

patient. The results were used to make a Kaplan–Meier plot containing two curves. The two curves were well-separated, where the separation was statistically significant ($P = 0.0001$). The issue was that Dukes' B colon cancer is treated with surgery, but that data on whether surgery should be followed by chemotherapy is conflicting, undecided, or controversial. The Wang study is expected to bring a decisive answer, by identifying patients likely to benefit from chemotherapy, prior to actually administering chemotherapy. In the authors' own words, "the prognosis signature would provide a powerful tool to select the patients who are at high risk and ensure that they receive adjuvant treatment."

Dukes' B colon cancer is not a specific type of colon cancer, but is part of a generic classification system for cancer of the large intestines (92). Dukes' A colon cancer involves invasion into but not through the bowel wall. Dukes' B involves invasion through the bowel wall, but not involving lymph nodes. Dukes' C involves invasion through the bowel wall, and also the lymph nodes, while Dukes' D involves all of the above, with widespread metastasis. This classification is similar to the more recently devised staging system, namely, Tumor (T), Node (N), Metastasis (M) staging (TNM staging) that is used for a variety of cancers.

c. Microarray Used in Liver Cancer—The Hoshida Study

In a study of hepatocellular carcinoma (HCC), Hoshida et al. (93) acquired tumor

biopsies from 307 patients, as well as biopsies from normal areas of the liver next to the tumor. In patients treated for HCC, what is desired is a diagnostic tool for predicting which patients are at greatest risk for recurrence. The researchers chose 6100 genes, and determined which of these genes were associated with long-term survival after surgery for HCC. In other words, the researchers determined whether there was a correlation between a change in expression (either an increase or decrease) for every single one of these 6100 genes, and long-term survival.

Gene expression data from *tumor samples* failed to show any correlation. To increase their chance of finding a useful result, the researchers also analyzed *normal liver samples* harvested from tissue adjacent to the liver tumor. This experiment worked. The authors arrived at a collection of 186 genes (a defined set of genes) useful for predicting risk for recurrence of HCC patients after "curative" surgery. The genes showing changes in expression, and that were most associated with poor prognosis, included *FSHB*, *SH3GL2*, *RBM34*, *NCAPH*, and *EGF*. The genes that showed changes in expression, and that were most associated with good prognosis, included *ALDH9A1*, *TTR*, *RLF*, *IPA1*, and *PFKFB1* (94). With the prognostic device in hand, the researchers then used it for testing liver samples from 234 other patients with HCC. The result was a success. The device predicted survival, and it predicted recurrence. The researchers concluded that their device can be used to identify patients in need of intensive follow-up after curative surgery.

⁹²Shampo MA. Dukes and Broders, pathological classification of cancer of the rectum. *J. Pelvic Surg.* 2001;7:5–7.

⁹³Hoshida Y, Villanueva A, Kobayashi M, et al. Gene expression in fixed tissues and outcome in hepatocellular carcinoma. *New Engl. J. Med.* 2008;359:1995–2004.

⁹⁴Further information on these genes can be found at a web site of the US government, www.ncbi.nlm.nih.gov/pubmed.