

Why is Immunohistochemical Detection of Metastasized Breast Cancer Cells in the Immunocompetent Host Not Always Easy?

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Abstract: Metastases of breast cancer cells from the tissue of origin to distant sites including vital organs commonly occurs in patients suffering from breast cancer. Such metastases are detrimental to the quality of life of these patients. Clinical pathologists and basic researchers in the field of oncology commonly use techniques like immunohistochemistry to detect disseminated cancer cells in metastasized regions in an attempt to improve patient outcomes. This review sheds light on genotypic and phenotypic changes in disseminated cancer cells that occur during the ongoing process of metastasis, thereby leading to continuous changes in the expression levels of different markers expressed by these cells and making the immunohistochemical detection of breast cancer cells in the non-cognate tissues difficult.

Keywords: Breast cancer, metastasis, genotypic and phenotypic changes.

Immunohistochemical assessments are commonly used by pathologists to detect metastasized cancer cells in the regions distant from the tissue of origin of the cancer as these assessments are considered to be a more direct method of detection of the cells, compared to other methods [1, 2]. However, the expression levels of such immunohistochemical markers in disseminated cancer cells can significantly vary from the cells in the tissue of origin. Heterogeneity of cancer cells is a very well-known phenomenon. In breast cancer, it may be difficult to clearly classify the cancer cells as marker-receptor- “positive” or “negative”, as there can be significant intra-tumoral heterogeneity in their expression [3, 4]. Her2, Muc1 and cytokeratins are some of the classical breast cancer markers [5, 6]. Intra-tumoral heterogeneity can typically be observed with such classical markers too, including Her2 [7-9], MUC1 [10] and cytokeratins [11, 12]. Such intra-tumoral heterogeneity in breast cancer occurs both at the genetic and morphological levels [13-17]. Due to the existence of mixed cell populations in the breast cancer tumours, they have the potential to differentially grow into diverse types like epithelial and fibroblastic, subject to different growth conditions [18].

One of the hallmark features of cancer cells is their genomic instability and this is what makes a cancer a cancer [19-21]. Cancer immunoediting comprises three Es- Elimination (immunosurveillance), Equilibrium and Escape; and the process leading from immunosurveillance to tumour escape in the immunocompetent host is well known [22]. As per the Darwinian selection theory, tumor-specific immune responses are

responsible for eliminating highly immunogenic tumor cells, while the tumor variants with reduced immunogenicity have a better chance of survival in the immunocompetent host [22-24]. Tumour cells have the ability to shed or restrict the presentation of ligands or antigens involved in their recognition by the host's immune system or down-regulate the expression of factors that promote activation of tumour-specific immune responses [25]. Due to the immune pressure, tumour cell variants with loss of such antigens emerge as a consequence of epigenetic mechanisms within the tumor [26, 27]. Likewise, the anti-tumor immune responses themselves can induce changes in antigen-positive cells, converting them into antigen-negative cells [28, 29]. Hence, discordance in receptor or biomarker status and genotypic heterogeneity between primary breast cancer cells and their metastasised lesions or circulating cells in the body is very common, because the biomarker expression of primary tumour cells can significantly change during the disease progression [30-39]. Similarly antigens that can be targeted by the immune system are also found to be lost in other types of human cancers [40-42]. Such immunoediting processes can be strong enough to induce very significant changes in morphology and microarray of the breast cancer cells, leading to failure in detection of earlier version of cells [43-50].

For example, Muc1 has several major limitations as a breast cancer marker and most cancer-expert panels around the world recommend against its use as a reliable marker even in the post-operative clinical setup in humans [5, 51]. Its expression is not always constant and changes massively based on the changes in endogenous biological processes [52]. MUC1 expression levels can change in cancer cell lines at the transcriptional level or even *in vivo* due to the effect of

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internal body hormones [53]. Muc1 is an epithelial marker [54], however, it is not necessarily expressed in all the cells within the tumour. For example, ovarian neoplasms constitute a heterogeneous group of tumours, of which 90% are of epithelial origin. Epithelial ovarian tumours are subclassified into various histological types, including ovarian mucinous tumours (OMTs), which account for 10–20% of all ovarian tumours. Of these OMTs (10-20 %) in humans, the positivity frequencies of MUC1 in OMTs range from 12 - 31.6 % which is very low [55]. Muc1 is known to serve as a target molecule in the killing of breast cancer cells by the body's immune system [56-59] and hence is also assumed to be a good candidate for immunotherapy against human cancers [60]. So as to avoid being detected and killed by the immune system, the cancer cells can undergo epigenetic changes [61] such that they lose Muc1 expression or modulate its antigenicity [62-69]. Similarly, downregulation of Muc1 can also be induced in cancer cells subjected to anti-cancer drugs, which in turn might protect tumours against host's immunity [70, 71]. It has also been seen in some cases that Muc1 is highly expressed in the normal mammary gland of an animal but not in a mammary tumour of the same animal, which suggests that *in vivo* factors could cause downregulation of Muc1 expression [72]. Similarly, the expression of MUC1 in breast cancer cells might also be linked with expression of other markers like HER2 [73-75].

Similar is the case with Her2. Cultured circulating tumour cells maintain discrete Her2+ and Her2- subpopulations and these cells can interconvert spontaneously *in vivo* just within few cell doublings [76, 77]. There can be certain factors that selectively pressurise the tumour niche such that breast cancer cells *in vivo* acquire a change in their Her2 status [78, 79]. The cancer cells may express Her2 primarily, but there could be discordance as the same cells that are metastasizing or circulating *in vivo* may not express Her2 or vice-versa [80-87]. So, in principle, the Her2 status of cancer cells in distant regions like bone marrow is independent of the primary tumour [88]. Her-2/neu antigen loss can actively occur in primary tumors (epigenetic changes) due to the neu-targeted anti-tumor immune responses, which might be a part of the selection process of a tumor variant that has reduced ability to induce danger signals [23, 43, 89-92]. Neu antigen-negative variants have been reported to be generated after neu-specific antibody therapy in a neu transgenic mice model of breast cancer [93], and a similar loss of Her2 is observed in humans with gastric

or gastroesophageal cancer following trastuzumab therapy [94].

On similar grounds dysregulation of expression of cytokeratins is also possible in cancer cells. For example, downregulation of cytokeratin 18 in breast cancer cells is observed in some cases [95] and such dysregulation might also be triggered due to the effect of drugs [96]. The anti-tumour action drives the process of epithelial-mesenchymal transformation of cancer cells, causing downregulation of epithelial markers such as cytokeratins [97]. Downregulation of cytokeratin 18 in metastatic cancer cells in distant regions like bone marrow can also commonly occur [98]. Such dynamic nature of expression of different markers in cancer cells following dissemination, makes the immunohistochemical assessments of these cells quite challenging.

A similar level of difficulty exists with detection of breast cancer cells in preclinical rodent models of experimental metastasis. Cell line misidentification is known to be a common problem [99]. On these grounds, a case of misidentification of a widely studied cancer cell line, U87MG glioma, was recently reported when it was found that the DNA profile of the cell line obtained from ATCC was different from that of the original cells, raising doubts on the authenticity of this ATCC cell line [100]. Similarly, although Walker 256 rat breast cancer cell line is commonly believed to be of epithelial origin, an old study had reported that epithelial cell markers were absent in Walker 256 cells [101]. Walker 256 cells have also been suggested to be of hematopoietic origin and not of epithelial origin, which was substantiated by the authors findings that these cells grew as non-adherent clumps of cells indicative of a lymphoid / leukemia cell culture rather than the sheets observed with epithelial cell lines [101-103]. Walker 256 cell tumour is also known to be able to give rise to a more fibroblastic cell line [104, 105]. It remains possible that Walker 256 cell line contains a heterogeneous population of different type of cells which are genetically programmed to change themselves from one state to other. For example, *in vitro* pure cultures of epithelial cells of Walker 256 tumour have been reported to transdifferentiate *in vivo* into tumours simulating fibrosarcoma [105]. Such cancer associated fibroblasts could be a cell state rather than a cell type, and origin of these cells could just be transdifferentiated epithelial cells [106]. Growth of epithelial components of Walker 256 tumour could be limited by the network of fibroblasts [107]. However, there is no specific marker for breast cancer associated

fibroblasts [108]. On these grounds, several terms have been coined to address the cancer produced by the same Walker 256 cells, viz. carcinoma, adenocarcinoma, carcinosarcoma, sarcoma and fibrosarcoma [105, 109-114]. Techniques like local intraosseous injection of cancer cells in rodents are commonly used to experimentally simulate metastasis of cancer cells to distant regions like axial skeleton [115-123]. However, there can be remarkable differences in the expression levels of different markers expressed by the cancer cells colonising the distant regions like bones due to the possible phenotypic and genotypic changes occurring in the cancer cells after experimental engraftment. To obtain detailed insights into these changes, one will require to perform comparative genomic and proteomic assessments of cell line cultured *in vitro* and bone-colonising tumours developed *in vivo* in these pre-clinical models.

Although it is generally expected that cancer cells in the metastasised regions might be detected in the local lymph nodes, this might not always be the case [124]. Lymph node negative breast cancer cases in humans are common, and metastases of cancer cells to distant regions like bones without presence of these cells in the lymph nodes is not unexpected [125-131]. If there are any cells from afferent lymph that reach the lymph nodes, it remains possible that these cells can transverse the lymph nodes and enter the efferent lymph [132] and might be subsequently eliminated by the immune system. The cancer cells don't necessarily need to grow in the lymph nodes as the transnodal passage of cells might occur [133]. For example, the Walker 256 rat breast cancer cells can pass the lymph nodes and enter blood circulation and hence may not even grow in the lymph nodes as shown in female wistar rats [134].

Another minor challenge with immunohistochemical assessment of cancer cells in distant regions like bones could be the experimental artefact introduced by the process of decalcification typically required to soften the osseous tissue. Although EDTA is commonly used for decalcification of tissues like bones [135] and normally considered safe, it can have detrimental effects on the cancer cells colonising the bones, thereby posing difficulties in immunohistochemical detection of these metastasized cells [136-148].

Additionally, breast cancer cells can change *in vivo* such that they are present in a non-proliferative state and might possess stem-cell like characteristics [149-153]. Transdifferentiation of cells from one cell type to

another is a commonly observed phenomenon with cancer cells [154-164]. Transdifferentiated cells thus formed can still be malignant in nature [165-179]. Breast cancer cell lines can co-express several types of differentiation markers, leading to aberrant multi-lineage transdifferentiation or lineage infidelity [180]. Hence, in the immunocompetent host, the possible dynamic nature of genotypic and phenotypic variations occurring in metastasized breast cancer cells, makes it difficult to immunohistochemically predict the molecular nature of metastasized tumours developed in distant tissues.

CONFLICT OF INTEREST

The author declares no conflict of interest.

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