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The conceptual evolution of genetic instability as a hallmark of cancer, with cumulative genetic and epigenetic advantageous mutations driving malignant transformation and progression, has led to a profound interest in mapping tumor genomes. We hypothesized that PMP genomes have clonally selected aberrations that, although highly variable in each patient, converge on essential tumor-specific cellular pathways. Thus, identification of these genetically-determined, disease-specific pathway aberrations will provide effective targeted treatment strategies in PMP. We have used high-throughput Comparative Genomic Hybridization Array (aCGH) technology to characterize the whole genome of human tumor samples of pseudomyxoma peritonei from appendiceal carcinoma and corresponding tissue from a unique murine xenograft model of PMP developed in our laboratory. We hypothesize that identification of unique or shared genetic aberrations in PMP will generate informative prognostic and predictive biomarkers. These data will help advance our efforts in delivering effective targeted therapies, based on patient-specific contexts and tumor vulnerabilities. We anticipate that the results of these studies will not only drive improved outcomes in this orphan tumor, but also serve as a paradigm for development of future personalized genomic approaches to cancer therapy in general.