

**2012 INTERAGENCY AUTISM COORDINATING COMMITTEE**  
**STRATEGIC PLAN UPDATE: QUESTION 2**  
**HOW CAN I UNDERSTAND WHAT IS HAPPENING?**

**WHAT IS NEW IN THIS RESEARCH AREA, AND WHAT HAVE WE LEARNED IN THE PAST TWO YEARS?**

In 2011 and 2012, significant progress has been made in understanding the underlying biology of ASD. This includes new observations about differences in neural connectivity in the brains of those with ASD, the discovery of molecular mechanisms that might cause autism symptoms, and insights from some of the conditions and disorders that co-occur with autism.

**Brain Imaging**

In the past two years there have been more than 225 research publications that have used neuroimaging of brain structure or connectivity to look for differences in autism. In response to the urgent need for sensitive and specific biomarkers for the diagnosis of ASD, many research groups have been studying patterns of brain development, including prospective longitudinal studies of infant siblings of children with ASD. Some traction has been gained by using diffusion weighted imaging (DWI, an imaging technique in which the diffusion of water molecules is mapped in order to reveal the underlying structure of the brain) to study white matter pathways. Research using this technique found atypical development of white matter pathways in high-risk infants (infants who had an older sibling with ASD) who later developed autistic symptoms (Weinstein et al., 2011). Abnormal white matter architecture was also found in three year old children with autism (Wolff et al., 2012).

Another recent trend is to use structural magnetic resonance imaging (structural MRI) to define neural phenotypes of autism. Several studies (e.g., Hoefft et al., 2011) have demonstrated that young boys with fragile X syndrome have different patterns of brain abnormalities than young boys with idiopathic autism. Other studies have shown that the accelerated brain growth associated with autism is observed mainly in young boys with regressive autism (Nordahl et al., 2011) and does not occur in girls with autism. Interestingly, enlarged brain size may be related to ethnicity, since macrocephaly (abnormally enlarged head) is not a common feature of autism in Israel (Davidovitch et al., 2011).

Over the past two years, an array of studies using functional magnetic resonance imaging (fMRI) and DWI has advanced understanding of the neural circuitry that is affected in ASD. These studies have most often highlighted differences in functional activation within specific brain regions known to be specialized for processing social information (e.g., social orienting, Greene et al., 2011; affective aspects of social processing, Gotts et al., 2012; gaze on emotional faces, Kliemann et al., 2012; attention, Redcay et al., 2012). Diffusion weighted imaging studies found disrupted pathways connecting language areas in children with autism (Lewis et al., 2012).

## **Neurophysiology**

Investigating neural circuits in the brain may reveal distinctions that cannot be observed by behavioral approaches alone. For example, brain activity has potential as an early predictor of subsequent ASD diagnosis. Electroencephalography (EEG) is a technique in which electrical activity along the scalp is used to measure current flow in the brain. EEG responses to dynamic eye gaze shifts (viewing faces with eye gaze directed toward versus away from the infant) during the first year predicted different clinical outcomes at 36 months (Elsabbagh et al., 2012). This difference in brain activity was apparent despite similar patterns of gaze as measured by eye tracking. Atypical audiovisual speech integration in infants at-risk for autism has also been shown (Guiraud et al., 2012). As the field strives for earlier methods of detecting autistic development, these findings, together with the neuroimaging findings described above, offer hope for the possibility of non-invasive, brain-based screening methods that could detect differences prior to the emergence of ASD behavioral symptoms.

## **Molecular Basis and Phenotyping**

Genetic studies continue to implicate dysfunction at the synapse—the junctions through which neurons transmit signals to each other—as part of the underlying biology of ASD. Of particular interest are the insights into the effects of gene mutations in animal models of syndromic autism, including FMRP (Fragile X Mental Retardation protein) in fragile X syndrome, MecP2 in Rett syndrome and TSC1/2 in tuberous sclerosis. Remarkably, these mouse studies support the hypothesis that many aspects of the ASD phenotype are reversible in both adults and infants; drugs influencing the mGluR5 receptor and the mTOR inhibitor, rapamycin, were found to be particularly effective (Tsai et al., 2012; Silverman et al., 2012; Auerbach, Osterweil & Bear, 2011). Rare mutations in genes that encode proteins forming large complexes at the synapse (Shank/ProSAP) are now known to be associated with autism. Deletions of these genes in mice were found to cause autism-like behaviors and alterations of synaptic function and glutamate neurotransmission (Schmeisser et al., 2012). Additionally, genetic deletions or duplications—called copy number variants (CNVs)—in other genes may interact with mutations in Shank to cause autism (Leblond et al., 2012).

As risk genes for ASD are identified at an increasing pace (see Question 3), the next step for brain imaging research is to determine how these risk genes impact the development of brain structure and function and contribute to the heterogeneity (diverse array of potential causes and presentation of symptoms) observed in people with ASD. For example, one fMRI study demonstrated that a common, functional ASD risk variant in the Met Receptor Tyrosine Kinase (MET) gene is an important regulator of key social brain circuitry in children and adolescents with and without ASD, with MET risk genotypes associated with atypical fMRI activation to emotional faces (Rudie et al., 2012). If validated, these findings highlight how different patterns in genetic variation may lead to an understanding of phenotypic heterogeneity in ASD and help to elucidate the key changes in neural circuitry.

A recent study examining gene expression in postmortem brains of individuals with autism showed a remarkable decrease in the typical variation seen between cortical regions in normal brains, a finding that suggests a simplification of cortical patterning in autism (Voineagu et al.,

2012). This study also uncovered patterns of neuronal gene expression in autism that paralleled and confirmed the role of genes known to be associated with autism risk. Surprisingly, the researchers also found a pattern of immune and glial cell gene expression in the autism brain that had not been identified in previous genetic studies, an observation that supports the view that brain immune system responses in autism are likely related to environmental events as well as genetic influences.

### **Immune System**

Recent findings in experimental animals are critical for understanding the role of glial cells (non-neuronal cells that maintain homeostasis, form myelin, and provide support and protection for neurons in the brain and nervous system) and immune pathways in the development of autism and its underlying biology. Models of microglia (glial cells that form part of the immune system) and immune pathway function during brain development and neuroplasticity in experimental animals, which have suggested involvement of microglia in normal neurodevelopmental activities such as the “pruning” of synapses, are the strongest demonstration of a potential role for the immune system in ASD pathogenesis (Schafer et al., 2012; Stephan, Barres & Stevens, 2012).

The potential role of adaptive immunity, environmental factors (such as maternal infections), and autoimmunity in the pathogenesis of ASD has also been identified using animal models. In some recent studies, for example, maternal immune activation resulted in long-term adaptive immune system abnormalities, in the offspring of mice exposed to immune challenges during pregnancy (Hsiao et al., 2012; Braunschweig et al. 2012). Interestingly, behavioral abnormalities observed in this model were reduced by reversing cellular immune deficits with immunologically normal bone marrow (Hsiao & Patterson, 2012), which has implications for development of new interventions for ASD.

Although human studies of immune function in ASD have been limited, some observations support a potential link between immune dysfunction and autism. One study that evaluated cytokines and chemokine expression in neonatal blood spot samples in the Danish Newborn Screening Bank suggested that an underactive immune system was present in infants that developed autism (Abdallah et al., 2012).

### **Co-occurring Conditions**

Over the past two years there has been increasing recognition of the substantial overlap between ASD and epilepsy. Past studies indicated that 10-20% of individuals with ASD have concurrent epilepsy. Within the past year, progress has been made on discovering the common roots of ASD and epilepsy, including identification of mutations in a gene coding for a metabolic enzyme (Novarino et al., 2012), and X-chromosome-linked mutations in a gene that produces proteins usually involved in cell adhesion (Marini et al., 2012).

Recent work has also reinforced the overlap between ASD and gastrointestinal disturbances. For instance, 24% of children with ASD enrolled in the Autism Speaks’ Autism Treatment Network (ATN) were shown to have one or more chronic gastrointestinal problems, and these problems

were associated with higher rates of both anxiety and sensory over-responsivity (Mazurek et al., 2012).

Sleep dysfunction is also associated with ASD and often correlates with its severity. Children with ASD who sleep fewer hours per night demonstrate lower overall IQ, verbal skills, overall adaptive functioning, daily living skills, socialization skills, and motor development. Furthermore, children who wake during the night in addition to sleeping fewer hours exhibit more communication problems (Taylor, Schreck & Mulick, 2012). Children with autism spend reduced time in the rapid eye movement (REM) phase of sleep, which has been hypothesized to play a role in neuroplasticity—the brain's ability to reorganize itself by forming new neural connections—and brain development (Buckley et al., 2010). Naturally occurring levels of a major metabolite of melatonin—which signals sleep onset—has been documented to be low in adolescents and young adults with autism compared to age and gender-matched controls (Tordjman et al., 2012). These findings provide the groundwork for treatment trials of melatonin in ASD (see Question 4).

### **WHAT GAPS HAVE EMERGED IN THE PAST TWO YEARS?**

Over the past two years several landmark efforts in biology have provided new tools and insights that may transform our understanding of ASD. While none of these efforts were focused on ASD, they provide unprecedented opportunities for future ASD research. The ENCODE project, for example, has demonstrated that the human genome is loaded with important biological signals beyond genes that code for proteins. While protein coding genes make up only 2% of the genome, new research revealed that about 80% of the genome is translated, resulting in some 20,000 non-coding RNA elements (Encode Consortium, 2012). Scientists working on ASD genetics have barely begun to explore these newly-discovered elements of the genome.

The Human Microbiome Project, which has mapped the microbial world of 18 different sites in the human body (Human Microbiome Consortium, 2012), has also provided important insights that have implications for many human conditions, including ASD. The results have altered thinking about what it means to be human, and the body is beginning to be viewed as more of a complex ecosystem in which human cells represent a paltry 10% of the population. But beyond the sheer numbers, this information brings new knowledge about the profound diversity of this ecosystem and striking individual differences. How these differences in the microbial world influence the development of brain, behavior, and neuroimmune function will be one of the great frontiers of clinical neuroscience in the next decade. In addition, the Human Connectome Project is providing the first detailed wiring diagram of the human brain, developing the tools for mapping the connections across distant regions of the cortex (Wedeen et al, 2012).

Turning to the basic issue of defining brain differences that contribute to autism, there continues to be a paucity of studies related to the cellular neuropathology of autism. The dearth of postmortem tissue has slowed research in every area addressed under this question. While this has been a challenge for many years, the loss of more than 50 brains after a freezer malfunction in June, 2012 has been an enormous setback. The loss represented about one third of the largest autism brain repository and will take years to replace (see Question 7).

In order to study the cellular and molecular underpinnings of autism, researchers also need appropriate cell culture models of neurons. In a landmark paper, investigators generated cortical neurons from induced pluripotent stem cells (iPSCs) derived from skin cells of two individuals with Timothy syndrome (Pasca et al., 2011). Interestingly, these neurons showed abnormalities in differentiation and neurotransmitter production that could be reversed by blocking the calcium channel known to be mutated in this monogenic, or single gene, cause of autism. iPSCs are promising both as a biological tool to uncover the pathophysiology of disease by creating relevant cell models and as a source of stem cells for cell-based therapeutic applications and drug discovery. It is noteworthy that for the first time, the derivation of iPSC lines from the whole blood of children with ASD was recently described (DeRoşa et al., 2012).

The lack of longitudinal studies in autism remains a striking gap in studies of brain function. While cross-sectional studies have provided important findings, there is a dearth of essential information about the time course of brain development from early infancy to adulthood (as well as the yet to be studied aging brain) in ASD. The power of longitudinal studies was recently reinforced by the results of a longitudinal structural MRI study that identified an increased rate of amygdala growth in very young children with ASD (Nordahl et al, 2012).

Although a network has been launched to study ASD in females, there remains a pressing need to conduct research aimed at understanding all aspects of ASD (genes, brain, and behavior) in females with ASD. ASD disproportionately affect males, and this skewed sex ratio has resulted in a bias of published research towards studies focused on males. Interestingly, girls are much less likely to be diagnosed with autism than are boys unless they also have intellectual or behavioral problems (Dworzynski et al., 2012), which might reflect either a gender bias in diagnosis or genuinely better adaptation/compensation in girls.

As more insight into the biological mechanisms underlying ASD is gained, one area that has been identified as a new gap is the role of the immune system and microglia in autism, which have recently been found to contribute to brain development and plasticity (Stephan, Barres & Stevens, 2012). Another is to understand the generalizability and pathophysiological significance of the findings of increased oxidative stress markers in plasma of children with autism (Melnyk et al., 2011). Further investigation into these and other gap areas will help explain the underlying biology of ASD, aiding in the identification of biomarkers for diagnosis and informing potential treatments and interventions in the future.

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