

Using Proteomics and Established Patient Cohorts to Address Relevant Clinical Biomarker Needs: The M.U.R.D.O.C.K. Study

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Perhaps the most challenging aspect of biomarker discovery for translational research purposes is refining the many important variables impacting ultimate success of the project, including: using the “correct” analytical and statistical approaches, finding the “best” clinical cohort, and of course addressing an unmet clinical need. Under funding provided by David H. Murdock, four collaborative biomarker studies in the areas of hepatitis C (HCV), osteoarthritis (OA), obesity, and cardiovascular disease (CVD) have been undertaken in the Duke University School of Medicine as part of the M.U.R.D.O.C.K. study (www.murdock-study.com). Biomarker studies requiring prospective collection and curation of clinical samples is time-consuming, therefore the M.U.R.D.O.C.K. Horizon 1 studies have focused specifically on utilizing biobanked and well-annotated clinical specimens to rapidly advance discovery of clinical biomarkers. Taking advantage of established patient cohorts at Duke, two teams of researchers in the School of Medicine have collaborated to perform open-platform biomarker discovery studies in the areas of Hepatitis C and Osteoarthritis, using liquid chromatography-mass spectrometry (LC-MS) based proteomics. Both studies have been successful in the OA and HCV biomarkers discovered are currently being verified in larger clinical cohorts. This presentation will utilize the OA and HCV case studies to highlight the technology used to perform biomarker discovery and verification efforts.