

University at Buffalo Institutional Review Board (UBIRB)

Office of Research Compliance | Clinical and Translational Research Center Room 5018

875 Ellicott St. | Buffalo, NY 14203

UB Federalwide Assurance ID#: FWA00008824

PROTOCOL TITLE: *"Spit for Buffalo" saliva sample collection project*

INSTRUCTIONS: Complete Research Protocol (HRP-503)

- *Depending on the nature of what you are doing, some sections may not be applicable to your research. If so, you must provide the reason why the section is not applicable for the response. For example, most behavioral studies would answer all questions in section 30 with words to the effect of "drugs and medical devices are not used in this study."*
- *When you write a protocol, keep an electronic copy. You will need to modify this copy when making changes.*
- *Do not remove the italics instructions or headings.*
- *If you are pasting information from other documents be sure to use the "Merge Formatting" paste option so that the formatting of the response boxes is not lost. If information is presented outside of the response boxes, it will not be accepted.*
- *If this study involves multiple participant groups who participate in different research procedures, consent processes, etc., be certain to provide information in each applicable section for each participant group and clearly label each participant group within a section or subsection.*

PROTOCOL TITLE:

Include the full protocol title.

Response: "Spit for Buffalo" saliva sample collection project

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VERSION NUMBER:

Include the version number of this protocol.

2/1/16

DATE:

Include the date of submission or revision.

1/5/16 submission, 1/14/16 revision, 2/16/16 revision, 3/25/16 revision

Grant Applicability:

Describe whether or not this protocol is funded by a grant or contract and if so, what portions of the grant this study covers.

Funds for sample collection kits will be requested from upcoming grant proposals from the Genome, Environment & Microbiome community and from the CTSA pilot grant program. Storage will be paid by the forthcoming UB BioBank project and sequencing will be paid by individual investigators or by the Buffalo Institute for Genomics (BIG).

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1.0 Objectives

1.1 *Describe the purpose, specific aims, or objectives.*

A project to establish a collection of patients from the UBMD practice plans consented for research purposes and who have given a saliva sample for future Genome and Microbiome studies.

1.2 *State the hypotheses to be tested.*

UB needs to establish a patient pool for Precision Medicine/Genomic/Microbiomic studies

2.0 Background

2.1 *Describe the relevant prior experience and gaps in current knowledge.*

Many diseases and conditions are related to specific genetic mutations or Microbiome status. We need a pool of patient whose genome and oral microbiome we know whose medical records can be queried for specific conditions and correlated with their genome or microbiome status.

2.2 *Describe any relevant preliminary data.*

None

2.3 *Provide the scientific or scholarly background for, rationale for, and significance of the research based on the existing literature and how will it add to existing knowledge.*

Many diseases and conditions are related to specific genetic mutations or Microbiome status. We need a pool of patient whose genome and oral microbiome we know whose medical records can be queried for specific conditions and correlated with their genome or microbiome status.

2.4 *Include complete specific citations/references.*

There have been many studies that have indicated that various genomic loci affect disease susceptibility for many conditions including sleep latency[1], obesity[2], coronary artery disease[3], Coeliac disease[4] and others[5]. Many studies have related the microbiome to human health[6-8]. Recently, one study has linked specific loci with specific microbiome composition[9]. The current study may lend new insights into medical relatedness of such phenomena in a Buffalo population.

1. Parsons, M.J., Lester, K.J., Barclay, N.L., Nolan, P.M., Eley, T.C., and Gregory, A.M. (2013). Replication of Genome-Wide Association Studies (GWAS) loci for sleep in the British G1219 cohort. *Am J Med Genet B Neuropsychiatr Genet* 162B, 431-438.

2. Shabana, Ullah Shahid, S., Wah Li, K., Acharya, J., Cooper, J.A., Hasnain, S., and Humphries, S.E. (2015). Effect of six type II diabetes susceptibility loci and an FTO variant on obesity in Pakistani subjects. *Eur J Hum Genet*.

3. Erdmann, J., Grosshennig, A., Braund, P.S., Konig, I.R., Hengstenberg, C., Hall, A.S., Linsel-Nitschke, P., Kathiresan, S., Wright, B., Tregouet, D.A., et al. (2009). New susceptibility locus for coronary artery disease on chromosome 3q22.3. *Nature Genet.* 41, 280-282.
4. Coleman, C., Quinn, E.M., Ryan, A.W., Conroy, J., Trimble, V., Mahmud, N., Kennedy, N., Corvin, A.P., Morris, D.W., Donohoe, G., et al. (2016). Common polygenic variation in coeliac disease and confirmation of ZNF335 and NIFA as disease susceptibility loci. *Eur J Hum Genet* 24, 291-297.
5. Lee, H.J., Woo, H.G., Greenwood, T.A., Kripke, D.F., and Kelsoe, J.R. (2013). A genome-wide association study of seasonal pattern mania identifies NF1A as a possible susceptibility gene for bipolar disorder. *Journal of affective disorders* 145, 200-207.
6. Slocum, C., Kramer, C., and Genco, C.A. (2016). Immune dysregulation mediated by the oral microbiome: potential link to chronic inflammation and atherosclerosis. *J Intern Med.*
7. Bravo-Blas, A., Wessel, H., and Milling, S. (2016). Microbiota and arthritis: correlations or cause? *Curr Opin Rheumatol* 28, 161-167.
8. Morgan, X.C., Kabakchiev, B., Waldron, L., Tyler, A.D., Tickle, T.L., Milgrom, R., Stempak, J.M., Gevers, D., Xavier, R.J., Silverberg, M.S., et al. (2015). Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease. *Genome Biol.* 16, 67.
9. Davenport, E.R., Cusanovich, D.A., Michelini, K., Barreiro, L.B., Ober, C., and Gilad, Y. (2015). Genome-Wide Association Studies of the Human Gut Microbiota. *PLoS One* 10, e0140301.

3.0 Inclusion and Exclusion Criteria

3.1 Describe the criteria that define who will be included or excluded in your final study sample.

Only patients in the UBMD practice plans.

3.2 Describe how individuals will be screened for eligibility.

Only adults (18 or older) will be recruited and no screening beyond confirmation of age will be done. Potential subjects will be informed that only individuals 18 years and older are eligible to participate. This will be stated in both the flyer and consent form.

3.3 Indicate specifically whether you will include or exclude each of the following special populations: (You may not include members of these populations as subjects in your research unless you indicate this in your inclusion criteria.)

- Adults unable to consent
- Individuals who are not yet adults (infants, children, teenagers)

- *Pregnant women*
- *Prisoners*

Exclude Adults unable to consent, not yet adults and prisoners. Pregnant women would be included.

3.4 *Indicate whether you will include non-English speaking individuals. Provide justification if you will exclude non-English speaking individuals.*

(In order to meet one of the primary ethical principles of equitable selection of subjects, non-English speaking individuals may not be routinely excluded from research. In cases where the research is of therapeutic intent or is designed to investigate areas that would necessarily require certain populations who may not speak English, the researcher is required to make efforts to recruit and include non-English speaking individuals. However, there are studies in which it would be reasonable to limit subjects to those who speak English: e.g., pilot studies, small unfunded studies with validated instruments not available in other languages, numerous questionnaires, and some non-therapeutic studies which offer no direct benefit.)

If we can translate our consent form we will include these patients.

4.0 Study-Wide Number of Subjects (Multisite/Multicenter Only)

4.1 *If this is a multicenter study, indicate the total number of subjects to be accrued across all sites.*

5.0 Study-Wide Recruitment Methods (Multisite/Multicenter Only)

If this is a multicenter study and subjects will be recruited by methods not under the control of the local site (e.g., call centers, national advertisements) describe those methods. Local recruitment methods are described later in the protocol.

5.1 *Describe when, where, and how potential subjects will be recruited.*

NA, single site

5.2 *Describe the methods that will be used to identify potential subjects.*

NA

5.3 *Describe materials that will be used to recruit subjects. (Attach copies of these documents with the application. For advertisements, attach the final copy of printed advertisements. When advertisements are taped for broadcast, attach the final audio/video tape. You may submit the wording of the advertisement prior to taping to preclude re-taping because of inappropriate wording, provided the IRB reviews the final audio/video tape.)*

NA

6.0 Multi-Site Research (Multisite/Multicenter Only)

6.1 *If this is a multi-site study where you are the lead investigator, describe the processes to ensure communication among sites, such as:*

- *All sites have the most current version of the protocol, consent document, and HIPAA authorization.*
- *All required approvals have been obtained at each site (including approval by the site's IRB of record).*
- *All modifications have been communicated to sites, and approved (including approval by the site's IRB of record) before the modification is implemented.*
- *All engaged participating sites will safeguard data as required by local information security policies.*
- *All local site investigators conduct the study appropriately.*
- *All non-compliance with the study protocol or applicable requirements will be reported in accordance with local policy.*

NA

6.2 *Describe the method for communicating to engaged participating sites:*

- *Problems.*
- *Interim results.*
- *The closure of a study*

NA

7.0 Study Timelines

7.1 *Describe the duration of an individual subject's participation in the study.*

We anticipate this project will continue for at least 10 years

7.2 *Describe the duration anticipated to enroll all study subjects.*

All subjects will be enrolled for an undetermined period.

7.3 *Describe the estimated date for the investigators to complete this study (complete primary analyses)*

Most likely never. The patients will be an ongoing resource for all future Precision Medicine/Genome/Microbiome studies

8.0 Study Endpoints

8.1 *Describe the primary and secondary study endpoints.*

Establishing of a set of patients with consented samples that can be used for future research in the relationship of genome and microbiome to health conditions.

8.2 Describe any primary or secondary safety endpoints.

There are no safety concerns as no interventions are planned in this protocol.

9.0 Procedures Involved

9.1 Describe and explain the study design.

Patients will be provided information about the study in the flyer and consent document. If patients have questions, other than simple questions, before signing, they will contact and speak with someone from the study team before providing their consent. At the Conventus site all consent documents and samples will be collected at the front desk, but details about the study will only be addressed by study team members (GEM coordinator) and not those at the front desk. At the Buffalo General Medical Center (BGMC) site patients will be provided information about the study in a flyer at the front desk and if they are interested will be given a consent form to read and complete, but details about the study will only be addressed by study team members (GEM coordinator). At the Conventus site, after signing the consent form and presenting it to the front desk patients will be given a saliva collection tube with instructions. At the Conventus site they will spit into a vendor labeled bar-coded saliva collection tube and return it to the front desk. At the BGMC site, after signing the consent form they will give it to a nurse when they are brought back to the examination area and will then be given a bar-coded saliva collection tube by the nurse who will collect it after filling. The bar code is printed on the tube and is a vendor generated alphanumeric identifier containing no patient information. The bar code for the sample will first be entered into the patients EHR by either scanning or manual typing by the UBMD personnel manning the patient intake area of the Conventus Building or by nurses at the BGMC site. It will then be transferred into the CIDR (Clinical Integrated Data Respository) by the Institute for Healthcare Informatics (IHI) in their quarterly synchronizing of the UBMD Allscripts EHRs with the CIDR. A marker indicating that a sample has been collected will be placed into the i2b2 database by the IHI. This ensures that the bar code is not available to anyone querying the i2b2 database. The samples will be stored in a filing cabinet behind the front desk to insure security and daily the sample will be collected by the UB Biobank and either stored, or DNA prepared from it for Genome and Microbiome sequencing by the UB Genomics and Bioinformatics Core or an outside entity. The bar code on the sample will be independently input by the Biobank so that only this coded information is associated with the sample within the Biobank or after sequencing. The Genome/Microbiome data will be stored in the GDW (Genomics Data Warehouse) at the

Buffalo Institute for Genomics and Data Analytics (BIG) and will be made queryable for investigators around the world searching for specific mutations. The i2b2 data will be queryable by investigators interested in specific diseases/conditions. The bar codes themselves will be unavailable to investigators unless they have obtained separate IRB approval for their use.

The UB Biobank is an entity under construction that will be housed in the Clinical and Translational Research Center (CTRC) and will have as its mandate the storage of DNA and tissue samples for clinical research performed at UB. The current version of the UB Biobank is being run by Dr. Andrew Talal for his patient liver studies but he has agreed in principal to store DNA samples for this project if needed until a permanent multi-user biobank is established. Until this is available unprocessed saliva samples will be stored in the Biobank room of the CTRC and any processed DNA samples will be stored in the UB Genomics and Bioinformatics core which is responsible for DNA preparation from the saliva samples.

The UB Genomics and Bioinformatic Core is a UB entity dedicated to Genomic research. They are located in the New York State Center of Excellence in Bioinformatics and Life Sciences (CBLS) and will prepare DNA from the saliva samples as funding is made available. They will either store the DNA within the Core or transfer it to the UB Biobank once it is established.

The Institute for Healthcare informatics is a UB entity whose mandate is to provide storage of EHR records of UBMD and other patients and to create a database of health records that can be queryable by researchers in a de-identified manner for translational research. They have established the CIDR database (Clinical Integrated Data Repository) and the de-identified i2b2 database. It is housed at the CBLS and Dr. Peter Winkelstein is its director. These databases are covered under IRB project 030-496602.

The Genome, Environment & Microbiome community of excellence (GEM) is a UB funded interdisciplinary group dedicated to understand the interactions between the Genome, the Environment and the Microbiome in human health. They are mandated both to perform research in these areas and to perform community outreach and educational activities on the Genome and Microbiome. Drs. Tim Murphy, Norma Nowak and Jennifer Surtees are its directors. The GEM Outreach Coordinator is currently Ms. Bridget Brace-MacDonald.

BIG is a UB entity funded by the State of New York to foster research and economic development in "Big Data" including Genomics data. It is housed in the CBLS and maintains a Genomics Data Warehouse (GDW) containing sequence information of patients included in a variety of research trials at UB. This database is searchable for genetic variations

present in patients. Access is by password and investigators are screened and approved by a data access committee. The director of BIG is Dr. Brian McIlroy and Drs. Norma Nowak and Tom Furlani are responsible for biological and computational data, respectively. The GDW is currently pursuing IRB approval. Any database requiring IRB approval, will not be used or involved until IRB approval has been granted.

The Center for Computational Research (CCR) is a UB owned and operated computer resource that provides computing functions for BIG and the UB Genomics and Bioinformatics Core.

The MDA (Muscular Dystrophy Association) clinic at the BGMC is a clinic run by Dr. Wolfe in the UB Neurology Dept. Dr. Wolfe has approved testing of the consenting and sample collection process at this clinic to ensure that procedures can be streamlined to minimize any effect on overall workflow at the clinic in anticipation of expanding it to other clinics and eventually the Conventus site.

The Global Alliance for Genomics and Health (GA4GH) is an international organization dedicated to promoting the safe and efficient exchange of information related to genomics and health. They have established protocols and recommendations for the secure storage and searching of genomic sequences and patient phenotype information. GA4GH was formed to help accelerate the potential of genomic medicine to advance human health. It brings together over 375 leading institutions working in healthcare, research, disease advocacy, life science, and information technology. The members of GA4GH are working together to create a common framework of harmonized approaches to enable the responsible, voluntary, and secure sharing of genomic and clinical data. The Genetics, Genomic & Bioinformatics Graduate Program at UB is an organizational member of GA4GH and promotes the use of its standards at UB. A URL for them is here: <https://genomicsandhealth.org>

9.2 Provide a description of all research procedures being performed and when they are performed, including procedures being performed to monitor subjects for safety or minimize risks.

Patients will be given a saliva collection tube with instructions and asked to fill it and return it. This is the only perceived procedure in which the patients will participate.

9.3 Describe procedures performed to lessen the probability or magnitude of risks.

There is little or no risk. Instructions for filling the saliva collection tube are relatively simple.

9.4 Describe all drugs and devices used in the research and the purpose of their use, and their regulatory approval status.

None

9.5 *Describe the source records that will be used to collect data about subjects. (Attach all surveys, scripts, and data collection forms.)*

None with this protocol. Future protocols that will use these patients may have re-contact requirements that would include data collection. Future protocols would be required to allow association of the bar-code with a patients name and address for future contact, but these protocols are theoretical and beyond the scope of this protocol.

9.6 *What data will be collected including long-term follow-up.*

No long-term follow up will be done under this protocol. Any recontact will be done under a separate IRB-approved protocol.

9.7 *For HUD uses provide a description of the device, a summary of how you propose to use the device, including a description of any screening procedures, the HUD procedure, and any patient follow-up visits, tests or procedures.*

None

10.0 Data and Specimen Banking

10.1 *If data or specimens will be banked for future use, describe where the data/specimens will be stored, how long they will be stored, how the data/specimens will be accessed, and who will have access to the data/specimens.*

Saliva samples both native and processed for DNA will be stored in the UB Biobank. They will be accessed only by Biobank personnel. Data generated by DNA sequencing will be stored in a coded manner using only the sample barcode on secure servers within the Biobank or at the Institute for Healthcare Informatics. At these sites only Biobank or IHI personnel will have access. Genomic sequence information will be stored on the secure GDW (Genomics Data Warehouse) servers at BIG that can be queried by investigators around the world but only the existence of a patient with a specific genotype will be available in a de-identified manner.

10.2 *List the data to be stored or associated with each specimen.*

Barcode data for each sample and DNA sequence information will be stored, both genomic and microbiomic

10.3 *Describe the procedures to release data or specimens, including: the process to request a release, approvals required for release, who can obtain data or specimens, and the data to be provided with specimens.*

Data will be made available through a layered process. Investigators will apply to the BIG for permission to search for specific patient types (age, disease, condition, etc.) and only de-identified statistics will be returned. Approval will be granted by a committee at the BIG. Mutation

information will be stored on a secure server that can be queried from around the world by GA4GH-approved investigators.

11.0 Data Management

11.1 Describe the data analysis plan, including any statistical procedures.

Genome data and Microbiome data will be analyzed by the BIG group.

11.2 Provide a power analysis.

None needed as this is not a study but a patient collection project.

11.3 Describe the steps that will be taken secure the data (e.g., training, authorization of access, password protection, encryption, physical controls, certificates of confidentiality, and separation of identifiers and data) during storage, use, and transmission.

The completed consent forms will be stored in a non-patient accessible filing cabinet behind the desk as will the collected saliva samples. The bar codes will not be associated with any specific consent form and will be stored only within the patients EHR. Bar code data from the collection tube will be input into the UBBiobank database by trained personnel on a password-protected computer system with encryption. The computer will be secured in a locked room in the BioBank with swipe card access. Sequencing data with the attached bar code information will be maintained on secured servers in the Center for Computational research within a password protected database on an encrypted hard drive accessible only by screened personnel who apply for access to a secured web-based search interface. When sequence information is placed on a publically accessible Global Alliance for Genomics and Health (GA4GH) compliant beacon server the bar code information will NOT be available, only the sequence information.

11.4 Describe any procedures that will be used for quality control of collected data.

Samples will be assessed for DNA degradation and poor quality samples will be discarded.

11.5 Describe how data and specimens will be handled study-wide:

See above. Saliva samples both native and processed for DNA will be stored in the UB Biobank. They will be accessed only by Biobank personnel. Data generated by DNA sequencing will be stored in a coded manner using only the sample barcode on secure servers within the GDW of BIG. At these sites only Biobank or BIG personnel will have access. Genomic sequence information will be stored on secure servers that can be queried by investigators around the world but only the existence of a patient with a specific genotype will be available.

11.6 What information will be included in that data or associated with the specimens?

Only the bar code of the sample will be associated with the data. All medical information will remain in the secure IHI database.

11.7 Where and how data or specimens will be stored?

UB Biobank (samples), UB Genomics and Bioinformatics core (samples), BIG (sequence data), IHI (de-identified or coded health data)

11.8 How long the data or specimens will be stored?

Undetermined

11.9 Who will have access to the data or specimens?

See above. Data will be made available through a layered process. Investigators will apply to the Institute for Healthcare Informatics for permission to search for specific patient types (age, disease, condition, etc.) and only statistics will be returned. Approval will be granted by a committee at the IHA. Mutation information will be stored on a secure GDW server that can be queried from around the world.

11.10 Who is responsible for receipt or transmission of the data or specimens?

GEM Coordinator (consent forms and samples) UB Biobank (consent forms and samples), BIG (sequence data) and IHI (health records) personnel.

11.11 How data and specimens will be transported?

Saliva samples will be transported on a cart between the Conventus building and the BGMC to the UB Biobank by personnel trained to carefully monitor the sample and not let them out of their sight during transport. At the time of DNA preparation the samples will be transported by cart to the UB Genomics and Bioinformatics Core facility (GBC) where they will be accepted by trained personnel who will monitor them during DNA processing. DNA will be produced in a 96-well format with a single bar code label and will be stored by the GBC in a locked -80 freezer until sequencing is performed. Depending on whether sequencing is performed within the GBC or an outside entity, the sample will either remain within the GBC or will be transported by courier in dry ice to any external sequencing facility. Any DNA remaining after initial sequencing will be stored in the UB Genomics and Bioinformatic core or the UB Biobank once it is fully operational. The only information associated with the DNA 96-well plate will be a single bar code associated with the plate and associated bar codes for each DNA sample in the plate. Data will be transported by ethernet over secure SFTP servers.

12.0 Provisions to Monitor the Data and Ensure the Safety of Subjects

12.1 Describe the plan to periodically evaluate the data collected regarding both harms and benefits to determine whether subjects remain safe.

NA

12.2 Describe what data are reviewed, including safety data, untoward events, and efficacy data.

None

12.3 Describe how the safety information will be collected (e.g., with case report forms, at study visits, by telephone calls with participants).

None

12.4 Describe the frequency of data collection, including when safety data collection starts.

None

12.5 Describe who will review the data.

The PI will monthly review the data to determine how collection is proceeding.

12.6 Describe the frequency or periodicity of review of cumulative data.

Monthly

12.7 Describe the statistical tests for analyzing the safety data to determine whether harm is occurring.

NA

12.8 Describe any conditions that trigger an immediate suspension of the research.

None are anticipated although if there were a data breach resulting in re-identification of patient name with their genomic data then procedures would be put in place to prevent it from reoccurring.

13.0 Withdrawal of Subjects

13.1 Describe anticipated circumstances under which subjects will be withdrawn from the research without their consent.

If a patients sample is deemed unsuitable for sequencing due to DNA degradation then that sample will be discarded and the patient will be removed from the research without their consent.

13.2 Describe any procedures for orderly termination.

Since the samples will remain the patients will not be contacted if they are removed from the research. The bar code will be deleted from the sample database as will the barcode identifier in the patients EHR.

13.3 *Describe procedures that will be followed when subjects withdraw from the research, including partial withdrawal from procedures with continued data collection.*

14.0 Patients will not be able to be withdrawn once samples are collected. In order to withdraw samples we would need to maintain a record of the sample number and the patient's name. After the sample is collected and the number entered we will not have access to the patients EHR. The number only goes into the CIDR database and we will not have access to that database either. Only future investigators who want to retrieve information and who have their own IRB approval will have access to the CIDR and/or EHR records. Therefore we cannot remove samples. We do not want to have access to the patients EHR or the CIDR so as to maintain as much confidentiality as possible and to minimize intrusion into the patients medical records.

Risks to Subjects

14.1 *List the reasonably foreseeable risks, discomforts, hazards, or inconveniences to the subjects related the subjects' participation in the research. Include as may be useful for the IRB's consideration, a description of the probability, magnitude, duration, and reversibility of the risks. Consider physical, psychological, social, legal, and economic risks.*

There are no known risks of contributing saliva samples for analysis. There is an unlikely risk for possible loss of confidentiality. And, in these types of large scale Genomic studies there is always the possibility that Genome or Microbiome data could somehow be associated with personal information. All reasonable and legally-required precautions will be taken to prevent this and it is not anticipated. A Federal law, called the Genetic Information Nondiscrimination Act (GINA), generally makes it illegal for health insurance companies, group health plans, and most employers to discriminate against patients based on their genetic information. This law generally will protect them in the following ways:

- *Health insurance companies and group health plans may not request your genetic information that we get from this research*
- *Health insurance companies and group health plans may not use your genetic information when making decisions regarding your eligibility or premiums.*
- *Employers with 15 or more employees may not use your genetic information that we get from this research when making a decision to hire, promote, or fire you or when setting the terms of your employment.*

14.2 *If applicable, indicate which procedures may have risks to the subjects that are currently unforeseeable.*

Storage of genome sequence data that could be reidentified

14.3 *If applicable, indicate which procedures may have risks to an embryo or fetus should the subject be or become pregnant.*

Response: NA

14.4 *If applicable, describe risks to others who are not subjects.*

Children of patients who have a genetic disease could be made aware of a lack of paternity or carrier status if they themselves are sequenced, but only if sequence data is reidentified, which is not planned.

15.0 Potential Benefits to Subjects

15.1 *Describe the potential benefits that individual subjects may experience from taking part in the research. Include as may be useful for the IRB's consideration, the probability, magnitude, and duration of the potential benefits.*

There are no benefits from your taking part in this research. We cannot promise any benefits to others from taking part in this research. However, participation may help medical research better understand a variety of medical conditions which may indirectly help others in the future.

15.2 *Indicate if there is no direct benefit. Do not include benefits to society or others.*

None

16.0 Vulnerable Populations

16.1 *If the research involves individuals who are vulnerable to coercion or undue influence, describe additional safeguards included to protect their rights and welfare.*

- *If the research involves pregnant women, review "CHECKLIST: Pregnant Women (HRP-412)" to ensure that you have provided sufficient information.*
- *If the research involves neonates of uncertain viability or non-viable neonates, review "CHECKLIST: Neonates (HRP-413)" or "HRP-414 – CHECKLIST: Neonates of Uncertain Viability (HRP-414)" to ensure that you have provided sufficient information.*
- *If the research involves prisoners, review "CHECKLIST: Prisoners (HRP-415)" to ensure that you have provided sufficient information.*
- *If the research involves persons who have not attained the legal age for consent to treatments or procedures involved in*

the research (“children”), review the “CHECKLIST: Children (HRP-416)” to ensure that you have provided sufficient information.

- *If the research involves cognitively impaired adults, review “CHECKLIST: Cognitively Impaired Adults (HRP-417)” to ensure that you have provided sufficient information.*
- *Consider if other specifically targeted populations such as students, employees of a specific firm or educationally/economically disadvantaged persons are vulnerable to coercion or undue influence. The checklists listed above for other populations should be used as a guide to ensure that you have provided sufficient information.*

None

17.0 Community-Based Participatory Research

17.1 Describe involvement of the community in the design and conduct of the research.

None

Note: “Community-based Participatory Research” is a collaborative approach to research that equitably involves all partners in the research process and recognizes the unique strengths that each brings. Community-based Participatory Research begins with a research topic of importance to the community, has the aim of combining knowledge with action and achieving social change to improve health outcomes and eliminate health disparities.

18.0 Sharing of Results with Subjects

18.1 Describe whether or not results (study results or individual subject results, such as results of investigational diagnostic tests, genetic tests, or incidental findings) will be shared with subjects or others (e.g., the subject’s primary care physicians) and if so, describe how it will be shared.

None

19.0 Setting

19.1 Describe the sites or locations where your research team will conduct the research.

UB CTRC, IHI, CBLS, CCR, Conventus Building and BGMC.

19.2 Identify where your research team will identify and recruit potential subjects.

As they come into the Conventus building or the BGMC UB Neurology MDA clinic for appointments.

19.3 Identify where research procedures will be performed.

CTRC Biobank, BIG, IHI, CCR, Conventus Building and BGMC.

19.4 Describe the composition and involvement of any community advisory board.

None

19.5 For research conducted outside of the organization and its affiliates describe:

- *Site-specific regulations or customs affecting the research for research outside the organization.*
- *Local scientific and ethical review structure outside the organization.*

None

20.0 Resources Available

20.1 Describe the qualifications (e.g., training, experience, oversight) of you and your staff as required to perform their role. When applicable describe their knowledge of the local study sites, culture, and society. Provide enough information to convince the IRB that you have qualified staff for the proposed research. Note- If you specify a person by name, a change to that person will require prior approval by the IRB. If you specify people by role (e.g., coordinator, research assistant, co-investigator, or pharmacist), a change to that person will not usually require prior approval by the IRB, provided that person meets the qualifications described to fulfill their roles.

Office Staff at the Conventus building and the BGMC clinic will show patients the brochure containing the consent form and say "If you are interested in participating in a UB research study, please take a look at this flyer. If you have any questions about it please call the number on the front page as we aren't allowed to provide any information about the study." Questions will be answered by the GEM outreach coordinator who will have completed CITI training in Human Subjects. Sample collection will be performed by the office staff (Conventus), by nurses (BGMC) and by the intake person/persons at the UB Biobank who will be trained in securely transporting samples to the Biobank and scanning sample bar codes into the database system of the Biobank and storing samples appropriately. DNA will be prepared by personnel trained in the UB Genomics and Bioinformatics Core in the use of robotic equipment to prepare DNA. DNA will be sequenced for BIG by the New York Genome Center by personnel trained in library preparation and sequencing using appropriate SOPs. Sequence information will be sent back to BIG to be analyzed by BIG bioinformatics personnel and sequence data will be stored in a secure server within the CCR that requires password-protected access and is encrypted. The IHI will maintain an i2b2 database

containing a notation that the sample has been collected and will allow searching for specific medical conditions in a de-identified manner.

Describe other resources available to conduct the research: For example, as appropriate:

20.2 Justify the feasibility of recruiting the required number of suitable subjects within the agreed recruitment period. For example, how many potential subjects do you have access to? What percentage of those potential subjects do you need to recruit?

Estimates are being prepared in consultation with UB Associates who are planning patient intake in the Conventus Building.

20.3 Describe the time that you will devote to conducting and completing the research.

The project will be conducted over the next 10 years and may continue indefinitely.

20.4 Describe your facilities.

Patients will be consented on the 4th floor of the Conventus Building which will contain desks for office staff and a waiting area for patient containing chairs and sofas. Consenting will also occur at the BGMC where patients will receive the flyer and consent form by front desk personnel in the waiting area and if interested will complete the form and give it to a nurse when they are taken back for examination. The UB Biobank will be located within the CTRC in a room to be determined. Access to this room will be by card-swipe only and will be secure. DNA will be prepared in the secure DNA-preparation room of the UB Genomics Core (initially) and eventually in the DNA-preparation room of the UB Biobank in the CTRC. DNA will be shipped by mail to the New York Genome Center for library preparation and sequencing in a secure facility as is done currently for other projects in the BIG. Sequence information will be identified only by bar code and will be stored on secure servers within the CCR for analysis by BIG.

20.5 Describe the availability of medical or psychological resources that subjects might need as a result of an anticipated consequences of the human research.

None are anticipated due to the perceived lack of medical or psychological risks.

20.6 Describe your process to ensure that all persons assisting with the research are adequately informed about the protocol, the research procedures, and their duties and functions.

Staff at the point of sample collection will be trained at answering simple questions about the project. Additional questions can be asked by phone or e-mail to the GEM administrator.

21.0 Prior Approvals

21.1 *Describe any approvals that will be obtained prior to commencing the research. (E.g., school, external site, funding agency, laboratory, radiation safety, or biosafety approval.)*

We are enlisting approval from each UB practice plan represented at Conventus.

22.0 Recruitment Methods

22.1 *Describe when, where, and how potential subjects will be recruited.*

Each patient will be contacted when they come to the Conventus building or UB Neurology MDA clinic at BGMC for an appointment. Their samples will be collected in the office by office staff (Conventus) or by nurses (BGMC).

22.2 *Describe the source of subjects.*

All adult patient coming into the Conventus building for a UBMD practice plan appointment and all patients coming into the UB Neurology MDA clinic at BGMC.

22.3 *Describe the methods that will be used to identify potential subjects.*

Any adult patient coming into the Conventus UBMD Medical offices or the UB Neurology MDA clinic for an appointment.

22.4 *Describe materials that will be used to recruit subjects. (Attach copies of these documents with the application. For advertisements, attach the final copy of printed advertisements. When advertisements are taped for broadcast, attach the final audio/video tape. You may submit the wording of the advertisement prior to taping to preclude re-taping because of inappropriate wording, provided the IRB reviews the final audio/video tape.)*

Current plans are for the consent form to contain all needed information regarding the project.

22.5 *Describe the amount and timing of any payments to subjects.*

None

23.0 Local Number of Subjects

23.1 *Indicate the total number of subjects to be accrued locally.*

100,000 eventually. We hope for 5-10K in the first year.

23.2 *If applicable, distinguish between the number of subjects who are expected to be enrolled and screened, and the number of subjects needed to complete the research procedures (i.e., numbers of subjects excluding screen failures.)*

NA

24.0 Confidentiality

Describe the local procedures for maintenance of confidentiality.

24.1 Where and how data or specimens will be stored locally?

The consent forms and saliva samples will be stored daily at the point of collection in a locked filing cabinet behind the front desk (Conventus) or in the examination room (BGMC) to insure security and then transferred on a daily basis to the secure swipe-accessed UB Biobank room where they will be stored in a locked filing cabinet to insure security for up to two months. Consent forms will be stored in a locked file cabinet accessible only by the GEM Outreach coordinator or the PI. Saliva sample will be stored in plastic boxes on a table in the room. The GEM Outreach Coordinator will pick up the consent forms on a 1-2 month basis depending on when there are 96 samples collected and transport them to their office where they will be stored in a locked filing cabinet. The saliva sample will be stored until after more than 96 samples are collected and then transported by cart to the UB Genomics Core Facility for DNA preparation. DNA will be stored within the Core Facility in a 96 well format. The bar code on the plate will identify only the plate and each sample will be identified by its location and the stored bar code from the saliva sample. Data will be stored on secured servers in the CCR or in locked rooms at the CTRC and BIG.

24.2 How long the data or specimens will be stored locally?

Over 10 years and for an undermined future period.

24.3 Who will have access to the data or specimens locally?

Response: Only BioBank and BIG personnel

24.4 Who is responsible for receipt or transmission of the data or specimens locally?

Response: BioBank and BIG personnel

24.5 How data and specimens will be transported locally?

Response: Specimens by foot and data by secure SFTP.

25.0 Provisions to Protect the Privacy Interests of Subjects

25.1 Describe the steps that will be taken to protect subjects' privacy interests. "Privacy interest" refers to a person's desire to place limits on whom they interact or whom they provide personal information.

Response: All data will be stored on secure servers that are password protected and encrypted. Volunteers are informed of this in the consent form.

25.2 Describe what steps you will take to make the subjects feel at ease with the research situation in terms of the questions being asked and

the procedures being performed. “At ease” does not refer to physical discomfort, but the sense of intrusiveness a subject might experience in response to questions, examinations, and procedures.

Response: We are making the consent form as friendly and easy to understand as possible, ensuring volunteers that everything practical is being done to protect their data.

25.3 *Indicate how the research team is permitted to access any sources of information about the subjects.*

Response: Only de-identified information will be available either on password protected servers or by web interfaces. No personal data will be made available to researchers.

26.0 Compensation for Research-Related Injury

26.1 *If the research involves more than Minimal Risk to subjects, describe the available compensation in the event of research related injury.*

Response: NA

26.2 *Provide a copy of contract language, if any, relevant to compensation for research-related injury.*

Response: NA

27.0 Economic Burden to Subjects

27.1 *Describe any costs that subjects may be responsible for because of participation in the research.*

Response: NA

28.0 Consent Process

28.1 *Indicate whether you will be obtaining consent*

Yes

28.2 *Describe where the consent process take place*

In the Conventus Medical Office of UBMD or the UB Neurology MDA clinic office at BGMC.

28.3 *Describe any waiting period available between informing the prospective subject and obtaining the consent.*

There is no waiting period. People will be able to take as much time as they need to decide about participating.

28.4 *Describe any process to ensure ongoing consent.*

It is clearly stated that samples once submitted cannot be withdrawn due to the lack of association of the bar code with the patient information unless one had access to the patients EHR, which the PI and the GEM Coordinator will not have.

28.5 Describe whether you will be following “SOP: Informed Consent Process for Research (HRP-090).” If not, describe:

- The role of the individuals listed in the application as being involved in the consent process.
- The time that will be devoted to the consent discussion.
- Steps that will be taken to minimize the possibility of coercion or undue influence.
- Steps that will be taken to ensure the subjects’ understanding.

Response: Flyers containing a cover page and two copies of the consent form will be sitting in a bin on the desk of the UBMD personnel who are logging the patients. Patients will be provided information about the study in the consent document. If patients have questions, other than simple questions, before signing, they will contact and speak with someone from the study team before providing their consent. All consent documents and samples will be collected at the front desk (Conventus) or in the examination room (BGMC), but details about the study will only be addressed by study team members (GEM coordinator) and not those at the front desk. Office Staff at the Conventus building will show patients the brochure containing the consent form and say "If you are interested in participating in a UB research study, please take a look at this flyer. If you have any questions about it please call the number on the front page as we aren't allowed to provide any information about the study." Questions will be answered by the GEM outreach coordinator who will have completed CITI training in Human Subjects, .

Non-English Speaking Subjects

28.6 Indicate what language(s) other than English are likely to be spoken/understood by your prospective study population or their legally authorized representatives.

“N/A”, non-English speakers are not being included at this time.

28.7 If subjects who do not speak English will be enrolled, describe the process to ensure that the oral and written information provided to those subjects will be in that language. Indicate the language that will be used by those obtaining consent.

N/A

Waiver or Alteration of Consent Process (consent will not be obtained, required information will not be disclosed, or the research involves deception)

28.8 Review the “CHECKLIST: Waiver or Alteration of Consent Process (HRP-410)” to ensure you have provided sufficient information for the IRB to make these determinations. Provide any additional information necessary here:

NA

28.9 *If the research involves a waiver the consent process for planned emergency research, please review the “CHECKLIST: Waiver of Consent for Emergency Research (HRP-419)” to ensure you have provided sufficient information for the IRB to make these determinations. Provide any additional information necessary here:*

NA

Subjects who are not yet adults (infants, children, teenagers)

28.10 *Describe the criteria that will be used to determine whether a prospective subject has not attained the legal age for consent to treatments or procedures involved in the research under the applicable law of the jurisdiction in which the research will be conducted. (E.g., individuals under the age of 18 years.) For research conducted in NY state, review “SOP: Legally Authorized Representatives, Children, and Guardians (HRP-013)” to be aware of which individuals in the state meet the definition of “children.”*

Consent will only be obtained from individual 18 years of age or older.

28.11 *For research conducted outside of NY state, provide information that describes which persons have not attained the legal age for consent to treatments or procedures involved the research, under the applicable law of the jurisdiction in which research will be conducted. One method of obtaining this information is to have a legal counsel or authority review your protocol along the definition of “children” in “SOP: Legally Authorized Representatives, Children, and Guardians (HRP-013).”*

NA

28.12 *Describe whether parental permission will be obtained from:*

- *Both parents unless one parent is deceased, unknown, incompetent, or not reasonably available, or when only one parent has legal responsibility for the care and custody of the child.*
- *One parent even if the other parent is alive, known, competent, reasonably available, and shares legal responsibility for the care and custody of the child.*

NA

28.13 *Describe whether permission will be obtained from individuals other than parents, and if so, who will be allowed to provide permission. Describe the process used to determine these individuals’ authority to consent to each child’s general medical care.*

NA

28.14 Indicate whether assent will be obtained from all, some, or none of the children. If assent will be obtained from some children, indicate which children will be required to assent.

NA

28.15 When assent of children is obtained describe whether and how it will be documented.

NA

Cognitively Impaired Adults

28.16 Describe the process to determine whether an individual is capable of consent. The IRB sometimes allows the person obtaining assent to document assent on the consent document and does not automatically require assent documents to be used.

“N/A”, cognitively impaired adults are not being included.

Adults Unable to Consent

When a person is not capable of consent due to cognitive impairment, a legally authorized representative should be used to provide consent and, where possible, assent of the individual should also be solicited.

28.17 List the individuals from whom permission will be obtained in order of priority. (e.g., durable power of attorney for health care, court appointed guardian for health care decisions, spouse, and adult child.) For research conducted in NY state, review “SOP: Legally Authorized Representatives, Children, and Guardians (HRP-013)” to be aware of which individuals in the state meet the definition of “legally authorized representative.” The list in the consent template signature section corresponds to the priority list for NYS.

NA

28.18 For research conducted outside of NY state, provide information that describes which individuals are authorized under applicable law to consent on behalf of a prospective subject to their participation in the procedure(s) involved in this research. One method of obtaining this information is to have a legal counsel or authority review your protocol along the definition of “legally authorized representative” in “SOP: Legally Authorized Representatives, Children, and Guardians (HRP-013).”

NA

28.19 Describe the process for assent of the subjects. Indicate whether:

- Assent will be required of all, some, or none of the subjects. If some, indicated, which subjects will be required to assent and which will not.

- *If assent will not be obtained from some or all subjects, an explanation of why not.*
- *Describe whether assent of the subjects will be documented and the process to document assent. The IRB allows the person obtaining assent to document assent on the consent document and does not routinely require assent documents and does not routinely require subjects to sign assent documents.*

“N/A”, cognitively impaired adults are not being included at this time.

29.0 Process to Document Consent in Writing

If your research presents no more than minimal risk of harm to subjects and involves no procedures for which written documentation of consent is normally required outside of the research context, the IRB will generally waive the requirement to obtain written documentation of consent.

(If you will document consent in writing, attach a consent document. If you will obtain consent, but not document consent in writing, attach a consent script. Review “CHECKLIST: Waiver of Written Documentation of Consent (HRP-411)” to ensure that you have provided sufficient information. You may use “TEMPLATE CONSENT DOCUMENT (HRP-502)” to create the consent document or script.)

29.1 Describe whether you will be following “SOP: Written Documentation of Consent (HRP-091).” If not, describe whether and how consent of the subject will be obtained including whether or not it will be documented in writing.

SOP will be followed and we will keep consent forms as paper copies until they can be scanned into our BioBank database.

30.0 Drugs or Devices

30.1 If the research involves drugs or device, describe your plans to store, handle, and administer those drugs or devices so that they will be used only on subjects and be used only by authorized investigators.

NA

If the drug is investigational (has an IND) or the device has an IDE or a claim of abbreviated IDE (non-significant risk device), include the following information:

30.2 Identify the holder of the IND/IDE/Abbreviated IDE.

NA

30.3 Explain procedures followed to comply with FDA sponsor requirements for the following:

<i>FDA Regulation</i>	<i>Applicable to:</i>		
	<i>IND Studies</i>	<i>IDE studies</i>	<i>Abbreviated IDE studies</i>
<i>21 CFR 11</i>	<i>X</i>	<i>X</i>	
<i>21 CFR 54</i>	<i>X</i>	<i>X</i>	
<i>21 CFR 210</i>	<i>X</i>		
<i>21 CFR 211</i>	<i>X</i>		
<i>21 CFR 312</i>	<i>X</i>		
<i>21 CFR 812</i>		<i>X</i>	<i>X</i>
<i>21 CFR 820</i>		<i>X</i>	

NA