Cancer of Unknown Primary Site

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Cancer of unknown primary site is a heterogeneous group of cancers for which the anatomical site of origin remains occult after detailed investigations. The emergence of sophisticated imaging, immunohistochemical testing, and molecular-profiling tools has influenced our approach to unknown primary cancer, although it has also increased the ambiguity of designations for this disorder. In the era of tailored therapeutic strategies, this situation presents both an opportunity and a challenge.

The past four decades have seen a shift in our understanding of unknown primary cancer (Fig. 1). First, improved imaging techniques increased our confidence in the classification of some cancers as having an occult primary origin. Later, subsets of unknown primary cancers with an apparently favorable prognosis were identified, primarily on the basis of histopathological findings, the pattern of spread, and serum markers. Subsequently, with the advent of new immunohistochemical markers and advances in diagnostic pathological tests, tissue-of-origin profiles were described that assigned additional putative primary sites to unknown primary cancer on the basis of immunohistochemical patterns. Current research involves the application of proteomic and genomic tools to unknown primary cancer.

Cancer of unknown primary site was once viewed almost as a separate type of cancer, with the assumption that, regardless of the site of origin, the tumors in unknown primary cancers shared biologic properties, perhaps including rapid progression and dissemination, which contributed to their presentation. This view drove the conduct of phase 2 empirical trials over the past three decades, with the goal of developing standard chemotherapy regimens that would be effective in all patients with unknown primary cancer. The underlying assumption was that variations in presentation would not have a substantial effect on therapeutic approaches or survival.

Our view of unknown primary cancer has evolved as our understanding of cancer biology in general has matured to become much more personalized. Many people now believe that tumors in unknown primary cancer may retain the signature of the putative primary origin and that extending the management of known cancers to subtypes of unknown primary cancer can contribute to advancements in therapies for this disease. Cancer of unknown primary site could even be seen as the epitome of personalized medicine, with individualized treatment driven by the mutational status of each patient.

The biologic events that allow the primary site to remain obscure after the development of metastases have not yet been defined. Studies that have shown chromosomal abnormalities, microvessel density, aneuploidy, and overexpression of several genes suggest that these abnormalities are not unique to unknown primary cancer. With the use of the Sequenom MassARRAY platform, a study involving consecutive patients with unknown primary cancer showed a low rate of mutations (in 18% of patients). No new, low-frequency mutations were found with the use of a panel of mutations involving the phosphatidylinositol 3-kinase...
(PI3K)–AKT pathway, MEK pathway, receptors, and downstream effectors. Furthermore, there are major obstacles to conducting the trials that would be required to show definitively that unknown primary cancer with a putatively identified source behaves the same way as metastatic disease with a similar, known primary site.

CLINICAL EVALUATION

FOCUSED IMAGING

In the absence of contraindications, a baseline computed tomographic (CT) scan of the chest, abdomen, and pelvis with the use of intravenous contrast material is the standard of care, as supported by the National Comprehensive Cancer Network and National Institute for Health and Clinical Excellence radiology guidelines for unknown primary cancer.15 Patients should then be approached in a directed fashion.15 Currently, magnetic resonance imaging (MRI) of the breasts is indicated in women presenting with isolated axillary adenopathy and adenocarcinoma, if findings on mammography and ultrasonography are negative. The absence of a breast mass on MRI is associated with a low probability of finding a tumor at mastectomy.16–18 Invasive testing (with bronchoscopy, upper endoscopy, colonoscopy, etc.) should be limited to symptomatic patients and to those with imaging or pathological abnormalities indicative of a primary cancer, since these patients may have a higher yield, as compared with asymptomatic patients without clinicopathological abnormalities, in efforts to detect a primary cancer.

CURRENT ROLE OF PET-CT IMAGING

In patients who have renal insufficiency or who cannot take iodine, positron-emission tomography (PET)–CT or MRI can be used. Elective use of PET-CT is currently limited to patients with squamous-cell lymphadenopathy of the neck (cer-
PATHOLOGICAL FEATURES AND MOLECULAR PROFILING

General Considerations

In most patients with unknown primary cancer, pathological findings supersede the interpretations of radiologic testing. Adequate tissue sampling, ideally by means of a core biopsy, is essential, as is communication between the treating oncologist and the pathologist. Most therapeutic phase 2 trials have defined unknown primary cancer as limited to epithelial cancers. In these trials, patients with metastatic lymphomas, melanomas, and sarcomas who presented without a known primary tumor were excluded, since management of these cancers is based on the specific stage and histologic findings. In practice, however, one must consider the expanded differential diagnosis, including nonepithelial tumors, when dealing with an unclassified cancer.

Light Microscopy

On light microscopy, cancers of unknown primary site include well-differentiated and moderately differentiated adenocarcinoma (in 60% of patients), poorly differentiated carcinoma or adenoscarcinoma (in 30%), poorly differentiated or undifferentiated malignant neoplasm (in 5%), and squamous-cell carcinoma (in 5%). In rare cases, patients with unknown primary cancer present with neuroendocrine cancer or mixed tumors, including sarcomatoid, basaloid, and adenosquamous carcinomas.25

SERUM TUMOR MARKERS

Tumor markers are generally not considered to be diagnostic, and among the adenocarcinoma markers, there is considerable variability. Elevated levels of carcinoembryonic antigen or cancer antigens 125, 19-9, and 27.29 are nonspecific and not helpful in identifying the primary tumor site. In men who present with adenocarcinoma and osteoblastic metastases, a prostate-specific antigen (PSA) test is recommended. Elevated levels of the beta subunit of human chorionic gonadotropin (hCG) and alpha-fetoprotein in men with undifferentiated or poorly differentiated carcinoma (especially those with a midline tumor) suggest the possibility of an extragonadal germ-cell (testicular) tumor.24 Alpha-fetoprotein should also be considered in patients with a potential diagnosis of hepatoma. Although tumor markers are not particularly helpful in diagnosing a specific primary tumor, they may be helpful in monitoring the response to treatment.
Figure 2. Drawback of Baseline ¹⁸F-fluorodeoxyglucose Positron-Emission Tomography (PET)–CT as the Initial Imaging Method in Unknown Primary Cancer.

A 51-year-old man who was a smoker presented with neck adenopathy. Biopsy of the left supraclavicular lymph node revealed metastatic, poorly differentiated carcinoma. Immunostains were negative for cytokeratin (CK) 7, CK20, synaptophysin, chromogranin, S-100, melanoma antigen recognized by T cells (MART-1), prostate-specific antigen, thyroid transcription factor 1 (TTF1), inhibin, and thyroglobulin. The tumor was focally positive for Hep Par-1, CD10, and low-molecular-weight keratin, and final pathological results were reported as nonspecific. A PET-CT scan that was ordered as the baseline study in the head and neck oncology clinic showed multiple hypermetabolic nodes in the neck (Panel A, arrow). The PET-CT scan did not show a renal primary cancer, although in retrospect there was a hint of a small lesion (Panel B, arrow). The patient received chemotherapy with paclitaxel and carboplatin for unknown primary cancer favoring a lung-cancer profile. He had mild disease progression while receiving this regimen. In parallel, he underwent a tissue-of-origin molecular-profiling study that showed a kidney-cancer profile. Additional renal-specific immunohistochemical testing on the nodal tissue showed the tumor to be positive for PAX-8, renal-cell carcinoma, CD10, epithelial membrane antigen, and vimentin — findings that are consistent with conventional-type, metastatic renal-cell carcinoma. A CT scan obtained with the use of intravenous contrast material showed a mass (1.0 by 1.2 cm) in the lower pole of the left kidney (Panel C, arrow). The patient was treated with targeted therapies, including everolimus, axitinib, and pazopanib; he had a mixed response initially, followed by disease progression in lymph nodes, liver, bones, and the primary site (Panel D, arrow). This patient did not have unknown primary cancer on presentation; instead, he had metastatic renal-cell cancer that had been evaluated with a suboptimal workup. Unfortunately, even with accurate diagnosis, directed therapies do not have a clear therapeutic effect in most patients with advanced renal-cell cancer.
**Immunohistochemical Testing**

The use of immunohistochemical testing in unknown primary cancer is based on the premise that there is concordance in the expression profiles of primary and metastatic cancers. Immunohistochemical tests are typically tests of peroxidase-labeled antibodies against specific tumor antigens that help suggest the tumor lineage and can establish most lineages (carcinoma, lymphoma, sarcoma, melanoma, etc.). Most researchers believe that a search for the putative primary cancer, performed by means of immunohistochemical testing, is helpful in detecting tumors with a favorable prognosis and in planning a tailored therapy for the patient. Although individual immunohistochemical tests have modest specificity and sensitivity (with the possible exception of the PSA test), their predictive value may improve with grouping and recognition of patterns that are strongly indicative of specific tumors.\(^{26}\) For example, the phenotype for positive thyroid transcription factor 1 (TTF1), with positive cytokeratin 7 (CK7), and the phenotype for positive cytokeratin 20, with positive homeobox protein CDX-2 and negative CK7, have been reported as very suggestive of lung and lower gastrointestinal cancer profiles retrospectively, although they have not been validated prospectively in the absence of a primary cancer. With the use of light microscopy and immunohistochemical testing, a single putative primary tumor may be assigned in up to 25% of cases of unknown primary cancer, and in the remaining cases, immunohistochemical testing is nonspecific.\(^{27}\)

Currently, we lack a tiered and uniform approach to performing the stains. Additional limitations of immunohistochemical testing include factors affecting tissue antigenicity, interobserver and intraobserver variability in interpretation, and tissue heterogeneity and inadequacy. Most important, the clinical efficacy of immunohistochemical test–based management of unknown primary cancer has not been shown adequately. In one retrospective study, patients with CDX-2–positive cancers who were treated with regimens used for gastrointestinal cancers had a survival of more than 30 months,\(^{28}\) but prospective validation of the therapeutic effect of immunohistochemical test–directed therapies for putative primary tumors is urgently needed. A differential diagnosis based on immunohistochemical testing can prompt more focused biomarker studies with potential therapeutic effect or actionable targets, which may allow patients with unknown primary cancer to enroll in biomarker-based early-phase studies.

**Tissue-of-Origin Molecular Profiling**

The premise for studying tissue-of-origin molecular-profiling assays in unknown primary cancers is that, when a large number of genes from known cancers are examined with the use of tools such as DNA microarray or quantitative real-time polymerase-chain-reaction (rt-PCR) assay, metastatic tumors have molecular signatures that match their primary origin. The performance of tissue-of-origin molecular-profiling assays in known cancers has been validated with the use of independent, blinded evaluation of sets of tumor samples, with an accuracy of approximately 90%.\(^{29-31}\) The feasibility of using formalin-fixed samples obtained from small, core-needle biopsy or using samples obtained by means of fine-needle aspiration makes this method practical for use in the clinic setting.

Tissue-of-origin assays based on messenger RNA (mRNA) or microRNA have been studied in prospective and retrospective trials involving patients with unknown primary cancer.\(^{32,33}\) Most of the studies have evaluated assay performance, although the challenge with validating the accuracy of an assay for unknown primary cancer is that, by definition, the primary cancer diagnosis cannot be verified. Thus, current estimates of the accuracy of tissue-of-origin testing have relied on indirect metrics, including comparison with immunohistochemical testing, clinical presentation, and the appearance of latent disease at the primary site. With the use of these measures, the assays suggest a plausible primary site in approximately 70% of the patients studied.\(^{34-37}\) In the remaining patients, the results are clearly discordant with the working differential diagnosis, the sample is insufficient despite repeat biopsy (an issue that occurs with bone samples), or the assay is unable to designate a primary origin from its panel of cancers.\(^{38}\)
At present, the only outcomes-based study has been a prospective, single-group study evaluating the role of the 92-gene assay to predict the tissue-of-origin and assay-directed, site-specific therapy in patients with unknown primary cancer. The investigators found that the median overall survival of 12.5 months (95% confidence interval, 9.1 to 15.4) among patients who received assay-directed, site-specific therapy compared favorably with the results of previous studies that used empirical therapy. Biliary and urothelial cancer profiles accounted for 33% of the predictions. Unfortunately, firm conclusions regarding therapeutic effect cannot be drawn from this study, given the nonrandomized design, statistical biases, confounding variables, including use of subsequent lines of (empirical) therapy, and the heterogeneity of unknown primary cancers.

Without randomized, controlled trials it is difficult to gauge the therapeutic effect of tissue-of-origin molecular-profiling assays. Creative trial designs are urgently needed in order to study subsets of unknown primary cancers and the effect of these assays on survival and quality of life of patients.

Two prospectively defined, blinded studies of difficult-to-diagnose primary cancers (several of them poorly differentiated cancers) have shown the cost-effectiveness of tissue-of-origin molecular profiling over immunohistochemical testing. Samples were evaluated by means of morphologic and immunohistochemical analysis or the tissue-of-origin molecular-profiling test. Accuracy was defined on the basis of comparison with the pathological features of a known primary cancer. In one study, the assay showed overall accuracy of 79% for tumor classification versus 69% for morphologic and immunohistochemical analysis (P = 0.02). The mean number of immunohistochemical stains used was 7.9 per case (range, 2 to 15). The other study had similar findings; the assay accurately identified 89% of the specimens, as compared with 83% accuracy with immunohistochemical testing (P = 0.01). In the subset of 33 patients with poorly differentiated or undifferentiated carcinoma, the accuracy was 91% with the assay versus 71% with immunohistochemical testing (P = 0.02). These results have important implications for the management of unknown primary cancers and warrant a study of an integrated algorithm evaluating tissue-of-origin molecular profiling to complement the use of immunohistochemical testing in selected patients.

TREATMENT IN THE GENOMICS ERA

Despite its heterogeneity, unknown primary cancer traditionally has been treated largely as a single entity, primarily with platinum-based combination chemotherapies. Over the past two decades, several combination treatments have been evaluated, and these have led to a range of therapies available for patients with unknown primary cancer. Phase 2 studies of empirical regimens have shown response rates of 25 to 35% and survival ranging from 6 to 16 months. Survival has been longer for patients with nodal, pleural, or serous peritoneal disease (14 to 16 months) than for patients with visceral metastatic disease (6 to 9 months). In most patients, the disease is disseminated and incurable. Additional prognostic factors guiding therapy decisions include lactate dehydrogenase and albumin levels, performance status, and number of sites of disease.

Historically, the “favorable subset” designation was based on a presentation that overwhelmingly suggested a specific primary origin. Patients who receive such a diagnosis often have a response to treatment that is based on the putative primary origin, and they may have prolonged survival and also a potential cure. These presentations (and their presumed primary origins) include adenocarcinoma in axillary lymph nodes in women (breast cancer), squamous-cell carcinoma in neck nodes (head and neck cancer), papillary or serous tumors in the peritoneal cavity in women (ovarian cancer), and poorly differentiated midline nodal disease in young men (germ-cell cancer), as well as metastatic neuroendocrine tumors and indolent, solitary metastases (the latter treated with definitive surgery, chemotherapy, radiation therapy, or a combination thereof). Some clinicians may view isolated or oligometastatic squamous-cell carcinoma in inguinal nodes as a favorable presentation, although the differential diagnosis is broader and includes anal, genitourinary, and gynecologic primary origins.

Case studies show the promise and challenge with determining the tissue of origin in
unknown primary cancer (Fig. 3 and 4). Patients with immunohistochemical test results suggesting a single diagnosis make up approximately 25% of patients with unknown primary cancer. Examples include the TTF1-positive and CK7-positive lung-cancer profile; the CDX2-positive, CK20-positive, and CK7-negative gastrointestinal-cancer profile; and the GCDFP (gross cystic disease fluid protein) 15-positive or mammaglobin-positive, CK7-positive breast-cancer profile. Frequently, the pattern of disease spread supports the immunohistochemical test results, and treatment algorithms are based on the putative primary origin. On occasion, the immunohistochemical and radiologic findings are discordant (Fig. 3A and 3B).

For the remaining 75% of patients, the differential diagnosis based on immunohistochemical testing is broad. Figure 4 shows a mass predominantly involving the liver that is suggestive of cholangiocarcinoma on the basis of radiologic findings. Pathological findings are typically nonspecific in such cases, and it is not unusual for cholangiocarcinoma to be called an unknown primary cancer. In patients without diagnostic (specific) results on immunohistochemical testing, a platinum-based regimen that is based on the clinicopathological presentation is often chosen, and protocol-based genomics studies, including tissue-of-origin molecular profiling and next-generation sequencing, may be useful. We lack specific and effective drugs for several cancer profiles, and treatments overlap for many cancers. However, as new therapies are developed for common known cancers, molecular tools for unknown primary cancers may be the cornerstone of decision making.

More broadly, there is an extensive push toward personalizing cancer care with the use of next-generation sequencing to identify driver mutations in individual tumors. Currently, we do not have a detailed understanding of the complex cross talk and signaling pathways involved in individual cancers. Vemurafenib, which targets the oncogenic BRAF V600E mutation, has...
though the management of unknown primary cancer is changing at a rapid pace, until new technologies have been validated and are widely available, we should not lose sight of the fundamental principle that the use of focused clinico-pathological testing and expert clinical judgment is critical in choosing the best therapies for patients.

**FUTURE DIRECTIONS**

Unfortunately, efforts to study unknown primary cancer with the use of collaborative research and new approaches have lagged behind efforts to study other solid-tumor types. Because of the heterogeneous presentations of unknown primary cancer, it is a challenge to adequately answer important questions involving new therapies, immunohistochemical testing, biologic features, and tissue-of-origin molecular profiling with the use of the traditional, prospective, phase 3 randomized designs. Innovative trial designs, the establishment of international consortia, and the application of genomic and proteomic techniques to subsets of unknown primary cancer will help us in our research efforts as we continue to expand therapeutic options to patients. The success of the next-generation sequencing approach will require both additional molecular insights and new drugs that are effective against specific mutations. Should this approach prove effective, the treatment of unknown primary cancers may merge with that of known primary cancers.

Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

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