MONDAY, July 15 (HealthDay News) -- U.S. National Cancer Institute scientists have generated an extensive data set of cancer-related genetic variations to help researchers better understand how cancer responds to drugs and can resist treatment.

"To date, this is the largest database worldwide, containing 6 billion data points that connect drugs with genomic variants for the whole human genome across cell lines from nine tissues of origin, including breast, ovary, prostate, colon, lung, kidney, brain, blood and skin," said Dr. Yves Pommier, chief of the NCI's Laboratory of Molecular Pharmacology.

"We are making this data set public for the greater community to use and analyze," Pommier said.

The research is published July 15 in the journal Cancer Research.

Opening this data set to researchers will expand understanding of the process by which normal cells are transformed into cancer, Pommier said in a journal news release.

"This comes at a great time, because genomic medicine is becoming a reality, and I am very hopeful this valuable information will change the way we use drugs for precision medicine," Pommier said.
The researchers conducted whole-exome sequencing of the NCI-60 human cancer cell line panel, which is a collection of 60 human cancer cell lines, and generated a comprehensive list of cancer-specific genetic variations.

Preliminary studies conducted by the NCI team indicate that the data set could dramatically improve understanding of the relationships between specific cancer-related genetic variations and drug response, which will accelerate the development of new drugs.

The NCI-60 human cancer cell line panel is used extensively by cancer researchers to discover new anti-cancer drugs.