Brief Study Description

The Chronic Renal Insufficiency Cohort Study (CRIC Study) is a multi-center, NIDDKsponsored, prospective cohort study. JH (PI: L. Appel) is one of 7 clinical center sites nationwide. In its ongoing recruitment drive, CRIC is enrolling participants who are adults, ages 45-79, with chronic kidney disease (eGFR of 45-69 ml/min/m²); 75% had to have proteinuria, defined by a urine dipstick of 1+ or spot urine albumin/creat ratio of \geq 300 mg/mg. The recruitment goal at Hopkins was 108. The recruitment drive lasted just 2 years (July 2013 – July 2015).

Extraordinary Recruitment Challenges

- The patients targeted in CRIC have subclinical kidney disease; they do not have advanced disease, i.e. ESRD. They have a laboratory abnormality without symptoms. In contrast to weight and blood pressure, most individuals, even those with CKD, do not know their level of urine protein excretion. Hence, the recruitment strategy required laboratory-based data mining to identify individuals with proteinuria and eGFR.
- 2. An elevated urine protein level, while one of the most important risk factor for CKD progression, is uncommon. Any one primary care provider has only a few patients who might be eligible. Nephrologists manage patients with advanced disease and less frequently those with subclinical disease. Still, in aggregate, across a large health care system such as JH, many persons are eligible.
- Several different laboratories measure protein excretion at Hopkins. The initial laboratory database that we used to search for participants had just urine protein excretion from the JH pathology laboratory, not commercial laboratories, e.g. Quest and LabCorps.
- 4. Search of laboratory databases requires a HIPAA waiver.
- 5. JH IRB required that primary care provider approve the recruitment of patients for this study.
- 6. The budget for recruitment was low.

Initial Recruitment Phase, Pre-Computational Phenotyping (Limited Success) Our initial efforts were resource intensive and unsuccessful, i.e., relying on prior study participants with known CKD, relying on a few enriched practices, and using the

database from the JH laboratory. After the first 6 months (25% of the recruitment period), we enrolled just 16 participants (expected=27), and very few had proteinuria. We were substantially behind schedule, and a change in recruitment strategy was needed.

Recruitment Using Center for Clinical Data Analysis (CCDA) Computational Phenotyping

The CCDA, conducted enterprise-wide searches that included the commercial laboratories. Search criteria were defined and refined to exclude as many individuals not meeting inclusion criteria as possible. Biweekly reports were generated to identify new potential study candidates. In the end, the site recruitment goal was exceeded (n=111, 103% of goal), ahead of schedule, with 54 of participants identified using the CCDA Computational Phenotyping strategy. See Figure 1. for flow diagram overview of the recruitment process.

Lessons Learned and Implications

- 1. Extensive local database management is required to process, manage, and track potential study candidates through the system. Support is needed for the development of secure local databases for individual investigators.
- 2. Initial yields from the biweekly CCDA searches were unexpectedly low. Twice, major code reviews were conducted. Through refinement, the programmer identified an error that led to a major new list, in addition to larger biweekly downloads. Support is needed for a systems analyst to develop and iteratively revise code for the search strategy and for team to estimate expected yield from other sources.
- 3. There were still many bottlenecks that impeded recruitment, e.g., need to avoid duplicate invitations to potential study candidates, need to identify correct primary care provider (which might differ from ordering provider), need to secure primary care provider approval, need to assess eligibility (not always evident using EHR data), need to provide transportation for potential study candidates, and need to pay for CCDA programming. In a few instances, primary care provider advised that a potential study candidate should not contacted, often because of concurrent medical problem. Much more common was potential study candidate refusal; many were not interested in participating in our study. A comprehensive approach to recruitment is required, one that involves much more than access to computational phenotyping.