The MURDOCK Study Community Registry and Biorepository

A diverse, longitudinal community-based cohort of 12,526 participants recruited from 20 zip codes in the Southeastern United States centered in Kannapolis, North Carolina. Managed by the Duke Clinical and Translational Science Institute (CTSI).

Overview and Unique Features

- The study was designed as a volunteer registry with open enrollment.
- First participant enrolled in February 2009; enrollment ended in February 2016.
- Enrollment was monitored to ensure that age and racial/ethnic representation in the accruing cohort reflected that of the catchment area.
- 25.7% non-white participants
- Ability to call-back for additional research studies (including basis by molecular/clinical phenotypes)
- Highly engaged cohort (>55% email open rate with 25% interested in new studies; 42% have enrolled in at least one ancillary study)
- Linkage to electronic health record (EHR) data
- Geospatial mapping; yearly follow-up
- Banked plasma, serum, stabilized RNA, DNA
- Diseases mapped: cardiovascular disease, aging and memory, diabetes, obesity, hypertension, kidney disease, oncology (lung, breast), autoimmune disease (rheumatoid arthritis, multiple sclerosis), physical performance, COPD

Cohort Details

Detailed enrollment (baseline) characterization includes:

- Date and place of birth
- 34 disease domains and related procedures (and menopausal status in women)
- Dietary and physical activity assessment; hours of sleep per night
- Tobacco and alcohol use; secondhand smoke exposure
- Selected PROMIS participant-reported outcomes domains
- Extensive socioeconomic data (SES) and social determinants of health data
- Brief physical exam (vital signs, height, weight, and waist circumference)
- Geospatial mapping at their home street address level to enable attribution of publicly available social, economic, and natural and built environmental features to the individual using geospatial information systems.
- Biospecimens collected at baseline include multiple aliquots of plasma, serum, whole blood (DNA), whole Blood (PAXgene RNA), buffy coat and urine. Serial sampling is available for some subcohorts.

Additional details:

- Ongoing access to electronic health records of many participants.
- Many participants have enrolled in additional studies that include serial assessments and sampling.
- Participants are followed yearly by repeating the baseline survey questions and self-reporting illnesses in the same categories surveyed at baseline. More than 65,000 years of longitudinal follow-up data are available.
- We anticipate genomic sequence data to be available in late 2023.