice given the same antimicrobials orally did not exhibit changes in behaviour, we can conclude that the increased exploratory behaviour in orally treated mice was due to changes in gut microbiota composition. Interestingly, germ-free mice displayed marked anxiety behaviour after colonization with commensal bacteria (Bercik et al., 2011). Overall these data suggest that intestinal microbiota has the capacity to modulate behaviour of the host.

To investigate this concept further, we have compared the behaviour and microbiota composition of NIH Swiss and BALB/c mice. While NIH Swiss are adventurous, with high exploratory drive, BALB/c mice are shy and cautious. Interestingly, these two mouse strains also had different microbiota composition. We thus derived both mouse strains under germ-free conditions and then colonized them with their own microbiota or with microbiota from the other mouse strain. While the mice colonized with the ho-

mologous microbiota displayed identical behaviour as their conventional counterparts, germ-free NIH Swiss mice colonized with BALB/c microbiota became more shy and hesitant, and germ-free BALB/c mice colonized with NIH Swiss microbiota became more daring and active (Bercik et al., 2011). The changes in mouse behaviour were accompanied by alterations in hippocampal BDNF levels, but no change in immune markers or gut neurotransmitter content was observed. Thus the intestinal microbiota can affect CNS function through immune-independent pathways.

In summary, accumulating data from animal studies suggest that gut inflammation and intestinal microbiota have a profound effect on gut function, behaviour and brain biochemistry of the host. Microbiota-gut-brain communication is complex and likely involves multiple pathways, including neural, immune and metabolic mechanisms. Up to date, human data on microbiota-gut-brain axis is limited and clinical trials are needed to extend our understanding on the role of bacteria in both health and disease.

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THE EFFECT OF INFECTION AND ANTIBIOTICS ON THE GUT BRAIN AXIS

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SUMMARY

Considerable experimental evidence largely from preclinical studies supports the concept of bidirectional interactions between the gut microbiota and the central nervous system. Multiple chemical, neural and immune signalling mechanisms have been identified which can mediate the transfer of information from complex microbial communities in the gut, to various cell types in the gut wall, including enterochromaffin cells and primary afferent nerves. In rodents, the perturbation of microbial homeostasis by introduction of pathogens can influence activity within brain circuits related to emotional behaviour, even before the development of gut inflammation. The suppression or perturbation of microbial communities by oral antibiotics can also influence such behaviours, and such behavioural changes can be associated with altered brain neurochemistry. Even though it is currently unknown if similar effects occur in adult humans on antibiotic therapy, it is intriguing to speculate that the regular antibiotic consumption early in life may affect brain development via the microbiota gut brain axis.

INTRODUCTION

The importance of interactions between the brain and the digestive system in health and disease has been recognized for many centuries (reviewed in *Mayer and Brunnhuber, 2012*). A major scientific breakthrough in understanding these interactions occurred with the discovery of the enteric nervous system (ENS) in the middle of the 19th century (*Costa et al., 1987; Furness et al., 1998; Furness, 2006; Gershon et al., 1994*). The ENS has been referred to as the “second brain,” based on its size, complexity and similarity in neurotransmitters and signalling molecules with the brain (*Gershon, 1998*). The topic of top-down modulation of gas-

trointestinal (GI) function by stress and emotions (*Cannon, 1929*), as well as bottom signalling from visceral afferents to the brain in abdominal pain syndromes, and possible emotion regulation (*James, 1884; Mayer, 2011*) has received increased attention during the past two decades, largely due to a series of independent, yet converging scientific discoveries from various fields of research, including enteric neuroscience (reviewed in *Furness, 2006*), neuro-imaging (reviewed in *Mayer, 2009*), intestinal microbiology and host microbial interactions (reviewed in *Artis and Grencis, 2008; Round and Mazmanian, 2009*), and more recently

microbial gut-brain signalling (reviewed in *Collins and Bercik, 2009; Collins et al., 2012; Cryan and Dinan, 2012; Forsythe et al., 2010; Forsythe and Kunze, 2012; Rhee et al., 2009;*),

which discusses emerging pre-clinical and some clinical evidence supporting a role of infections and antibiotic treatment on bi-directional signalling between the gut and the brain.

THE GUT BRAIN AXIS IN HEALTH

There are an estimated 200-600 million neurons in the human ENS, equal to the number of neurons in the spinal cord (*Furness, 2006*). These neurons have been classified on the basis of their morphology, electrophysiological properties and chemical coding into distinct classes of functional specific neurons, including several classes of afferents (*Furness, 2006; Wood, 1987*). The size and complexity of the ENS is not surprising when considering some of the unique challenges posed by the interface of the organism with its luminal environment: It interfaces closely with our largest body surface (the intestinal surface area [100 m²] is approximately 100 times larger than the surface area of the skin), with the largest population of commensal microorganisms of all body surfaces (100 trillion, 40,000 species, 100 fold greater number of genes

compared to the human genome (*Kurokawa et al., 2007*), with the gut-associated immune system (containing two-thirds of the body's immune cells), and with thousands of entero-endocrine (EE) cells (containing more than 20 identified hormones). These unparalleled relationships between the GI tract and the brain, with multiple, bi-directional and often interacting interoceptive communication systems emphasize the importance of this system in the maintenance of homeostasis, and make the brain gut axis unique amongst all viscera. A rapidly growing body of evidence supports a crucial role of the gut microbial ecology in the normal functioning of the gut brain axis, with gastro-enteric infections and suppression of the normal microbial ecology by antibiotic treatment representing major threats to its homeostasis.

THE EFFECT OF INTESTINAL INFECTION ON GUT BRAIN INTERACTIONS

From a clinical perspective, profound behavioural changes, as well as changes in mood, affect, cognitive function (attention, concentration) and motivation have long been known as characteristic features of most acute gastro-enteric infections in humans. Similarly, the clinical presentation of

patients with diarrhoea and cramp like abdominal pain are hallmarks of these enteric infections. However, the neurobiological mechanisms underlying the effects of gastro-enteric infections on the human gut brain axis are largely unknown.

GASTRO-ENTERIC INFECTIONS IN RODENTS WITH VARIOUS PATHOGENS

The cellular and molecular mechanisms underlying the symptoms of acute abdominal pain in enteric infections have been identified in the form of peripheral and central sensitization of visceral afferent pathways. Similarly, many of the molecular immune and neurobiological mechanisms that mediate the behavioural changes associated with acute enteric infections, including the so-called sickness syndrome (Watkins and Maier, 1999) have been identified (Bercik et al., 2012). More recently a series of intriguing studies from a small number of laboratories have identified behavioural, cognitive and neurobiological effects resulting from perturbations of the normal gut microbiota by different pathogens, and have described similarities and differences in the way the signals from the gut are transmitted to the brain.

Campylobacter jejuni

A pivotal study by Lyte and colleagues demonstrated that mice display altered, anxiety-like behaviour during the early phase of acute infection with *C. jejuni*, a common food-borne pathogen (Lyte et al., 1998). This abnormal behaviour consisted of decreased exploratory and increased non-exploratory behaviour during elevated plus-maze task on the second day after oral infection with the intestinal pathogen, compared to saline-treated animals. Interleukin-6 (IL-6) levels and peripheral blood leukocyte populations did not differ significantly between infected and control animals indicating the absence of a fully engaged immune response at the time of the behavioural tests. Based on these findings, the authors suggested that the behavioural changes were not a consequence of cytokine-induced sickness behaviour

but were rather mediated by neuronal pathways transmitting information about the shift in gut microbiota to the brain. A subsequent study showed that infection with *C. jejuni* activated sensory visceral structures in the brainstem, on both the first and second day post-oral inoculation, in the nucleus tractus solitarius (NTS) and lateral parabrachial nucleus (LPBN) (Gaykema et al., 2004). On the second day, an increase in c-FOS mRNA expression, an indicator of neuronal activity, was observed in the hypothalamic paraventricular nucleus, a brain region involved in the stress response. Since serum levels of IL-6, IL-1 β , and tumour necrosis factor- α (TNF- α) were unchanged over both days, the data are most consistent with vagal transmission of pathogen-related signals to the CNS. Mediation by the vagal afferent pathways was confirmed by the combined result of bilateral increase of c-FOS expression in the NTS, 4-12 hours post oral inoculation with *C. jejuni*, and unchanged levels of circulating pro-inflammatory cytokines (Goehler et al., 2005). Other studies focusing on early (7-8 hours) responses to oral inoculation have demonstrated that infection with *C. jejuni* increased anxiety-like behaviour during the hole-board task, accompanied by activation of brain circuits related to emotional behaviour. Increased c-FOS mRNA expression was observed in central autonomic regions, including the paraventricular, basolateral nuclei of the amygdala and parts of bed nucleus striae terminalis. This data is consistent with previous studies as these brain regions are purportedly relaying the viscerosensory stimuli from vagal afferent pathways to higher order regions mediating behavioural stress responses (Goehler

et al., 2008). Together with the earlier identification of vagal afferent pathways in mediating cytokine triggered sickness behaviour (Watkins and Maier, 1999) these studies illustrate an important role of vagal afferents in detecting an acute pathogen induced change in the gut and transmitting this signal to central fear circuits, even though the peripheral encoding mechanisms of such signals (e.g. inflammatory, pathogen related) may differ.

Citrobacter rodentium

Oral inoculation of mice with another pathogen, *C. rodentium*, has been found to be associated with cognitive dysfunction in non-spatial and working memory, 10 days (time of maximal inflammation) and 30 days post-inoculation (Gareau et al., 2011). However, these inflammation associated behavioural effects were only seen in the context of an acute water avoidance stress. On the other hand, germ-free mice, 10 days post oral pathogen inoculation had an exaggerated stress response regardless of the presence or absence of the acute stressor, presumably due to an alteration in responsiveness of the hypothalamic-pituitary-adrenal axis (Gareau et al., 2011). When a Lactobacillus-containing probiotic regimen was given to non-germ-free mice before and during infection, serum corticosterone responses to stress were attenuated, c-FOS expression and BDNF levels in the CA1 region of the hippocampus stabilized, and cognitive dysfunction was prevented. Based on these findings, the authors made several speculations:

1. Information about specific enteric bacterial infection reaches the brain through either enterochromaffin cell derived serotonin or corticotropin-releasing factor, priming the HPA-axis to stress.
2. At the time of the stress, abnormal

behaviour is observed due to HPA axis induced alterations in hippocampal memory.

3. The primed stress response is heightened in germ free mice due to an absence of a gut microbiome.

Cognitive dysfunction and anxiety-like behaviour 7-8 hours after oral inoculation with *C. rodentium* was most likely mediated by vagal afferent pathways since vagal sensory ganglia from infected mice had higher c-FOS expression (Lyte et al., 2006). The data from various pathogenic infections suggests that vagal afferent transmission from gut to brain plays a crucial role in mediating the behavioural and cognitive changes, as well as the observed activation of brain circuits observed during gut infection.

Helicobacter pylori

Studies in chronic *H. pylori* infection of mice have also shown correlation with abnormal feeding behaviour consisting of frequent bouts of feeding with less food consumed per feeding than control animals. Increased levels of plasma ghrelin and postprandial CCK, higher TNF- α in the hypothalamic median eminence (ME), and lower pro-opiomelanocortin (POMC) expression in the arcuate nucleus were associated with the observed delay in gastric emptying and the development of visceral hypersensitivity in infected mice. The ME of the circumventricular organ contains a leaky area of the blood-brain barrier of the CNS, thus allowing metabolites and molecules from the systemic circulation to enter the brain directly rather than being mediated by neuronal activation (Bercik et al., 2009). Another study from the same group of mice chronically infected with *H. pylori* found delayed gastric emptying and visceral sensitivity associated with an up-regulation of substance P and calcitonin gene-related

peptide expression in the gut and spinal cord (Bercik et al., 2002). Bacterial eradication normalized gut dysfunction symptoms, but did not alter abnormal feeding behaviour and the increase in TNF- α in the brain and gastric CD3(+) T-cell counts remained elevated, suggesting different pathways monitor post-infective gut dysfunction. Interestingly these behavioural feeding changes and the biochemical changes both lasted for 2 months after the bacteria were eradicated, implying that the effects of chronic infection in GI tract can be long lasting (Bercik et al., 2009). When the infected animals were given probiotics, abnormal feeding behaviour was normalized and CD3(+) T-cell counts decreased, further suggesting that there are various mechanisms at play during recovery from infection that are not well understood and need further investigation (Verdu et al., 2008).

Trichuris muris

Chronic intestinal infestation of mice with *T. muris*, a close relative of the human parasite *Trichuris trichiura*, was accompanied by increased anxiety-like behaviour, as well as decreased expression of brain-derived neurotrophic factor (BDNF) in the hippocampus, a multifunctional brain region involved in memory formation and in the inhibition of the central stress response. Intestinal inflammation, observed by the increased plasma levels of pro-inflammatory cytokines TNF- α and interferon- γ , was also accompanied by an increase in the plasma kynurenine:tryptophan ratio, reflecting an alteration of tryptophan metabolism in the mice. The *T. muris* infection induced anxiety-like behaviour was not affected by a vagotomy performed prior to the infection, arguing against an important role of afferent vagal pathways in mediating the observed behavioural effects during this

type of infection. In contrast, anxiety like behaviour was not observed when mice were treated with the anti-inflammatory agents etanercept (a TNF- α inhibitor) and the steroid budesonide after infection, even though hippocampal BDN expression was similar to the infected-only mice. These findings suggest that in this model, the observed anxiety-like behaviour is induced by inflammatory mediators originating in the gut, and exert their effects either via circulating cytokines and inflammation-related changes in altered tryptophan metabolites, rather than mediation by vagal afferents. On the other hand, the authors reported that administration of the probiotic *Bifidobacterium longum* was able to restore normal behaviour and hippocampal BDNF expression, while plasma cytokine and kynurenine levels remained unaffected. Even though the precise mechanisms and pathways underlying the infection induced behavioural changes in this model remain to be determined, the findings suggest that multiple signalling mechanisms can be involved in the transmission of gut pathogen-related information to the brain (e.g. vagal afferents, inflammatory mediators, amino acid metabolites), and that the engagement of these mechanisms can vary depending on the pathogen and the experimental model (Bercik et al., 2009). Bercik and co-workers have shown similar results in SCID mice, which had been orally administered chronic *T. muris*, which caused anxiety-like behaviour and also expressed higher levels of BDNF mRNA in the hippocampus using *in situ* hybridization. The effect of BDNF was avoided when *B. longum* was introduced, although anxiety-like behaviour remained; and the introduction of *L. rhamnosus* normalized anxiety-like behaviour but not BDNF mRNA expression. This further confirms the plethora

of data to date suggesting strongly that there are different signalling mechanisms for how information on the state of the gut's microbiota, specifically its contents work (Bercik et al., 2009).

In summary, considerable preclinical evidence has been reported to clearly support the ability of enteric pathogens to signal to the central nervous system and affect behaviour. This pathogen to gut to brain communication system is capable of detecting acute changes in the gut microbial ecology, and of selectively signalling the presence of a pathogen to brain circuits, which are involved in the stress

response, behaviour, memory, and learning. Furthermore, there is good evidence to support the existence of multiple pathways or mechanisms mediating the transmission of pathogen related information from the GI tract to the brain. One may speculate that, while signalling via circulating immune mediators plays the dominant role during fully developed mucosal inflammation, peripheral afferent pathways, including enteric and vagal afferents may play an important role at the earliest stages of infection, prior to the full engagement of the immune response (Bercik et al., 2012).

THE EFFECT OF ANTIBIOTICS ON GUT BRAIN INTERACTIONS

Despite the well known side effects of orally ingested antibiotics reported in human patients, there are no reports in the literature or anecdotal reports suggesting that suppression of normal microbiota by antibiotics (dysbiosis) are associated with significant changes in mood, affect, cognition or behaviour. This is surprising, given the widespread use of antibiotics both in paediatric and adult populations, the now well established communication between the gut microbiota and the central nervous system, and the recent results from rodent studies suggesting that antibiotic induced suppression of the normal flora is associated with significant behavioural and even neurochemical changes in the brain.

Antibiotic treatment of experimental mice has become one of the most commonly used methods to induce artificial intestinal dysbiosis. Perturbation of the microbiota in adult mice by oral administration of non-absorbable antibiotics neomycin and bacitracin and the antifungal agent nystatin has been shown to increase a viscerosomatic nociceptive reflex to

colorectal distension consistent with the development of visceral hypersensitivity following antibiotic induced dysbiosis (Verdu et al., 2006). In the same study, the antibiotic induced visceral hypersensitivity was reversed by the oral administration of the probiotic *Lactobacillus paracasei*. This study demonstrated that antibiotics can severely disrupt the central processes responsible for visceral responses by altering the neurotransmitter content of the colon, while certain probiotics may be able to re-establish intestinal symbiosis and neurotransmitter content, thereby normalizing visceral function. In another study by the same group (Bercik et al., 2011a), oral administration of neomycin and bacitracin along with the antifungal agent pimaricin to adult BALB/c mice, did not lead to quantitative changes in culturable bacteria but was associated with a transient change in microbial ecology: Antibiotic ingestion was associated with an increase in Actino-bacteria and Lactobacillus species and decrease in c-proteobacteria and bacteroidetes. The antibiotics also induced changes in be-

haviour, with treated animals demonstrating evidence of increased exploratory behaviour in both the step-down and light/ dark preference tests, indicating reduced levels of anxiety. As was demonstrated in comparisons between germ-free and conventional animals, behavioural changes in antibiotic-treated animals were associated with reduced BDNF levels in the amygdala, and increased levels in the hippocampus (*Bercik et al., 2011a*). The effects of antibiotic treatment on the composition of the intestinal microbiota and on behaviour were transient with treated mice resembling controls after a 2-week washout period. In these studies, a causal relationship between microbiota changes and behavioural effects is supported by the demonstration that, in

contrast to oral antibiotic treatment, i.p. treatment did not influence behaviour. Furthermore, antibiotic treatment had no effect on the behaviour of germ-free animals (*Bercik et al., 2011a*). Whether the behavioural changes can be attributed to specific alterations in the microbiota, e.g., increased lactobacilli and acinto- bacteria or decreased c-proteobacteria and bacteroidetes, was not investigated. However, this is an intriguing idea especially given subsequent studies demonstrated anxiolytic effects of feeding certain lactobacilli and bifidobacterium strains (*Bercik et al., 2011b*), and as such it would be interesting to assess the effects of prebiotics, e.g. agents that promote the growth of bifidobacteria and lactobacilli, on behaviour.

SUMMARY AND CONCLUSIONS

Growing preclinical literature supports the concept of bidirectional microbiota gut brain communications providing the basis for interactions between three “super systems” within the body: The gut microbiome, the gut associated immune system and the central nervous system. However, despite the excitement about the recent findings demonstrating important influences of the gut microbiota on behaviour and brain signalling systems in rodent models, caution is in place when extrapolating the findings obtained from perturbations of the gut microbiota from rodent behaviours to complex human experiences and subjective symptoms.

In the case of gastro-enteric infections, characteristic human symptoms of nausea, fatigue, lack of motivation, anxiety, depression and abdominal pain may be the human homologues of rodent behaviours and molecular mechanisms reported in the publications discussed above. Functional brain imaging

studies in human subjects may provide further evidence to support the translational significance of these observations.

In the case of antibiotics, there is currently no convincing clinical or experimental evidence in human subjects to mimic the dramatic findings observed in rodent models. The reason for this translational gap is currently unknown, but may in part be related to the fact that antibiotics are generally not given to otherwise healthy subjects, but generally in the context of on-going infections. It is conceivable that targeted evaluations of cognitive function, affect and mood in subjects undergoing oral antibiotic therapy will reveal subtle effects in these domains. In view of the widespread use of non-absorbable antibiotics for the treatment of patients with irritable bowel syndrome and symptoms of bloating and abdominal distension, it would be important to know if such treatments have effects on

the CNS. An important aspect of suppression of normal gut microbiota by antibiotics and the resulting effects on the gut brain axis may be related to brain development. Germ-free conditions, an extreme form of dysbiosis, have been found to profoundly influence brain development in rodents. Given the widespread use of antibiotics in neonatal intensive care units, and in paediatrics for common diseases as si-

nusitis, bronchitis and respiratory tract infections, it is conceivable that the dysbiosis resulting from these interventions may affect brain development in children. Future studies evaluating possible correlations between antibiotic use, dysbiosis and cognitive and emotional functioning and underlying brain networks in children should address this important question.

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IMPACT OF ENTERIC INFECTIONS ON COGNITIVE DEVELOPMENT: FIELD AND ANIMAL STUDIES OF PROTECTION BY ApoE4

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SUMMARY

Although diarrhoeal diseases in early childhood remain important causes of mortality, the long-term impact of enteric infections, with or without overt diarrhoea, may impair child growth and development. Repeated dehydrating or malnourishing infections can compound other causes of mortality and may also have lifelong consequences for those who survive. This includes a cognitive decrement that may average up to 10 IQ points by 7-9 years of age that can be attributed to diarrhoeal illnesses in the first 2 years of life alone. The cognitive function most affected is semantic, rather than phonemic, fluency, a deficit also seen in early Alzheimer's (vs. Parkinson's) dementia. These effects may be lifelong and may have selected for surprising "survival" or "thrift" genetic alleles like ApoE4 that we have shown to *protect* against the cognitive deficits seen in children with heavy diarrhoea burdens as well as providing protection against the growth and histopathologic impact of enteric infections in a murine model of malnutrition and infection.

In this overview, we review these long-term growth and cognitive effects of early childhood diarrhoea, the Alzheimer-like deficits seen and the surprising protection provided by the ApoE4 allele that increases Alzheimer risk in later life, a new example of "antagonistic pleiotropy". We also show this protection in our murine model of cryptosporidiosis using targeted transgenic mice with the human E4 allele and how the molecular mechanism of this benefit can lead to novel interventions to break the vicious cycle of diarrhoea and malnutrition and their devastating consequences for child development.

BETTER COGNITION AND IQ CORRELATE WITH FEWER INFECTIONS

Over 200 million of the world's children less than 5 years of age fail to achieve their developmental potential, are stunted and live in poverty. These children do poorly in school and go on

to have low incomes, high fertility and provide poor care for their children, contributing to what Dr. Grantham-McGregor has called "intergenerational transmission of poverty" (*Grantham-*

McGregor et al., 2007). Eppig and colleagues recently suggested that the “Flynn Effect” of improving IQ with development correlates with decreasing “infectious diseases burden”, even when controlling for GDP per capita, education, temperature and malnutrition; i.e. the recognized correlation of nutritional deficiencies with IQ is lost when the effects of infectious diseases are removed which they interpret as suggesting that the malnutrition-IQ link

appears to occur through infectious diseases (Eppig et al., 2010). Whether there is an effect of infections on cognitive development that is independent of their effects on malnutrition is less clear. Although this is a controversial area, our data on diarrhoeal illness correlations also appear to be independent of stunting (<1HAZ) (which is itself also correlated with diarrhoea in the first 2 years of life) (Pinkerton et al., 2012).

INFECTION OR STUNTING IMPAIRS COGNITION

Convincing support for the effects of infection on child development came from albendazole trials in Kenya and Jamaica, suggesting that intestinal helminths impair growth and cognitive development. These were the basis of our studies of heavy early childhood diarrhoea burdens in Fortaleza. Stephenson and colleagues reported that, among Kenyan schoolchildren, even a single dose of albendazole showed a benefit in fitness, appetite and weight and height gains within 2 to 4 months when compared with double blinded placebo-treated controls (Stephenson et al., 1989, 1990, 1993). Similarly, in studies of schoolchildren in Jamaica, Nokes et al. (1992) showed improved fluency (long term memory and retrieval) and digit span backwards/forwards (from WISC, involves attention and distractibility) 2 months after a 3-day course of albendazole (vs. placebo). Since HAZ-2 may be a surrogate for early childhood diarrhoea burdens (Dillingham and Guerrant, 2004), it may also be relevant that Chang and co-workers described better arithmetic scores at 10 years old with higher HAZ-2 (height for age Z scores at 2 years old) (Chang et al., 2011). Although these brief anti-helminthic treatments did not necessarily eradicate intestinal geohelminths (and certainly did

not prevent common re-infections), the 2-3 log reduction in major geohelminths provide impressive evidence for the importance of heavy intestinal nematode infections in the physical and cognitive development of schoolchildren. Our own data from Northeast Brazil also suggests that geohelminth infections in early childhood (i.e. from birth to 2 years old) have important, lasting effects on subsequent child growth and development (Moore et al., 2001). We and others are now exploring whether stunted children may also be at greater risk for later obesity, diabetes and metabolic syndrome in what we have called a ‘collision of bad water with bad diets’ (DeBoer et al., 2012).

The importance of stunting on cognitive development is clear from several studies (Grantham-McGregor, 1995). In studies of nonverbal intelligence at 8-11 years old in the Philippines, Mendez and Adair’s group has shown that moderate to severe stunting (i.e. HAZ-2 <-2) at 2 years is associated with a 0.25 to 0.61 standard deviation lower mean cognitive test Z score by age 8 (p<0.001) (Mendez and Adair, 1999). They also noted that stunting (i.e. progressing from -1.5 to -3.3 HAZ) at 2 years correlated with progressive delays in age at starting school from 5 to 8+ years, and that, even

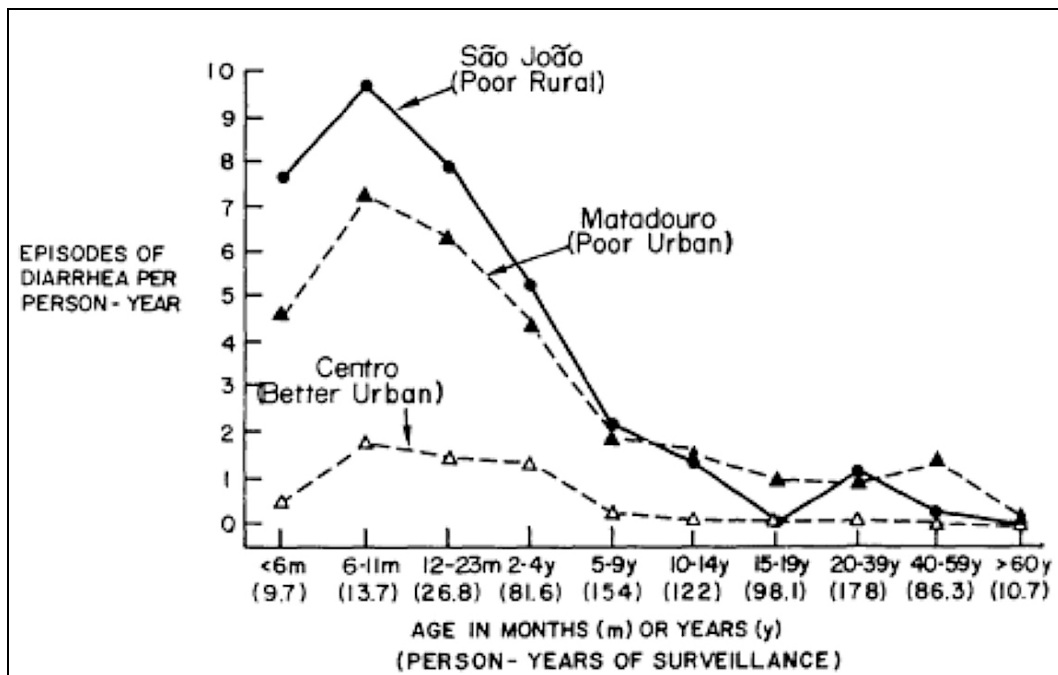


Figure 1: Age specific diarrhoea attack rates in rural and urban communities (Pacatuba and Gonçalves Dias) in Northeast Brazil (Guerrant et al., 1983; Lima et al., 2000).

though schooling (achieving 2-6 years of education) improves mean cognitive test scores, there remains a 30% dec-

rement in the stunted children at 11 years; i.e. stunting limits what education can accomplish!

THE CRITICAL 4-24 MONTH AGE “WINDOW” FOR CHILD DEVELOPMENT

Leonardo Mata, in studying The Children of Santa Maria Cauque (Mata, 1978) described how even impoverished children often start off on their growth curves reasonably well, only to fall progressively off with the onset of diarrhoeal and other common early childhood infections over the critical first 2 years of life. Precisely the same pattern of fall-off in linear growth (i.e. HAZ) occurs worldwide, with remarkably similar findings in Asia, Africa and Latin America described by Victora and Shrimpton (Victora et al., 2010) in 2010, much as they had shown nearly a decade earlier in 2001 (Shrimpton et al., 2001).

Feeding studies also confirm the importance of early childhood (3 years) in cognitive development. For example, in the two Guatemalan villages given an “atole” vegetable-protein supplement (163kcal with 11.5g protein) vs. “fresco” sugar sweetened beverage (59kcal and no protein) in two control villages in INCAP studies from 1969-1977. A follow-up 25-35 years later showed that those in the supplemented villages had a 10% better IQ, even after, adjusting for schooling (Stein et al., 2008), and that the 25-42 year old males had 46% higher wages, with the females having 8-20% higher reading, Raven scores and schooling if they had

been in the supplemented villages compared with the non-supplemented villages some 40 years before. However these benefits were seen only in those who had been in the supplement program in their first 2-3 years of life, showing the crucial timing of early life in cognitive development (*Hoddinott et al., 2008*).

We also have found increasingly impressive correlations in our Fortaleza studies of early childhood diarrhoea (ECD) that heavy diarrhoea burdens in the first two years of life are associated with impairments in cognitive function (TONI, WISC-III coding and digit span and WRAML mazes) several years later (*Guerrant et al., 1999; Niehaus et al., 2002*). Furthermore, these heavy diarrhoea burdens in the first 2 years of life also correlate with impaired schooling (both age at starting school and age-four-grade) several years later (*Lorntz et al. 2006*). Early heavy diarrhoea burdens are also associated with stunting at 2 years of age in our as well as in other multi-country studies (*Moore et al. 2001; Checkley et al., 2008*) and, as noted above, stunting at the second birthday (HAZ-2) is clearly associated with impaired cognition as assessed later in life. Although some suggest that the effects of diarrhoea on cognition may be only through its effects on stunting, as noted above, like Eppig, we find that the association of diarrhoea with cognitive impairment remains even when controlling for anthropometry. Thus heavy early childhood diarrhoea burdens clearly associate with lasting effects on stunted growth, and, in turn on impaired cognition. Whether the cognitive impact of early childhood diarrhoea is independent of (i.e. even greater than) the also significant effects of diarrhoea on stunting remains controversial. Nevertheless, the huge effects of early childhood diarrhoea on child growth and

development are critical to recognize and ameliorate.

The reasons for the first 2 years of life being so critical are likely at least two-fold: first is the obvious vulnerability to the heaviest burdens of diarrhoea and enteric infection (with rates clearly highest in that age range) (*Guerrant et al., 1983; Lima et al., 2000; Fischer Walker et al., 2012*) (Figure 1) Second is the rapid development of brain growth and synaptogenesis and myelination in humans in this window from birth to 2 years. Unlike some other species in which brain development occurs predominantly *in utero*, human infants are born with small brains and sparse synapses relative to their near adult levels of brain weight-for-height and even synaptic density by 2 years of life (*Dobbing and Sands, 1973; Corel, 1975; Rice and Barone, 2000; Thompson and Nelson, 2001*) (Figure 2). Not only does the human brain double in size in the first year of life, by 3 years of age it reaches 80% of its adult volume (The Urban Child Institute: Baby's brain begins now, Conception to age 3. URL: www.theurbanchildinstitute.org/why-0-3/baby-and-brain, 2012; *Nowakowski, 2006*). Furthermore, synapse formation occurs predominantly between birth and 2-3 years of age (by which time the human brain has nearly 200% of its adult number of synapses); after which "blooming and pruning" gradually eliminate nearly half of these synapses throughout childhood and adolescence (*Corel, 1975; Huttenlocher, 2002*). These anatomic observations are even more apparent when one considers the impressive incapacity of the human new-born infant compared with the remarkable appearance of motor and cognitive skills including walking, running, talking and personality which develop by the child's second birthday.

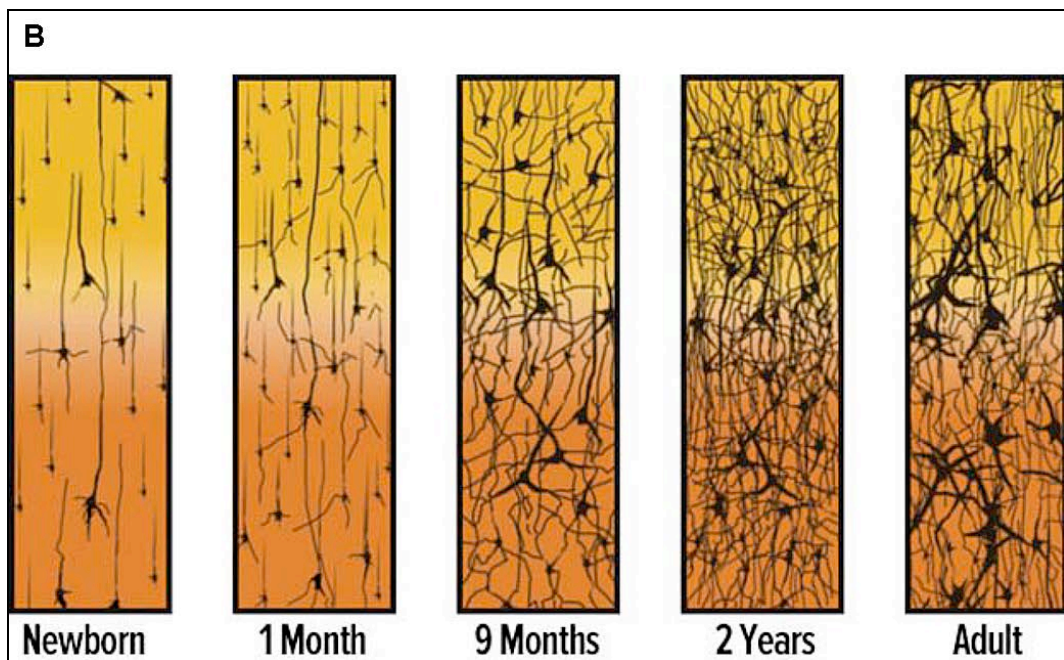
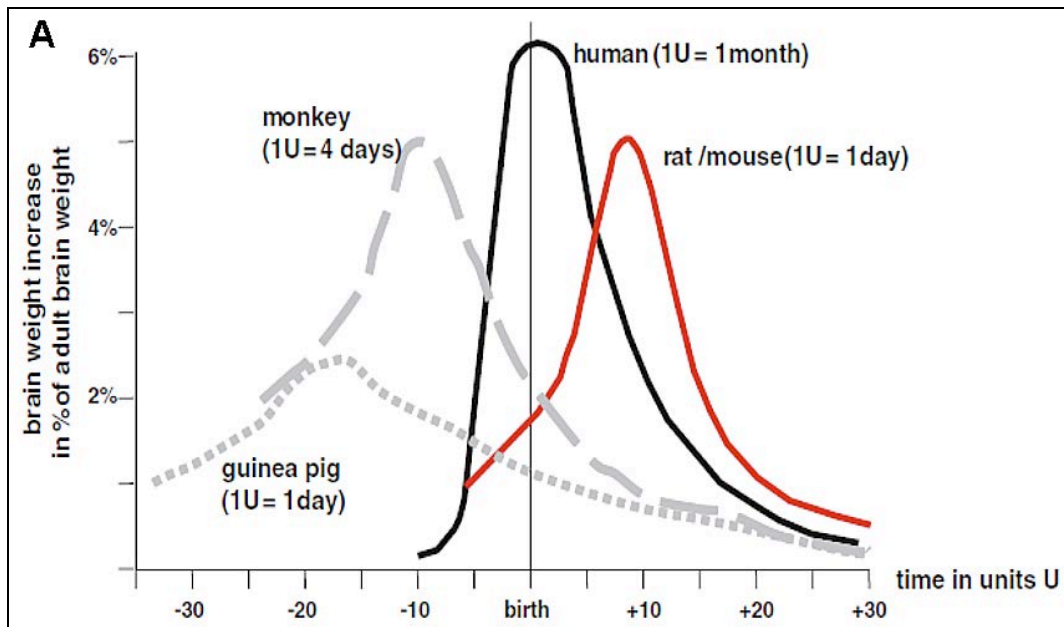


Figure 2: Age of brain development in humans and other animals, showing that most human brain development (by A: weight or by B: synapse formation) occur in the first 2 years of life. Adapted respectively from *Dobbing and Sands* (1973) and from *Corel* (1975).

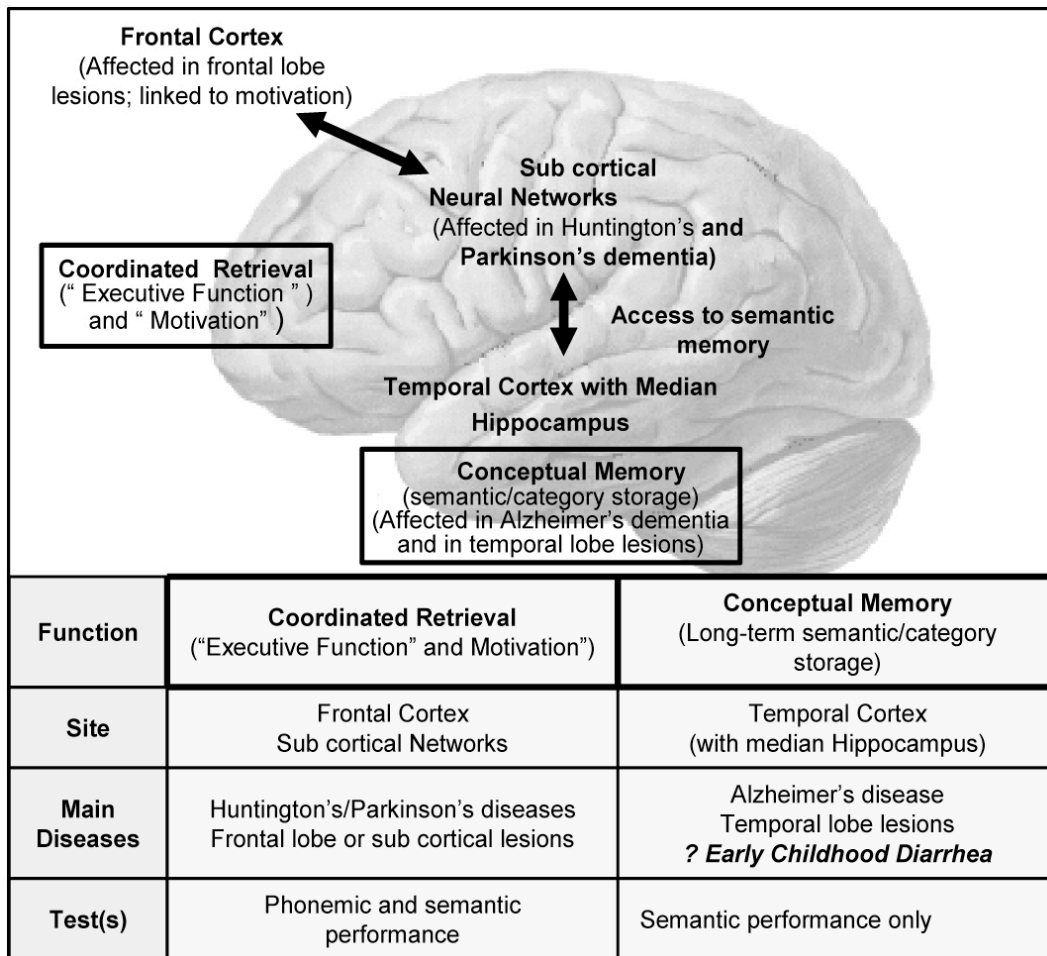


Figure 3: Brain regional development and function.

EARLY CHILDHOOD DIARRHOEA AND GIARDIASIS IMPAIR SEMANTIC FLUENCY (LIKE ALZHEIMER'S DISEASE) AND ApoE4 PROTECTS

When we examined the specific areas most affected by early childhood diarrhoea, it was striking that these were predominantly functions similar to those lost in early Alzheimer's disease. These include higher executive function and semantic (vs. phonetic) fluency (Patrick et al., 2005; Oriá et al. 2009), with brain regions that likely differ from the predominant ones involved in phonemic fluency or in Parkinson's dementia (Figure 3).

Because of the semantic fluency predominance of the deficits, we examined the ApoE4 allele frequencies and found, to our initial surprise, that ApoE4 was protective of the cognitive function and against diarrhoea, the former only in the children with heavy diarrhoea burdens (Oriá et al., 2005, 2007, 2010). Some early investigations into this link are beginning to support a host benefit of ApoE4 against enteric protozoa. The positive correlation

between *Giardia lamblia* and diarrhoea ($p < 0.01$) in ApoE4 negative children in our study was lost in the presence of an ApoE4 allele ($p = 0.53$) (Oria et al., 2005). Moreover, the ApoE4 allele appears to be protective against cognitive impairments due to early *Giardia* infections in Egypt (Yahya et al., 2009a, 2009b), although these findings should be further confirmed with larger numbers and better control for confounding factors. The association of potential protection against symptoms with this parasite by the host ApoE4 allele may be related to the *Giardia*'s requirement to obtain host cholesterol for its own growth (since *Giardia* is unable to synthesize cholesterol) thus needing to divert host cholesterol to the parasite from the intestinal milieu, which may deleteriously affect the developing brain (Oria et al., 2007). These effects may require an evolutionarily conserved LDL-receptor pathway, which is found to be down-regulated in ApoE4 carriers (Mahley and Rall, 2000). Recently, a putative *Giardia lamblia* low-density lipoprotein receptor-related protein (GLRP), a type I membrane protein, which shares the substrate N-terminal binding domain and an FXNPXY-type endocytic motif with human LRP, was identified (Mahley and Rall, 2000; Rivero et al., 2011).

In addition, Colton and colleagues (Colton et al., 2001; Czapiga and Colton, 2003) have shown that ApoE4 increases NO production in microglial macrophages by stimulating arginine uptake via an arginine-selective cationic amino acid transporter (CAT1). Hence we examined the ability of arginine to enhance parasite killing with *Cryptosporidium* infections in our murine model (Castro et al., 2012) and also the ability of targeted transgenic C57Bl6 mice with the human ApoE4 allele to resist cryptosporidial infec-

tions or their growth impairment in our murine model. We found that arginine is the most effective "anticyptosporidial drug" we have encountered in our murine model, with a 10-fold reduction in the number of parasites per milligram of intestinal tissue. These effects were only partially blocked by L-NAME (NG-nitro-arginine methyl ester) (Castro et al. 2012) or by BEC (S-(2-boronoethyl)-L-cysteine) (Castro et al., unpublished data), suggesting that the protection from arginine was through both the iNOS and the arginase pathways to kill the parasite and repair epithelial cell injury respectively. Furthermore, in studies that are being submitted for publication elsewhere, C57BK6J ApoEko mice expressing the human ApoE4/4 gene under murine ApoE promoter lost less weight, had better villus-to-crypt ratios and shed fewer parasites than ApoE 3/3 target replacement and wild-type mice, suggesting that understanding how ApoE4 may be protective can open novel approaches to better controlling protozoal infections. Interestingly, supporting the concept that ApoE4 may improve innate immunity against enteric pathogens, data from the Tsimane population in lowland Bolivia, (an indigenous forager-farmer population living under conditions resembling pre-industrial European populations with high infectious morbidity, high infection and inflammation, and shortened life expectancy) when bearing ApoE4 show lower serum C-reactive protein levels (Vasunilashorn et al., 2011), suggesting that ApoE4 bearers had lower rates of environmental-related infections.

Our data support that ApoE4 behaves as antagonistic pleiotropy, where the presence of ApoE4 in our gene pool was associated with increased needs for fat energy storage and improved innate immunity adaptations against enteric

infections in times where those were critical for human survival in the pre-industrialized era. However this once beneficial gene becomes potentially quite detrimental in the presence of longer life expectancy, reduced physical exertion and westernized diets.

There are other postulates and literature evidence for an antagonistic pleiotropy described for ApoE4 during human early development and in adulthood (*Prentice et al., 2005; Alexander et al., 2007; Finch and Morgan, 2007; Beeri et al., 2009; Chang et al., 2011*).

EFFECTS OF MALNUTRITION AND OF MICRONUTRIENTS ON BRAIN ANATOMY AND FUNCTION

Especially vulnerable in the first two years of life in humans (analogous to the first few weeks of life in rodent models) is the postnatal brain plasticity, particularly in dynamic hippocampal, neocortical and cerebellar regions (*Frankova and Barnes, 1968; Rice and Barone, 2000*). It is these areas that are potentially altered by nutrients or micronutrients in critical developmental windows (*Georgieff, 2007; Pinero et al., 2001; de Souza et al., 2011*). Hence we examined the effects of malnutrition and of zinc and glutamine therapy in our murine model of litter clustering induced malnutrition. There we found that malnourished mice (with breast-milk restriction by increased litter size) had growth impairment and deficits in early post-natal behaviour ontogeny, associated with reduced serum and brain zinc levels. In addition, we found reduced hippocampal GABA levels and reductions in hippocampal synaptophysin (as a marker for synaptic density) expression, associated with malnutrition. Furthermore, malnutrition-induced CA-1 neuronal hypertrophy was found with litter size clustering, likely related to CA-1 cell death changes. All effects improved with glu-

tamine and/or zinc treatment (*Ladd et al., 2010*).

We next examined the effects of zinc, vitamin A and glutamine supplementation on the growth and cognitive responses in 213 undernourished children from the favela in Fortaleza and found that lower vitamin A and glutamine levels were associated with disrupted intestinal barrier function (by lactulose/mannitol absorption ratios). There was also a significant correlation between vitamin A supplementation of apolipoprotein E4(+) children and improved lactulose/mannitol absorption ratios. In addition, only the ApoE4 positive children (37/213, 13.9%) who received glutamine supplementation (10 day glutamine treatment either with or without zinc or vitamin A supplementation) showed significant positive Pearson correlations between the changes in height-for-age z-scores over four months with delayed verbal learning scores, along with correlated changes over the same period in weight-for-age z-scores and weight-for-height z-scores that were associated with non-verbal intelligence quotients (*Mitter et al., 2012*).

CONCLUSIONS

In conclusion, we find profound and lasting effects of early childhood enteric infections and diarrhoea on chil-

dren's growth and cognitive development. While these "vicious cycles of poverty" are only now being dissected

at the levels of molecular causality, genetic predispositions and potential novel interventions can already be designed that hold promise for interrupt-

ing these vicious cycles of diarrhoea, stunting, cognitive impairment and poverty.

ACKNOWLEDGEMENTS

Some of the work in this review was supported in part by the NIH National Institute for Allergy and Infectious Diseases, ICIDR (International Collaborations in Infectious Diseases Research) grant No. U01AI026512, by the NIH Fogarty International Center GIDRT Training grant No. D43TW006578, and MARCE grant No. U54AI057168. Additional support came from the NIH *Eunice Kennedy Shriver* National Institute of Child Health and Human Development (NICHD: ApoE grant No. RO1HD053131) with co-funding from the NIH Office of Dietary Supplements (ODS). Dr. Bartelt was supported in part by the Research Training in Digestive Diseases grant No. 5T32 DK007769.

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THE GUT MICROBIOME AND THE NERVOUS SYSTEM: SUMMARY OF THE SEMINAR

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When this symposium was being planned, very little information existed as to the potential role of commensal bacteria in the gut in modulation of the peripheral or central nervous systems. A limited number of reviews were extant (*Collins and Bercik, 2009; Forsythe et al., 2010*) and to the knowledge of the planners, a symposium devoted to this subject was novel if not unique. In the course of 2011-2012 a significant number of reviews of the subject appeared and since June 2012, there has been an explosion of interest in this area so that the numbers of reviews may now equal or even be in excess of original articles in the field (*Grenham et al., 2011; Bravo et al., 2012; Collins et al., 2012; Cryan and Dinan, 2012; Dinan and Cryan, 2012; Forsythe and Kunze, 2012, Saulnier et al., 2012*)! Many of the participants in this symposium have been contributing authors to these reviews.

The concept of the gut microbiome as a “forgotten organ” and the complexity of the effects on the host of the more than 3 million genes which it contains have opened biologists’ eyes to how little we know in this area. Initial major emphasis has been placed on the interactions between bacteria in the gut and the immune and endocrine systems and this has recently been extended to the nervous system. These pathways have been loosely termed the gut-brain or microbiome-gut-brain axis, however they have largely failed to take into account the enormous contri-

bution of the fungal and viral genomes, which also contribute, to these inter-kingdom communications. The fungal contributions have recently been highlighted by *Iliev et al. (2012)* who termed this the “mycobiome” and showed that this “eukaryotic fungal communitycoexists with bacteria and substantially expands the repertoire of organisms interacting with the intestinal immune system to influence health and disease”. The virome has also just started receiving attention in this respect (*Reyes et al., 2012*).

The fact that the microbiome may influence animal behaviour has been known for a number of years and was recently reviewed by *Ezenwa et al. (2012)*. The choice of mates by *Drosophila* was shown to depend on specific gut Lactobacilli which, when eliminated, restored typical random mating. This was thought to depend on the influence of cuticular pheromone production (*Sharon et al., 2010*). The swarming of locusts depends upon the production of an aggregation pheromone, which in turn depends on the presence of 2 or 3 specific gut bacteria (*Dillon et al., 2002*). The nerves responsible for this phenomenon have been identified, as has serotonin as the neurotransmitter involved (*Anstey et al., 2009*). Several other animal behaviours have been associated with specific characteristics of the gut microbiome (*Ezenwa et al., 2012*).

The symposium began with an overview by Bud Craig who summa-

rized his relevant work on interoception which has focused attention on the way in which a particular neuroanatomical area of the brain, the insula, integrates sensory input from the body (Craig, 2002, 2010, 2011). The activation of the anterior insula correlates with subjective feelings and thereby emotions and the right and left insulae are probably asymmetrically organized, and possibly this is done in an opposite fashion. This is particularly evident in primates and presumably humans, and the data are striking and indicate that the non-dominant (i.e. mostly left) insula contains an answer to the question “how do you feel?”. While this work has not yet identified the role of the gut microbiome, the evidence in rodents of commensal effects on brain neurochemistry and behaviour strongly predict a neuroanatomical target, possibly via the vagus nerve (Bravo et al., 2011a). Emeran Mayer, another symposium speaker, has published together with Bud Craig a major review on the brain-gut axis, incorporating modern concepts of how gut feelings are generated and integrated with special reference to functional gastrointestinal disorders such as irritable bowel syndrome (IBS) and gut pain (Mayer et al., 2006).

Paul Forsythe drew especial attention to the bidirectional interaction between the gut microbiome and the brain and stressed the fact that while the vagus nerve carried much of the information generated in the viscera to the brain, additional pathways exist, ranging from hormonal to possibly direct effects of bacterial products such as GABA or results of fermentation such as fatty acids. A recent publication showed that feeding of *L. rhamnosus* (JB-1) resulted in anxiolytic behavioural changes accompanied by alterations in specific GABA receptors in the brain and a blunted corticosterone re-

sponse to stress, all of which were abrogated by prior vagotomy (Bravo et al., 2011a). The same bacterium causes increased electrical activity in the vagus nerve (Perez-Burgos et al., 2012). While the efferent vagal pathway has been identified by Tracey and colleagues (Olofsson et al., 2012) as part of a cholinergic anti-inflammatory reflex, the extent to which the afferent and efferent pathways are part of a reverberating network is not known. Commensal bacteria such as probiotics may well stimulate immediate functional immunoregulatory activity locally as well as through efferent vagal pathways and therefore in turn influence stress and low-grade inflammation associated conditions such as depression (Raison et al., 2010; Dantzer, 2012). Wolfgang Kunze was more concerned with how bacteria may be communicating with the enteric nervous system and thereby the brain. Several approaches were identified, both *in vivo* (long-term) and *ex vivo* (short-term). Bacteria placed in the lumen of a small bowel segment communicate within seconds with sensory afferent nerve fibres in the myenteric plexus and within minutes, decrease the amplitude of gut motor contractions. These effects are accompanied by inhibition of a specific calcium activated potassium channel (KCa 3.1) in AH cells of the myenteric plexus. Interestingly, mast cells from rats fed *Lactobacillus rhamnosus* (JB-1) also showed inhibition of this channel (Forsythe et al., 2012). These data clearly point to a generalized systemic effect of an ingested probiotic. At the same time, activation of vagal fibres by luminal JB-1 but not by another lactobacillus (*L. salivarius* that does not affect gut motor contractions) supports the vagal activation by these bacteria en route to the brain. While components of bacteria responsible for these effects are not

totally characterized, an exopolysaccharide of *B. fragilis*, PSA, recapitulated the effects of the parent bacteria. A very recent important report from Mazmanian's laboratory suggests that this may be occurring through outer membrane micro-vesicles shed by the bacteria, offering a novel bacteria-host communication pathway (Shen et al., 2012).

Michiel Kleerebezem drew attention to the molecular consequences of interactions between the microbiome and the host at the transcriptomic and metabolomic levels. The complexity of these interactions was highlighted by the fact that in a double-blind placebo controlled cross-over design with 3 different probiotics in young healthy adults, each bacterium induced a different pattern of response in regulatory and other drug-like pathways in host tissues (van Baarlen et al., 2011). An additional problem facing the whole field is to define the "normal" microbiome in health and the emerging definition of a molecular 'bandwidth of human health' might provide an important window for further exploration (Bron et al., 2012). Recent just published papers have identified surprising and dynamic patterns of transcriptional signatures of intestinal adaptive and innate immunity, metabolism and neuronal development in response to a changing microbiome in conventionalized germ-free mice (El Aidy et al., 2012a, 2012b, 2012c).

Elaine Holmes focused on metagenomic and metabolomic approaches to studying the role of the gut microbiome in human health and disease and highlighted the value of studying microbial metabolites as specific biomarkers in urine and serum (Holmes et al., 2012). These may reflect primary or secondary changes in microbial communities or their consequent effects on host pathways. For example,

antibiotic induced effects on gut microbial composition can be analysed in this way and valuable information obtained on relative dysbiosis through a non-invasive approach (Swann et al., 2011). Extensive studies are building an archive of data in health and disease and demonstrate the power of combining different molecular approaches in microbe-host interactions (Kinross et al., 2008; El Aidy et al., 2012b). The application of urinary metabolic phenotyping to patients with and without autism have shown differences in certain microbial co-metabolites and suggest intriguing gut microbial disturbances in this developmental disorder (Yap et al., 2010).

Many chronic diseases are thought to be associated or initiated by stress. Chronic stress is correlated with subsequent low-grade inflammatory changes and is thought to cause or exacerbate conditions as varied as depression, anxiety and IBS. John Cryan offered examples and experimental models and the ways in which gut microbes could influence the hypothalamic-pituitary-adrenal (HPA) axis and how this in turn could change microbial composition (Bravo et al., 2011b; Cryan and Dinan, 2012; Dinan and Cryan, 2012). Exploration of such changes in the germ-free state and the effects of when (neonatal, post-weaning or adult) they occurred in conventionally housed animals has provided new insights into the programming of immune, endocrine and nervous systems. Such experiments have also revealed significant gender differences that may have their human counterparts in chronic disorders that may involve the nervous system (Clarke et al., 2012).

Major depressive disorder is accompanied by increases in serum of inflammatory markers such as C-reactive protein and TNF (Dantzer et al., 2011; Dantzer, 2012) and Graham

Rook persuasively argued that this was associated with a change in composition of the gut microbiome in the last few decades (*Raison et al., 2010*). This imbalance may have involved the loss of beneficial commensal bacteria (*Rook and Lowry, 2008*). This concept is an important variation on what is commonly termed “the hygiene hypothesis” and raises serious questions while offering possible answers as to why there is an increased prevalence of diseases such as depression, autism and autoimmunity in recent times (*Rook, 2010; Rook et al., 2012*).

IBS is co-morbid with psychiatric manifestations (*Whitehead et al., 2002*) and Premysl Bercik discussed experimental evidence linking dysbiosis with changes in the brain and behaviour including germ-free models and effects of antibiotic or probiotic treatment (*Bercik et al., 2012; Collins et al., 2012; Saulnier et al., 2012*). He adduced evidence that changes in the microbiome could be accompanied by alterations in the neurochemistry of the brain and behaviour in both vagotomised and non-vagotomised mice (*Bercik et al., 2011, 2012*). Therefore not all psychoactive effects of bacteria are mediated via the vagus nerve. Perhaps the most striking examples involved demonstration that faecal transplants from donor mice with defined phenotypic behavioural characteristics to others with equally stereotypic, but different behaviours resulted in the hosts displaying the behaviour of the donor animals (*Bercik et al., 2011*).

Emeran Mayer summarized information from many of the speakers listed above and integrated these into clinical knowledge. He stressed the fact that clinical infections may lead to alterations in behaviour and brain neurochemistry without necessarily involving changes in the gut microbiome (*Mayer, 2011*). These alterations may

in turn influence, and be influenced by antibiotic and possibly probiotic treatment. IBS may represent a combination of these effects and the outcome and presentation not only may be influenced by these factors, but also by early life trauma (*Berman et al., 2012*). It is therefore not surprising that patients’ symptoms may be treated by psycho-educational intervention (*Labus et al., 2012*). Many of these behavioural and neurochemical brain changes are reflected in the use of non-invasive functional magnetic resonance imaging (fMRI) and many of the important studies in this respect emanate from Emeran Mayer’s laboratory. It is therefore fitting that a recent study by *Larsson et al. (2012)* involves Bud Craig as a co-investigator, and finally, that evidence of fMRI changes has been observed in as yet unpublished studies of probiotic ingestion.

Richard Guerrant brought the symposium down to earth with a practical clinical reminder of the major potentially permanent detrimental effect on cognition of repeated childhood dehydrating or malnourishing infections, with and without diarrhoea (*Guerrant et al., 2012*). Prior to this presentation, little discussion had occurred about the role of diet and nutrition on the gut microbiome and consequent effects on the host. Indeed, this area has to date received scant attention in the literature. Because of its importance to health and well-being in developing countries as well as in the industrialized world, it will be crucial to extend research efforts into this subject. Possession of the ApoE4 allele was shown to be a protective factor against the development of cognitive and growth defects in children with heavy diarrheal burdens (*Mitter et al., 2012*), and a murine model supporting this observation was described.

In conclusion, many aspects of the emerging evidence for a microbiome-gut-brain axis were energetically discussed during this symposium. They revealed many convergent pieces of evidence in support of the concept and importance of the subject. However, they also showed up areas in which little effort had yet been placed, such as the role of nutrition and diet and the lack of definition of what constitutes a normal microbiome in a healthy adult. A recent study on the composition of the microbiome in a healthy and elderly population has shown an interesting role of diet (Claesson et al., 2012). The effects of ethnicity, culture and gender are only just beginning to be explored.

Furthermore, our ignorance of the possible roles of the mycobiome and virome is huge. We have not even touched upon the recent flurry of papers suggesting that the enteric nervous system may be involved in the earliest manifestations of Parkinson's disease, even before classical symptoms appear (Forsyth et al., 2011; Natale et al., 2011). Whether this represents an imbalance of organisms that together make up the normal microbiome or an example of an unusual pathogen, which enters the body through the enteric nervous system, remains unknown.

We greatly look forward to the next symposium on this subject.

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