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## Identification of circulating tumor cells: a prognostic marker in squamous cell carcinoma of the head and neck?

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In 2010, according to the NCI, 49,260 new cases of oral cavity, pharyngeal, and laryngeal cancer were estimated to occur in the United States; approximately 11,480 deaths were attributed to these cases. More than 95% of these cases are squamous cell carcinomas (1, 2). For all stages combined, the 5-year survival rate is approximately 50% (3), and this rate has not changed significantly in the last several decades. Treatment failure in patients with squamous cell carcinoma of the head and neck (SCCHN) can include local recurrence, regional recurrence (cervical lymph nodes), distant metastasis, or development of a second primary cancer. There is certainly a need for a reliable blood test to determine prognosis in SCCHN patients, specifically those patients who may be at increased risk of locoregional recurrence or distant metastasis.

Cancer metastasis may develop when cells from the primary tumor become invasive, making their way into the surrounding lymphatic or vascular channels. Lymph node involvement may only be microscopic, and therefore not always clinically or radiographically evident. In cancer of the oral cavity, about 25% of patients will have microscopic disease in the lymph nodes, despite a clinically negative neck (4, 5). The

presence of regional lymphatic metastasis in SCCHN is currently the most significant prognostic factor impacting survival, reducing survival by 50% (6–8). When cancer cells invade into the intravascular space, they are referred to as circulating tumor cells (CTCs). The exact mechanisms by which tumor cells leave the primary tumor, invade local tissues, and go on to develop in distant sites is not yet known.

From a clinical standpoint, the presence of CTCs may impact prognosis and treatment by providing: 1) early, definitive evidence of occult cancer spread, 2) a quantifiable risk factor for the development of distant metastatic disease, 3) the opportunity for further genetic analysis for targeted treatment strategies such as radiation or chemotherapy sensitivity, 4) a biomarker for post-treatment cancer surveillance. Studies have linked disseminated tumor cells to poor prognosis in breast (9), lung (10, 11), prostate (12), and colorectal cancers (13) but limited work has been done with regard to the role of CTCs in SCCHN.

While a milliliter of human blood contains an average of 5 billion RBCs, 7 million WBCs, and 295 million platelets, it is certainly a diagnostic challenge to identify a CTC (14). Researchers have taken several different approaches to accomplish this task. One approach is RT-PCR analysis of cancer-specific antigens, which are presumed to not be found in the blood, without visual cellular confirmation; this has been reported in SCCHN (15–19). Although this appears promising in melanoma (20–23), this technique may result in the detection of false positives due to non-specific amplification of genetic material. Other methods have used filtration to detect CTCs by size alone (24, 25), which implies that all CTCs are indeed larger than WBCs.

More commonly, the use of positive selection of CTCs by binding an antibody to a cancer-specific antigen on the cell surface has been performed. The most well-known are the CellSearch system by Veridex (26, 27) and the CTC-chip technology (28). Both of these methods rely on epithelial cell adhesion molecule (EpcAM) expression on the cell surface of CTCs in order to isolate and identify the cell (although other markers are also used for further analysis). While this is effective for identification of EpcAM positive cells, it may not be adequate for those cells which do not express this marker. The use of positive selection techniques for CTCs creates a significant intrinsic bias into the detection process since it is assumed that a CTC must express the cell surface marker targeted. Although such positive selection methods have not yet been described in the study of SCCHN, this potential diagnostic limitation has already been experimentally confirmed with another epithelial cancer, breast cancer. It has been demonstrated that the recovery of spiked breast cancer cells into the blood is a function of EpcAM expression. Those cell lines that highly expressed EpcAM were well-recovered using CellSearch; however other more aggressive breast cancer cell lines, which were high in CD44 expression, were poorly recovered, and 98% of these cells were missed (29). There is a growing body of evidence that epithelial to mesenchymal transition (EMT) takes place in the primary tumor, and it is possible that these cells may alter expression of their typical surface markers. EpcAM may be down-regulated during EMT, a process in which cancer cells acquire a more invasive and migratory phenotype (30–34).

In contrast to the positive selection approaches, we have developed an enrichment methodology which is based only on depletion of normal cells. We have demonstrated that this optimized methodology is able to obtain an average 5.66 log<sub>10</sub>, and as high as >7 log<sub>10</sub> total enrichment of CTCs in the blood of patients with SCCHN (35). To date, we have not found any evidence of CTCs in healthy patients. Such a method leaves CTCs in their native state (without binding of surface antibodies) to allow further unaltered cellular characterization. The RBCs are removed by lysis, followed by magnetic separation of immunomagnetically labeled CD45+ leukocytes, leaving potential CTCs for further characterization. Immunocytochemical staining can then be performed using nuclear staining, cytokeratin, and other markers. Using confocal imaging, we have found a number of patients expressing cytokeratin positive CTCs (36), but also what appear to be tumor microemboli. Most interestingly, we have found nucleated cells with weak or no cytokeratin expression, but rather mesenchymal characteristics. It is tempting to speculate that such cells have undergone EMT and are in circulation in patients with SCCHN; certainly more research is needed to further define such CTC phenotypes. We have not found these cells in healthy human blood samples, and the biologic behavior of these cells in SCCHN is not known.

There is promising evidence that CTCs are predictive of prognosis in SCCHN. Although there is no visual confirmation of the presence of a CTC, RT-PCR studies such as mRNA expression of cytokeratin 20 in the blood of patients with oral cavity squamous cell carcinoma, have been linked to reduced disease-free survival and increased frequency of lymph node metastasis (16). Partridge et al. (2003) used a negative depletion methodology to identify disseminated tumor cells in SCCHN patients and correlated outcomes. They found that the detection of disseminated tumor cells pre-operatively or intra-operatively indicated an increased risk of local/distant recurrence and reduced survival (37). We have published our early prospective clinical results of 48 patients with SCCHN with a mean follow-up of 19 months, showing a statistically significant worse disease-free survival in patients with CTCs present at the time of surgical resection. We also observed that the presence of an increasing number of CTCs correlated with a worse outcome. There was no correlation between the presence of CTCs and lymph node metastasis, which suggests that with further study of additional patients, CTCs may turn out to be an independent prognostic marker in SCCHN (38).

We have developed a high-performance negative depletion technique for the identification of CTCs in the blood of patients with SCCHN, and our early clinical follow-up to date has been encouraging, suggesting that the presence of CTCs may be designated as a potential novel prognostic marker. The biologic mechanisms underlying CTCs and cancer recurrence or distant metastasis are not yet well-established, and until greater knowledge is acquired, techniques using cancer specific markers to potentially select out only a subpopulation of CTCs, may miss abnormal cells in cancer patients. With regard to CTCs, there are numerous unanswered questions, and we suggest that in order to objectively find answers, an unbiased approach may be best. With further clinical follow-up, we will continue to elucidate the long-term significance of CTCs in patients with SCCHN; certainly, larger prospective studies are warranted.

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