UChicago Postdoctoral Symposium 2021

Lesson from COVID-19: Postdoc and Beyond

September 20–24th (Virtual)

Poster Abstracts

Poster Session Schedule

Session 1 (10 am – 11 am) – Join here

Jiajin Luo – *Urban spatial accessibility of primary care and hypertension management on the south side of Chicago: a study from COMPASS cohort*

Rebecca Turcios – *Exploring genetic etiologies for arrhythmogenic right ventricular cardiomyopathies in chimpanzees*

Kiranj Chaudagar – *Co-targeting PI3K/MEK/Wnt signaling drives tumor-associated macrophage-mediated control of PTEN/p53-deficient murine prostate cancer*

Oscar Jara Leiva – *Do Connexin Mutants Cause Cataracts by Perturbing Glutathione Levels and Redox Metabolism in the Lens?*

Session 2 (10 am – 11 am) – Join here

Minhui Chen – *A new method to quantify cell type-specific genetic effects on gene expression using single-cell RNA-sequencing*

Olivia Gozel – *Low-dimensional shared variability affects communication between brain areas*

Frederic Labbe – *A computational model for the interaction between epidemiological dynamics and antigenic diversity in Plasmodium falciparum*

Gregory Handy – *Computational investigation of gamma rhythm synchronization across space via cortical VIP neurons*

Session 3 (11 am – 12 pm) – Join here

Bridget Clancy – *Identification of Ornithonyssus bacoti Infestation via an Exhaust Air Dust Health Monitoring Program*

Xinhai Chen – *Engineered human antibodies for the opsonization and killing of Staphylococcus aureus*

Srikrishnan Rameshbabu – *NLRP3 Activation Controls Prostate Cancer via Induction of Macrophage-mediated Phagocytosis*

Jenna Guthmiller – *Broadly neutralizing antibodies commonly target a membrane-proximal epitope of influenza virus hemagglutinin*

Session 4 (11 am – 12 pm) – Join here

Abhimanyu Thakur – *Engineering exosomes for targeted drug delivery for Alzheimer's disease therapy*

Shabana Shaik – *Translational profiling identifies sex-specific metabolic and epigenetic reprogramming of microglia in gut microbiome perturbed AD model*

Jenna Shoenberger – *Biocompatibility of a Novel Cranial Implant in a Rhesus Macaque*

Poster 1

Presenter: Jiajun Luo

Department: Public Health Sciences

Title: Urban spatial accessibility of primary care and hypertension management on the south side of Chicago: a study from COMPASS cohort

Abstract:
Background: Hypertension is preventable. Primary care facilities are able to detect hypertension and provide effective drugs for hypertension management. We aim to investigate how spatial accessibility (SA) of primary care affect the hypertension management.

Method: 5,096 participants from the Chicago Multiethnic Prevention and Surveillance Study were included. Addresses of these participants and primary care providers in selected Chicago communities were geocoded. An SA score was generated using enhanced two-step floating catchment area method. Logistic regression was used to estimate the odds ratio (OR) and 95% confidence interval (CI) for hypertension status according to SA score quartiles with adjustment for demographic covariates.

Results: The study population was predominantly non-Hispanic black (84.0%), over 53% reported an annual household income less than $15,000, and 37.3% were obese. Hypertension prevalence was 78.7% in this population, among which 37.7% were uncontrolled and 41.0% were unaware. Higher SA score was associated with less hypertension prevalence. Compared to the 1st quartile of SA score, the OR strengthened from 0.82 (95% CI: 0.67-1.01) for the 2nd quartile, to 0.75 (95% CI: 0.62-0.91) for the 3rd quartile, and further to 0.73 (95% CI: 0.60, 0.89) for the 4th quartile. Similar associations were observed for both uncontrolled and unaware hypertensions. When stratified by neighborhood socioeconomic status, better SA of primary care was associated with less unaware hypertension in both disadvantaged and non-disadvantaged neighborhoods.

Conclusion: Better SA of primary care can improve hypertension management. Residents in disadvantaged neighborhood can also benefit from interventions that increase the number of primary physicians.

Poster 2

Presenter: Rebecca Turcios

Department: Surgery

Title: Exploring genetic etiologies for arrhythmogenic right ventricular cardiomyopathies in chimpanzees

Abstract:
Approximately 30% of captive chimpanzees (P. troglodytes) are affected by primary structural heart diseases- one of which is arrhythmogenic right ventricular cardiomyopathy (ARVC). ARVC is a fibrofatty replacement of the myocardium which may lead to systolic dysfunction, arrhythmias and sudden cardiac deaths. Familial ARVC in humans has genetic associations in desmosomal genes, with most causal mutations occurring in PKP2. Whole genome sequencing of sub related ARVC affected P.troglodytes identified a nonsense (stopgain) variant in exon 6 of PKP2 in affected individuals. Given the close genetic relatedness to humans, variations observed in P.troglodytes PKP2 may result in an ARVC phenotype. Isoform analysis in human PKP2 has revealed isoforms with exon 6 retained and with exon 6 spliced out. We hypothesize that P.troglodytes PKP2 exon 6 is retained, which results in the inclusion of the identified stopgain variant in the gene transcript and causes a nonfunctional, truncated protein. An isoform analysis to characterize splicing of PKP2 in P. troglodytes is needed to detect the potential pathogenicity of this mutation. P. troglodytes derived induced pluripotent stem cells will be cultured and differentiated into cardiomyocytes. RNA will be isolated for transcriptomic analysis using Oxford Nanopore long read sequence technology. Isoforms with the retained exon 6 will support the hypothesis that the identified variant likely results in disease phenotype in P.troglodytes. With this information an improved understanding of ARVC in P.troglodytes could improve efforts to maintain healthy captive populations.

Poster 3

Presenter: Kiranj Chaudagar

Department: Medicine/Hematology/Oncology

Title: Co-targeting PI3K/MEK/Wnt signaling drives tumor-associated macrophage-mediated control of PTEN/p53-deficient murine prostate cancer

Abstract:
PTEN loss-of-function occurs in >50% of mCRPC patients and is associated with poor prognosis, therapeutic outcomes and resistance to immune-checkpoint inhibitors. The combination of PI3K/AKT-pathway inhibition and androgen blockade has demonstrated only a modest improvement in progression-free survival in PTEN-deficient mCRPC patients, highlighting the critical need for definitive therapeutic strategies that render long-term tumor control. As a first step towards understanding the mechanistic basis of this resistance, we performed a co-clinical trial in a prostate-specific PTEN/p53-deficient genetically engineered mouse model, and discovered that recruitment of non-phagocytic-PD-1-expressing tumor-associated macrophages (TAM) thwarts anti-tumor efficacy of degarelix (chemical castration)/copanlisib (PI3K-inhibitor) combination. Strikingly, we observed a ~3-fold enhancement in the response rate with the addition of PD-1 antibody (aPD-1), which was abrogated by TAM depletion. Mechanistically, decreased lactate production from copanlisib treated tumor cells resulted in suppression of histone lactylation (H3K18lac) and enhanced TAM activation. Addition of castration/aPD-1 blockade further augmented TAM activation; however activation of Wnt/MEK signaling pathways restored H3K18lac within TAM and led to treatment resistance. We therefore tested the combination of trametinib (MEK-inhibitor) with copanlisib which phenocopied degarelix/copanlisib/aPD-1 treatment and demonstrated an 80% response rate with corresponding suppression of H3K18lac within TAM. However, enhanced Wnt/□-catenin signaling was also responsible for resistance to copanlisib/trametinib combination in the 20% non-responder mice. Critically, the addition of LGK`974 (Porcupine-inhibitor) to trametinib/copanlisib combination resulted in complete tumor control without significant short-term toxicity. Collectively, the combination of copanlisib/trametinib/LGK`974 achieves significant TAM-driven tumor control in murine PTEN/p53-deficient prostate cancers, and warrants further investigation in PTEN-deficient mCRPC clinical trials.

Poster 4

Presenter: Oscar Jara Leiva

Department: Pediatrics

Title: Do Connexin Mutants Cause Cataracts by Perturbing Glutathione Levels and Redox Metabolism in the Lens?

Abstract:
Cataracts of many different etiologies are associated with oxidation of lens components. The lens is protected by maintenance of a pool of reduced glutathione (GSH) and other antioxidants. Because gap junction channels made of the lens connexins, Cx46 and Cx50, are permeable to GSH, we tested whether mice expressing two different mutants, Cx46fs380 and Cx50D47A, cause cataracts by impairing lens glutathione metabolism and facilitating oxidative damage. Levels of GSH were not reduced in homogenates of whole mutant lenses. Oxidized glutathione (GSSG) and the GSSG/GSH ratio were increased in whole lenses of Cx50D47A, but not Cx46fs380 mice. The GSSG/GSH ratio was increased in the lens nucleus (but not cortex) of Cx46fs380 mice at 4.5 months of age, but it was not altered in younger animals. Carbonylated proteins were increased in Cx50D47A, but not Cx46fs380 lenses. Thus, both mouse lines have oxidizing lens environments, but oxidative modification is greater in Cx50D47A than in Cx46fs380 mice. The results suggest that GSH permeation through lens connexin channels is not a critical early event in cataract formation in these mice. Moreover, because oxidative damage was only detected in animals with significant cataracts, it cannot be an early event in their cataractogenesis.

Poster 5

Presenter: Minhui Chen

Department: Medicine/Genetic Medicine

Title: A new method to quantify cell type-specific genetic effects on gene expression using single-cell RNA-sequencing

Abstract:
Gene expression levels vary across individuals, tissues, cell types, and recent evidence shows that genetic effects on gene expression often differ between cell types. Rapid growth in throughput and experimental methods for single-cell RNA-sequencing now allow this technology to be applied to sufficient sample sizes for genetic studies. In this study, we develop a new method to leverage these emerging datasets to dissect gene expression variability among cell types and individuals. To accommodate heterogeneous gene expression across cell types, we propose diverse statistical models to powerfully characterize the distribution of cell type-specific variation. Further, we extend these models to quantify cell type-specific genetic effects on expression. Through simulation, we found that our method was well powered when the population reached a moderate sample size (100 individuals). We will deploy these methods on multiple large-scale datasets, including a cohort of hundreds of lupus cases and controls from diverse populations, and link our inference with genetic risk factors for lupus to understand causal cell types.

Poster 6

Presenter: Olivia Gozel

Department: Neurobiology

Title: Low-dimensional shared variability affects communication between brain areas

Abstract:
Neuronal dynamics range from asynchronous spiking to richly patterned spatio-temporal activity and are modulated by external and internal sources. Although the activity of individual neurons is heterogeneous and within-area dimensionality of the response space is high, numerous experimental datasets exhibit low-dimensional shared variability between neurons, which can be modulated by cognitive states. Besides, cortical areas are connected through long-range excitatory projections and in non-human primates, it has been shown that there exists a low-dimensional communication subspace between visual areas that predicts spiking activity in a downstream area using upstream activity. However, little is known about the effect of neuronal dynamics on interactions between brain areas.

To investigate how low-dimensional shared variability affects communication between brain areas, as assessed by a communication subspace measure, we use a 3-layer spiking network. Neurons in L0 are homogeneous Poisson processes with a uniform rate. L1 and L2 consist of excitatory (E) and inhibitory (I) neurons which are recurrently connected. In randomly connected networks, asynchronous activity is generated when E inputs are approximately balanced by I inputs. However, brain connectivity is spatially structured, hence we model within- and between-layer connectivity using two-dimensional wrapped Gaussians. In both L1 and L2, we set a larger width for the recurrent than the feedforward connections, because such networks have been shown to transition from a stable to a pattern-forming regime as recurrent inhibition is broadened.

We observe that as the width of recurrent inhibitory connections is increased in L2, spatio-temporal patterns emerge within L2. By using the peak of the normalized power over all temporal frequencies and spatial wavenumbers as a measure of pattern-formation, we observe a decrease in prediction performance of L2 activity by L1 activity. However, when recurrent inhibition is instead broadened in L1, prediction of L2 activity becomes highly accurate. We can compute shared dimensionality using the participation ratio of the shared covariance matrix obtained by Factor Analysis when we sample neurons from a disc area with varied radiuses. Interestingly, pattern formation decreases within-area dimensionality identically when spatio-temporal patterns emerge in L2 or when they are inherited from L1.

Poster 7

Presenter: Frederic Labbe

Department: Ecology & Evolution

Title: A computational model for the interaction between epidemiological dynamics and antigenic diversity in Plasmodium falciparum

Abstract:
The microbiological paradigm for disease surveillance of diverse pathogens requires studying the variation of major surface antigens under the most intense immune selection. The major target of naturally acquired antibodies in the malaria parasite Plasmodium falciparum is the surface protein PfEMP1, encoded by the hyper-diverse var multigene family, whose variation should play a key role in transmission dynamics within and between hosts. To investigate the population structure of the parasite from the perspective of such diversity and the way it influences epidemiology, we previously developed a stochastic agent-based model (ABM) that tracks the dynamics of unique var repertoires within genomes and the individual immune memory in a population of hosts. However, the parasite harbors more conserved antigens and immunity to malaria is not determined by the var system alone. P. falciparum has many single-copy blood-stage antigen encoding genes of relatively low diversity that contribute to a generalized immunity influencing parasitemia and reducing the incidence of clinical episodes. To extend our ABM and further confront theory with epidemiological data obtained over the last six years in a high transmission setting in Ghana, we have incorporated generalized immunity together with parasitemia, a key epidemiological variable, into our computational formulation. The resulting model combining specific and generalized immunity is described here, together with its application to investigate the population dynamics of malaria in endemic high-transmission regions. This modelling and analytical work will provide a platform for understanding the impact of strain diversity on the overall parasite load in infected individuals and the response of the transmission system to intervention.

Poster 8

Presenter: Gregory Handy

Department: Neurobiology

Title: Computational investigation of gamma rhythm synchronization across space via cortical VIP neurons

Abstract:
Inhibitory neurons play a crucial role in many components of sensory processing, including modulating feature selectivity, mediating response suppression, and maintaining an asynchronous network state. Past mathematical models have successfully replicated and furthered our understanding of some of these processes by considering a recurrent network of excitatory and inhibitory neurons. However, experimental evidence has shown that significant diversity exists within this inhibitory population, with 80% of neurons falling into one of three major subtypes: parvalbumin (PV)-, somatostatin (SOM)-, and vasointestinal peptide (VIP)-expressing neurons. Here, we investigate how a division of labor among these interneuron subtypes enables the cortex to handle more elaborate computations than those previously considered.

In this talk, we will considering gamma band synchronization in the primary visual cortex (V1), which is thought to facilitate local and long-range communication in neural circuits. We observe through optogenetic suppression experiments that VIP neurons specifically suppress gamma synchronization between spatially separated cortical ensembles when they are processing non-matched stimulus features. We use a straightforward and minimal computational model of V1 to show how well-known features of the V1 circuit, namely like-to-like connectivity across retinotopic space, and specific, but powerful VIP->SST inhibition, are sufficient to capture these experimental observations.

Poster 9

Presenter: Bridget Clancy

Department: Surgery

Title: Identification of *Ornithonyssus bacoti* Infestation via an Exhaust Air Dust Health Monitoring Program

Abstract:
Ornithonyssus bacoti, the tropical rat mite, is a zoonotic bloodsucking mite which may infest mouse colonies via wild rodent vectors. Heavy infestations in mouse colonies have been documented to cause anemia, alopecia, and decreased reproductive performance. In mid 2020, our institution experienced increased levels of wild mice, which were found to be infested with O. bacoti diagnosed by microscopic exam and confirmed by fur swab PCR. We elected to add O. bacoti to our quarterly PCR health monitoring exhaust air dust (EAD) testing, increase wild mouse control measures, and treat the environment with a permethrin spray in an attempt to prevent colony animal infestation. Initial quarterly EAD health monitoring results in September of 2020 were negative for O. bacoti. However, in early 2021, multiple IVC racks tested positive for O. bacoti via quarterly testing. Historically in the literature, O. bacoti outbreaks of research mice were not identified until mite burden was high enough to cause dermatitis on animal care workers. Due to modern molecular diagnostics and proactive EAD surveillance, our institution was able to identify and initiate eradication measures in a timely manner. To the best of our knowledge, this is the first report to successfully identify O. bacoti using environmental PCR techniques. This outbreak demonstrates the importance of screening for O. bacoti in facilities with wild rodent issues, and highlights unique considerations when managing O. bacoti infestations.

Poster 10

Presenter: Xinhai Chen

Department: Microbiology

Title: Engineered human antibodies for the opsonization and killing of Staphylococcus aureus

Abstract:
Gram-positive organisms with their thick envelope cannot be lysed by complement alone. Nonetheless, antibody binding on the surface can recruit complement and mark these invaders for uptake and killing by phagocytes, a process known as opsonophagocytosis. The crystallizable fragment of immunoglobulins (Fcg) is key for complement recruitment. The cell surface of S. aureus is coated with Staphylococcal protein A (SpA). SpA captures the Fcγ domain of IgG and interferes with opsonization by anti-S. aureus antibodies. In principle, the Fcγ domain of therapeutic antibodies could be engineered to avoid the inhibitory activity of SpA. However, the SpA binding site on Fcγ overlaps with that of the neonatal Fc receptor (FcRn), an interaction that is critical for prolonging the half-life of serum IgG. This evolutionary adaptation poses a challenge for the exploration of Fcγ mutants that can both weaken SpA-IgG interactions and retain stability. Here, we use both wild type and transgenic human FcRn mice to identify new antibodies with enhanced half-life and increased opsonophagocytic killing in models of S. aureus infection and demonstrate that antibody-based immunotherapy can be improved by modifying Fcg. Our experiments also show that by competing for FcRn binding, staphylococci effectively reduce the half-life of antibodies during infection. These observations may have profound impact in treating cancer, autoimmune, and asthma patients colonized or infected with S. aureus and undergoing monoclonal antibody treatment.

Poster 11

Presenter: Srikrishnan Rameshbabu

Department: Medicine/Hematology/Oncology

Title: NLRP3 Activation Controls Prostate Cancer via Induction of Macrophage-mediated Phagocytosis

Abstract:
Immunotherapy has demonstrated limited efficacy in metastatic castrate-resistant prostate cancer (mCRPC) patients. This poorly immunogenic phenotype is mediated in part by a paucity of an immune cell infiltrate and a predominance of myeloid immunosuppressive cells, including tumor-associated macrophages (TAM). We hypothesized that strategies to re-invigorate anti-cancer innate immunity could provide durable benefit in PC. Here, we tested the impact of activating the NLRP3 inflammasome complex with a novel NLRP3 agonist BMS-392959 in an immunotherapy-refractory murine c-myc driven PC tumor model. Our results demonstrate significant single-agent tumor control in BMS-392959 treated mice, which is accompanied by a global increase in immune cell infiltration. Mechanistic studies revealed a tumor cell extrinsic macrophage-mediated innate response driven by enhanced M1 polarization and phagocytosis of tumor cells, that was significantly enhanced by the addition of androgen deprivation therapy (ADT). Strikingly, combination with ADT led to robust and in some cases, complete tumor control and extended survival compared to monotherapy. Collectively, our results demonstrate that NLRP3 is a promising therapeutic target that drives macrophage-mediated anti-cancer innate immunity, and warrants further investigation in neoadjuvant clinical trials in high-risk PC patients.

Poster 12

Presenter: Jenna Guthmiller

Department: Medicine/Rheumatology

Title: Broadly neutralizing antibodies commonly target a membrane-proximal epitope of influenza virus hemagglutinin

Abstract:
Broadly neutralizing antibodies targeting epitopes of the influenza virus hemagglutinin (HA) have the potential to provide near universal protection against influenza virus infection, however, viral mutants that escape broadly neutralizing antibodies have been reported. Therefore, the identification of broadly neutralizing antibody classes that can neutralize viral escape mutants is critical for universal influenza virus vaccine design. Here, we report a distinct class of broadly neutralizing antibodies targeting an epitope toward the bottom of the HA stalk domain where HA is "anchored" to the membrane. Anchor epitope targeting antibodies are broadly neutralizing across H1-expressing viruses and can cross-react with pandemic-threat H2 and H5-expressing viruses. Antibodies targeting this anchor epitope utilize a highly restricted repertoire, which encode for two conserved motifs that make extensive contacts with conserved residues in the HA fusion peptide. Moreover, anchor epitope targeting B cells are common in the human memory B cell repertoire and were recalled in humans by a chimeric HA vaccine, a potential universal influenza virus vaccine. Altogether, our study reveals an unappreciated class of broadly neutralizing antibodies against group 1 influenza A viruses. We demonstrate that current seasonal influenza vaccines do not induce anchor-targeting antibodies, while properly designed universal influenza virus vaccine candidates, including the chimeric HA approach, can induce antibodies against this conserved anchor epitope. To maximize protection against seasonal and pandemic influenza viruses, vaccines should aim to boost this previously untapped source of broadly neutralizing antibodies that are widespread in the human memory B cell pool.

Poster 13

Presenter: Abhimanyu Thakur

Department: Cancer Research (Ben May)

Title: Engineering exosomes for targeted drug delivery for Alzheimer's disease therapy

Abstract:
Alzheimer's disease (AD) is a neurodegenerative disease, characterized by damage of hippocampus neurons, and the formation of amyloid plaques, hyperphosphorylated tau protein, and neurofibrillary tangles. In an AD brain, amyloid-β precursor protein (APP) is highly upregulated, which binds with FE65 protein via interaction between Fe65-PTB2 and APP intracellular domain (AICD), leading to the release of amyloid-β, supporting AD pathogenesis. Therefore, targeting the interaction between APP and FE65 could be a potential therapeutic approach for AD. Recently, exosomes, a set of nanovesicles with diameter in the range of 30-100 nm have been widely studied as a drug delivery carrier for various diseases including brain disorders such as AD, Parkinson's disease, and glioma; owing to its ability to cross the blood-brain barrier, and its modifiable surface with target specific moieties. Therefore, a novel exosome-based targeted drug delivery system was developed via engineering the surface of neuron cells-derived exosomes to achieve APP targeted delivery in the brain of AD mouse models. The engineered exosomes encapsulating an autophagy inducing agent could seize and block the collaboration between Fe65-PTB2 and AICD, followed by the delivery of the cargo, implying its role as potential therapeutics for AD.

Poster 14

Presenter: Shabana Shaik

Department: Neurobiology

Title: Translational profiling identifies sex-specific metabolic and epigenetic reprogramming of microglia in gut microbiome perturbed AD model

Abstract:
Microglia, resident macrophages of CNS constantly screen the brain and engage in pathological processes by changing their morphology and expressing various antigens. They play a central role in mediating phagocytic clearance of Aβ peptides, a pathological hallmark of Alzheimer's disease (AD). While sex-specific differences in etiopathology are not evident in the brains of AD patients, females show more incidence for reasons largely unknown. Studies from Sisodia lab showed that antibiotic (ABX) mediated alterations of the gut microbiome in APPPS1-21 transgenic mice resulted in a significant decrease in amyloidosis and altered microglial phenotypes that are specific to male mice. To understand sex-specific changes in amyloidosis and the molecular players involved in mediating microglial function in response to ABX, we generated 'APPPS1-21-CD11br' microglia reporter mice. Consistent with our previous studies, ABX-treatment in these mice led to reduced amyloidosis in male mice with no significant changes in the females. Quantitative profiling of newly synthesized peptides was performed from immunoprecipitation of cortical homogenates of WT-CD11br and APPPS1-21-CD11br male and female mice treated with ABX or vehicle. First, we identified variants proteins expressed in microglia due to expression of mutant APP/PS1 transgenes and revealed sex-specific cellular stress responses, due to the deposition of Aβ plaques. Next, the variant proteins identified with ABX-treatment revealed sex-specific metabolic and epigenetic reprogramming associated with microglial function. ABX-treated male mice showed a metabolic shift to meet the energetic demands for amyloid clearance while the female mice showed loss of energy homeostasis due to dysfunctional mitochondria leading to impaired lysosomal clearance.

Poster 15

Presenter: Jenna Schoenberger

Department: Surgery

Title: Biocompatibility of a Novel Cranial Implant in a Rhesus Macaque

Abstract:
Cranial implants have proven to be indispensable to neurophysiology research in nonhuman primates. Since their inception centuries ago, cranial implants have continuously improved with one recent innovation being 3-D printing. This technology takes advantage of computed tomography and magnetic resonance scans to allow for individual customization, enhancing function and fit. Using 3-D printed devices evades the tedious task of reshaping metal implants during cranial implantation surgeries, hence minimizing anesthesia/surgery time and risk of infection. The reduced space between implant and skull facilitates implant integration and decreases postoperative complications. In addition, material modifications using polyamides, a synthetic polymer with proven human biocompatibility, has improved flexibility, and decreased weight and cost of implants. Polyamide 12 (PA12) has been used to develop hip and knee implants for humans. Given this information, construction of PA12, 3-D printed, cranial implants for rhesus macaques was explored. As part of biocompatibility testing, we tested tissue reactivity to PA12 by surgically placing a small sample into the subcutaneous tissue between the scapulae of a rhesus macaque. During six weeks it was in place, examination of the implant site occurred at least once per week, and no tissue reaction was ever noted. After explantation, no gross or histopathological foreign body reaction was seen in the tissue surrounding the PA12 implant. PA12 was then used to create a 3-D printed microelectrode array connector, which was successfully placed onto the skull of this same rhesus macaque. To our knowledge, this is the first 3-D printed microelectrode array connector produced from PA12.