Findings from breast and gynecological cancer study may have potential for future clinical applications

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Researchers from The University of Texas MD Anderson Cancer Center have found a startling amount of new information about molecular features of tumors as well as identified previously unknown cancer subtypes based on a comprehensive analysis of 2,579 tumors from breast and four different types of gynecologic cancers. These new findings potentially could serve as a launching pad for future therapeutic studies.

Results from the multi-institutional effort, led by Rehan Akbani, Ph.D., associate professor of Bioinformatics & Computational Biology were published this week in the online issue of *Cancer Cell*.

The study is part of the Pan-Cancer Atlas, which has aimed to answer overarching questions about cancer by examining the full set of tumors available via The Cancer Genome Atlas (TCGA), a joint effort of the National Cancer Institute and the National Human Genome Research Institute. Akbani's investigation is one of several that conclude the Pan-Can Atlas and TCGA missions of mapping key genomic changes in an array of cancer types. "Our aims were to identify shared and unique molecular features, clinically significant subtypes and potential therapeutic targets," said Akbani. "We confirmed similarities previously identified in the five breast and gynecologic tumor types and discovered intriguing molecular relationships not observed in previous studies of these diseases. A number of the observations have possible prognostic and/or therapeutic relevance, although any clinical possibilities

illuminated by this study would require extensive additional research before they would be ready for practical application."

Key results of the study included:

- Using 16 key molecular features, the team identified five prognostic cancer subtypes and developed a decision "tree" that classified patients into the subtypes based on six features assessable in clinical laboratories.
- Identifying other subtypes with high leukocyte counts, raising potential implications for immunotherapy treatment in the future.
- Discovering the presence of significant estrogen receptor-regulated long non-coding RNAs (lncRNAs) and interaction "networks" between genes and lncRNAs.
- Observing many genetic aberrations including 61 somatic copy-number alterations (SCNAs) and 46 significantly mutated genes (SMGs). Eleven each of the SCNAs and SMGs had not been identified in previous TCGA studies of five tumor types.

"This study presents a broad-based, curated atlas of gynecologic and breast cancer molecular features that we believe will be useful as a starting point for researchers in the field for many years to come," said Akbani.

John Weinstein, M.D., Ph.D., chair of Bioinformatics & Computational Biology, and a member of the research team added that "the study complements other integrative TCGA Pan-Cancer Atlas projects that have painted molecular portraits of about 11,000 patient tumors in 33 cancer types."

Provided by University of Texas M. D. Anderson Cancer Center