NF Research Initiative

3/19/18 – Steering Committee Meeting Minutes

Meeting Attendees: David Miller (BCH), Sarah Berns (BCH), Katherine Piculell (BCH), Anthony Griffin (Mount Sinai), Douglas Stewart (NCI), Xia Wang (Moffitt), Nicky Ullrich (BCH), Jesse Hart (Lifespan), Christopher Moertel (UMinn), Raymond Kim (Mount Sinai)

DM: *Our protocol is now active*, so we are eager to move ahead with getting MTA language and everyone's IRB protocols

New chairpersons: Adrienne Flanagan is Pathology & Oncology Co-Chair, Nischalan Pillay is the Genomics Informatics Co-Chair

DM presents Dr. Flanagan's slides -

- We want a 2 to 1 ratio of sporadic to NF-1 related
- When we talk about molecular analysis, what should we do?
    - Looking at MPNST (and subtypes) including atypical neurofibromas
    - Tumor heterogeneity and tumor evolution
    - Have the potential to do interesting studies related to circulating tumor DNA

Frozen Tissue

- RNOH: 30 cases of NF1 available
- We have at least double this number of NF1 related MPNSTs with the rest of the consortium
- Whole genome sequencing – at what depth? Would it be worthwhile to do whole genome at a standard depth and overlay with exome sequencing at a higher depth?
    - We would have to match what we are doing with WGS with what we are doing on normal paired sample
- RNA seq analysis on frozen samples
- On all samples we would try to do some type of epigenomic analysis

Tumor Heterogeneity – FFPE samples

- Gene list (30 genes of previously published or pre-publication genes)
- Hybrid capture assay
    - Half of samples are from London
    - Other half are remaining consortium samples
- Propose to sample 5 or 6 areas from the same tumor with very good histological correlation

Tumor Evolution – more challenging

- Collection of samples over space and time with progressive histological features
- A lot of this would be with FFPE

Circulating Tumor DNA

- Work prospectively within the consortium to see if we can identify molecular signatures
    - May be able to correlate with circulating tumor DNA samples

Single Cell Analysis: WGS, RNAseq

- Not an immediate goal but worthwhile to consider if we should leverage this for understanding tumor evolution as well

Feedback?

Xia Wang: For epigenetics, is there any room to add something for IHC analysis for certain proteins?

- DM: We have talked about this before with our pathology team and we have a standard group of stains here that would be part of the data set
- *NFRI to circulate Case Review Form*

Raymond Kim: What is the con of going deep on a whole genome?

-DM: Quite expensive – we'd have to make multiple library preps. It ends up being 200x for deep whole genome.

- You can go deeper and cheaper for whole exome

Doug Stewart: Jack Shern has a particular interest in single cell analysis tumors. It's something that he is working on.

-DM: I think everyone is open to collaboration. I think it's something the London group is interested in and it hasn't been put into place yet. We also have an interest in that here. We should loop Jack in and figure out how we can work on it together.