Analysis of Surveillance, Epidemiology, and End Results Database for Carcinoid Tumors

To the Editor:

We read with great interest the article by Raz and colleagues in CHEST (April 2015), in which the authors use public data from the Surveillance, Epidemiology, and End Results (SEER) program to demonstrate that individuals who undergo complete oncologic surgical resection of their typical carcinoid tumors have the best overall and disease-specific survival. In their analysis, the authors excluded a series of cohorts, such as cases with nodal positivity, distant metastases, prior cancers, and previous therapy, and maintained a significant cohort of 4,111 cases for their final dataset. Although the SEER database has some limitations, the size of the cohort under study provides for a variety of investigations not typically available to individual or collective researchers.

The size and accuracy of the SEER database can be used additionally in probing another consideration in the natural history of carcinoid tumors, namely, the lack of malignant cellular transformation of carcinoids to small cell carcinomas of the lung, a high-grade pulmonary cancer that, like carcinoid tumors, derives from endogenous neuroendocrine cells. It has been established that small cell carcinomas are typically associated with cigarette smoking, whereas carcinoid tumors do not have this epidemiologic causative factor. An additional demonstration that these two neuroendocrine tumors have disparate carcinogenic pathways may be achieved by the mathematical approach of multistage carcinogenesis depicted graphically by the log (age-specific incidence) vs log (age at presentation). The log-log plot generates a straight line whose slope represents a mathematical function of the aggregate of cellular and molecular events in the carcinogenic process. The size of the SEER cohorts for these two neuroendocrine tumors permits this analysis. As displayed in Figure 1, the two neuroendocrine carcinomas have markedly different patterns on the log-log plot. This mathematical approach and graphical representation may also be used to suggest that similar histopathologic tumors from different organs may share a field effect or, as in this case, that separate tumors, despite similar cells of origin, may differ in their carcinogenic sequence and consequently do not demonstrate malignant evolution or transformation to a higher-grade subtype within their natural history.

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References

