Phosphotyrosine Signaling Analysis in Human Tumors Is Confounded by Systemic Ischemia-Driven Artifacts and Intra-Specimen Heterogeneity

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Abstract

Tumor protein phosphorylation analysis may provide insight into intracellular signaling networks underlying tumor behavior, revealing diagnostic, prognostic or therapeutic information. Human tumors collected by The Cancer Genome Atlas program potentially offer the opportunity to characterize activated networks driving tumor progression, in parallel with the genetic and transcriptional landscape already documented for these tumors. However, a critical question is whether cellular signaling networks can be reliably analyzed in surgical specimens, where freezing delays and spatial sampling disparities may potentially obscure physiologic signaling. To quantify the extent of these effects, we analyzed the stability of phosphotyrosine (pTyr) sites in ovarian and colon tumors collected under controlled ischemia and in the context of defined intratumoral sampling. Cold-ischemia produced a rapid, unpredictable, and widespread impact on tumor pTyr networks within 5 minutes of resection, altering up to 50% of pTyr sites by more than 2-fold. Effects on adhesion and migration, inflammatory response, proliferation, and stress response pathways were recapitulated in both ovarian and colon tumors. In addition, sampling of spatially distinct colon tumor biopsies revealed pTyr differences as dramatic as those associated with ischemic times, despite uniform protein expression profiles. Moreover, intratumoral spatial heterogeneity and pTyr dynamic response to ischemia varied dramatically between tumors collected from different patients. Overall, these findings reveal unforeseen phosphorylation complexity, thereby increasing the difficulty of extracting physiologically relevant pTyr signaling networks from archived tissue specimens. In light of this data, prospective tumor pTyr analysis will require appropriate sampling and collection protocols to preserve in vivo signaling features. Cancer Res; 75(7); 1–9. © 2015 AACR.

Introduction

Protein posttranslational modifications (PTM), such as phosphorylation, regulate the stability, localization, and activity of cellular components (1–3). Accordingly, dynamic phosphorylation plays a vital role in coordinating information flow within the cell and regulating emergent tumor responses ranging from proliferation to invasion and angiogenesis. Phosphorylation occurs predominantly on serine and threonine residues with tyrosine phosphorylation accounting for only approximately 0.05% of all phosphorylation events in eukaryotic cells (4). Although tyrosine phosphorylation is rare and tyrosine kinases represent only 0.3% of the genome, these enzymes represent close to 30% of the known oncoproteins such as SRC, EGFR, and BCR-ABL (5). Their disproportionate role in oncology, combined with their structural druggability, makes tyrosine kinases highly desirable therapeutic targets. Quantitative analysis of protein tyrosine phosphorylation in human tumor tissue specimens can provide insight into intracellular signaling networks underlying tumor behavior while identifying activated kinases and their substrates, signaling components that may represent druggable targets.

Human tumors collected by The Cancer Genome Atlas (TCGA) program potentially offer the opportunity to characterize activated signaling networks driving tumor progression, in parallel with the genetic and transcriptional landscape already documented for these tumors (6–8). The National Cancer Institute’s Clinical Proteomic Tumor Analysis Consortium (NCI-CPTAC) seeks to provide proteomic characterization of tumors genomically annotated by TCGA programs (9). State-
of-the-art mass spectrometry (MS)-based proteomics provides quantitative, systematic analysis of protein phosphorylation profiles (10–12) with the potential to directly identify activated signaling networks in tumors; information that is difficult to derive from genetic-based studies. However, tumor specimen analysis is complicated by possible temporal delays in tissue acquisition and processing along with spatial sampling differences due to the heterogeneous nature of human tumors. Freezing delays following sample resection and processing subject the specimen to ischemia; unfortunately the exact time to freezing for archived tissue specimens is often undocumented. To date, studies on the effects of ischemia on tissue phosphorylation have been reported, yet the sample collection and analysis approaches used did not allow assessment of short periods of ischemia (13) or permit comprehensive analysis of pTyr signaling (14).

The heterogeneous nature of human tumors has been widely documented (15, 16). Inter-patient and intratumoral variations are evident at a macroscopic histologic level and at molecular, genetic, and epigenetic levels through clonal evolution and tumor microenvironment influences (17, 18). A previous report investigated phosphorylation patterns across distinct anatomic metastatic lesions of prostate cancer. However, the number of phosphorylation sites probed was limited and intralesion comparison was not performed (19). The influence of proximal spatial heterogeneity within a tumor specimen on pTyr signaling networks has yet to be determined. Collectively, these preanalytical factors may influence protein phosphorylation measurements, thereby obscuring physiologic signaling networks (20). Therefore, we sought to investigate how preanalytical variations in sample collection and processing can ultimately affect downstream pTyr signaling analysis of human tumors.

Materials and Methods

Human ovarian and colon tumor collection

High-grade serous ovarian carcinoma tissue from 5 patients was collected as previously reported (21). Colon adenocarcinoma biopsy tissue was collected from five patients at the Cooperative Human Tissue Network at Vanderbilt University Medical Centre (CHTN-VUMC; Nashville, TN), in accordance with Institutional Review Board–approved protocols. Following vessel ligation, surgical specimen removal was performed and the first core biopsy was taken immediately thereafter (t = 0), transferred to prechilled cryovials, and snap frozen in liquid nitrogen. Further core biopsies were collected and frozen after 10, 30, and 60 minutes of cold ischemia. Only specimens meeting pathology quality inclusion criteria of left-sided colon adenocarcinoma cancers in which clamp time could easily be determined, minimal tumor diameter of 4 cm, and no prior chemotherapy and/or radiation were released for analysis.

Protein extraction, digestion, and iTRAQ labeling of peptides from ovarian and colon tumors

Approximately 50 to 100 mg (total wet weight) of each of the timepoint samples was homogenized separately for protein extraction and digestion as described previously (22). Desalted peptides were labeled with multiplex iTRAQ (Isobaric Tags for Relative and Absolute Quantification) reagents as reported previously (22). Briefly, 800 μg peptide per sample for each of the ovarian and colon tumor timepoints was labeled with two tubes of iTRAQ reagent (according to the labeling scheme shown in Supplementary Figs. S2 and S5).

Phosphotyrosine peptide enrichment

Phosphotyrosine peptides were enriched before mass spectrometry analyses using a cocktail of anti-phosphotyrosine antibodies followed by immobilized metal affinity chromatography as previously described (22).

Mass-spectrometry–based phosphotyrosine analysis

Peptides were chromatographically separated and subsequently analyzed by Orbitrap Elite mass spectrometer (Thermo Scientific), database-searched, validated, and normalized as previously reported (22).

Phosphotyrosine data analysis

The total list of peptides and proteins identified and quantified can be found in Supplementary Tables S1, S2, and S4. All mass spectra, in the original instrument vendor format, contributing to this study may be downloaded from: https://cptac-data-portal.georgetown.edu/cptacPublic/

Mass-spectrometry–based protein expression analysis

Approximately 10% (~300 μg) of iTRAQ-labeled peptides from each colorectal tumor pTyr IP supernatant was separated off-line on C18 column. A total of 80 fractions were collected, noncontiguously pooled into 20 final fractions, and each subjected to an independent LC/MS-MS analysis. Each fraction was separated by reverse phase UHPLC (Easy-nLC 1000, Thermo Scientific) before nanoelectrospray directly into a Q-Exactive mass spectrometer (Thermo Scientific).

Protein expression data analysis

Peptide and protein identification was performed with the Proteome Discoverer software (version 1.4; Thermo Scientific) using Mascot search engine (version 2.4.1, Matrix Science). MS-MS spectra were searched against a human protein sequence database (NCBIInr, 2012 release, 35,586 sequences). For each protein expression experiment, one combined database search was performed where the data files from all 20 independent MS fraction analyses were searched collectively as a single input dataset. The total list of peptides and proteins identified and quantified can be found in Supplementary Table S5.

Affinity propagation clustering analysis

Quantitative temporal profiles of all pTyr sites within an individual patient dataset were clustered using the affinity propagation algorithm proposed by Frey and Dueck (23). Individual patient datasets were subjected to independent analysis (see Supplementary Fig. S4) as described previously (22).

Statistical analysis and annotation

Hierarchical clustering analysis and heatmap construction were performed using the built-in Bioinformatics Toolbox function “Clustergram” in Matlab (R2013b, The Mathworks Inc.) with Euclidean pairwise distance metric. Statistical analysis was conducted using GraphPad Prism 5.0a software. Pearson correlation analysis (two tailed), and pairwise Student t tests (two-tailed) were
used for calculating the significance of the differences and significance was accepted when $P<0.05$. Kinase enrichment analysis was performed using the webtool at http://amp.pharm.mssm.edu/lib/kea.jsp and conducted as described previously (24). The input dataset was compiled from the union of ischemia-regulated pTyr sites found in $\geq4$ ovarian tumor samples and $\geq4$ colon tumor samples. Predicted kinases were plotted onto a dendrogram of the human kinase (25) using the webtool at http://web.cec.pdx.edu/~josephl/kinome-cluster/. Panther Gene ontology (GO) annotations were identified by uploading UniProt ID lists to the Protein Analysis Through Evolutionary Relationships (PANTHER) classification system (http://www.pantherdb.org/).

**Results**

Postexcision ischemia induces rapid, widespread, patient-dependent alterations to pTyr networks

Postexcision ischemia time is generally undocumented in TCGA samples but may range from minutes to an hour during processing and pathologic inspection. To understand the effect of cold-ischemia on protein tyrosine phosphorylation, we collected patient-derived ovarian tumor samples from five individuals undergoing debulking surgery and performed a controlled ischemia 4-point time-course (Supplementary Fig. S2). Ischemia time-course sets from each patient were analyzed separately, providing detection and quantitation of several hundred pTyr sites per patient (Supplementary Table S1). Within 5 minutes of cold-ischemia, the fraction of pTyr sites within a specimen that showed quantitative fluctuations ranged from 29% to 55%, depending on the patient (Fig. 1A and Supplementary Table S1). Intriguingly, the temporal response to ischemia was patient specific. Two patients, 39 and 67, showed a predominant decrease across many pTyr sites within the first 5 minutes, whereas the other patients had a more mixed response, with comparable proportions of increasing and decreasing sites. We hypothesized that some of the inter-patient differences in response to ischemia could be attributed to patient-specific baseline phosphorylation profiles. To investigate this possibility, the "0 minute" samples from each ovarian patient were analyzed simultaneously, providing detection and quantitation of several hundred pTyr sites per patient (Supplementary Table S1). Within 5 minutes of cold-ischemia, the fraction of pTyr sites within a specimen that showed quantitative fluctuations ranged from 29% to 55%, depending on the patient (Fig. 1A and Supplementary Table S1). Intriguingly, the temporal response to ischemia was patient specific. 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Figure 1.

Postexcision ischemia induces rapid, widespread, patient-dependent alterations to pTyr networks. A, heatmaps of all quantified peptides from individual patient-derived ovarian tumor 4-timepoint ischemia study. Rows indicate mass spectrometry-derived quantitative levels of pTyr sites in log2 scale relative to t = 0 minute, rank ordered by value at t = 60 minutes. Onset of color in the heatmaps corresponds to changes > 3 SD from value at t = 0 (red, increasing; blue, decreasing). See Supplementary Table S1 for details. B, hierarchical-clustered heatmap of quantitative pTyr profiles of individual ovarian tumors at resection. Quantitative levels of pTyr sites grouped in rows, in log2 mean normalized scale. C and D, select examples of distinct inter-patient ischemia regulated temporal dynamics. Colored lines represent relative inter-patient phosphorylation levels; mean ± SD of technical replicates is shown. Temporal data values shown are derived from independent patient datasets and normalized with t = 0 value measured in B (see Supplementary Fig. S3 for additional examples). E, affinity propagation-derived clusters for pTyr sites detected in patient 27 (See Supplementary Fig. S4 for affinity propagation clusters of other patients). Subplots signify groups of pTyr sites with similar quantitative trends across time (x-axis). Solid lines denote trends of individual pTyr sites. Mean log2 temporal values relative to t = 0 minute are shown. Exemplar pTyr site of each cluster shown in blue. F, ischemia-regulated phosphorylation sites common to all patients with functional categorization. Ischemia index (y-axis) for each site represents absolute sum of the log2 changes relative to t = 0 at 5, 30, 60 minutes. Mean value ± SEM from all patients is plotted. Asterisks denote sites known to be implicated in protein activity or function.
provided different signaling profiles (Fig. 2C; 10, 30, 60 minute pairs).

Spatial and temporal protein expression differences are minimal in tumor samples

To evaluate whether intratumor protein expression heterogeneity contributed to the observed spatial and temporal pTyr differences, we performed protein expression analysis of the colorectal specimens (Supplementary Fig. S8 and Supplementary Table S5). Unsupervised hierarchical clustering indicated that protein expression is mostly uniform temporally and spatially (Fig. 3A). Where quantitative protein expression differences were observed between paired timepoints, they were muted compared with the large differences identified in pTyr profiles. To systematically evaluate the relationship between protein expression heterogeneity and pTyr levels, we identified 76 pTyr sites where corresponding protein levels were also available (Fig. 3B and Supplementary Table S6). Although protein expression was invariant with both spatial location and ischemia, pTyr levels showed dramatic spatial and ischemic time-dependent variation. These results suggest that differential ischemic responses could occur in adjacent parts of a tumor. For example, selected pTyr sites in patient 041 exhibited spatially distinct changes during ischemia, despite uniform expression of the corresponding proteins (Fig. 3C).

Ischemia alterations occur across tumor types, impacting a core set of functional classes, yet have the potential to affect biologically diverse pTyr pathways

To reduce the impact of spatial heterogeneity on phosphorylation and identify consistent ischemia-related changes, we averaged the pTyr measurements from paired-timepoint samples. As with the ovarian tumors, a large proportion of pTyr sites showed significant quantitative changes following delayed freezing (Fig. 4A and Supplementary Table S4). These results demonstrate that delayed-freezing effects can alter tyrosine

Figure 2.
Spatial phosphorylation heterogeneity is apparent in human colon tumors. A, separate unsupervised hierarchical-clustered heatmaps represent the spatial and temporal sample set of each patient-derived colon tumor. Patient identifier shown to top left of each heatmap. Rows indicate mass spectrometry-derived quantitative levels of pTyr sites in log2, mean normalized scale. Onset of saturated color in the heatmaps corresponds to changes ≥2-fold from the mean (red, increasing; blue, decreasing). B, Pearson correlation analysis was used to quantify the direction and magnitude of correlation among the spatially distinct colorectal tumor samples. Data points presented in each plot are the log2 mean-centered value for a given pTyr site between paired spatially-distinct samples at the indicated timepoints in patient 323. $r = \text{Pearson correlation coefficient}; 95\% \text{CI}, 95\% \text{confidence interval of } r; P = \text{two-tailed } P \text{ value. See Supplementary Fig. S7 for correlation analysis of other patients. C, phosphorylation levels of clinically useful pTyr sites are plotted for each patient spatial and temporal sample set. Samples are shaded according to patient and columns grouped to indicate identical timepoint samples that are spatially distinct. Mean value ± SEM is plotted. Statistically significant differences are indicated. }^*; P = 0.001 \text{ to } 0.01; ^\dagger; P = 0.01 \text{ to } 0.05.$
phosphorylation in multiple tumor types. As with the ovarian cancer samples, inter-patient differences were observed for temporal dynamics (Supplementary Table S4). From these data, we extracted a minimal ischemia-regulated signature of 12 pTyr sites common to both ovarian and colorectal samples; adhesion and migration, proliferation, and stress response pathways are represented within this signature (Fig. 4B). Because of the inter-patient biologic variation, many additional specimen-specific ischemia-driven pTyr perturbations were documented. Accordingly, when all tumor variation is considered, it becomes apparent that extensive ischemia-dependent alterations affect most tyrosine kinases (Fig. 4C and Supplementary Table S7). The pathways impacted by ischemia encompass diverse kinases and downstream effectors across broad biologic functions and processes (Supplementary Fig. S9). Therefore, ischemia, particularly of unknown duration, may distort pTyr network profiles to an extent that cannot be reliably corrected.

Discussion

There is a strong impetus to comprehensively integrate genetic profiles of tumors with corresponding proteomic expression and protein phosphorylation datasets (9). The salient findings of this study indicate that measurement of pTyr signaling nodes in human tumors is (i) susceptible to extensive postresection ischemia effects creating rapid and systemic changes that alter the initial in situ tumor phosphorylation profile, and (ii) distinct intratumor phosphorylation profiles are apparent, indicating spatial microheterogeneity and presumably signaling differences within specimens.

Our findings suggest that the tumor specimens are actively regulating signaling events despite their loss of blood supply and attachment to the surrounding tissue. Hypoxia, hypoglycemia, acidosis, hyperthermia, and osmotic disturbances are perturbations to which the tumor acutely responds until cryopreservation. The immediate implication is that insight about tumor pTyr signaling in human tumor specimens may be greatly misleading or incorrect depending on the nature and duration of tumor harvesting/processing before analysis. Unfortunately, retrospective extrapolation of an accurate in vivo phosphorylation state appears to be prohibitively difficult due to unique dynamics on each pTyr site coupled with unpredictable patient specific responses to ischemia (Fig. 1C and D and Supplementary Fig. S3).

The temporal trends and directionality of pTyr fluctuation observed are consistent with the physiologic effects of tumor

Figure 3.

Spatial and temporal protein expression differences are minimal in colorectal tumors. A, separate unsupervised hierarchical-clustered heatmaps represent the spatial and temporal sample set of each patient-derived colon tumor. Patient identifier shown to top left of each heatmap. Rows indicate mass spectrometry-derived quantitative levels of protein expression in log2 mean normalized scale. Onset of saturated color in the heatmaps corresponds to changes >2-fold from the mean (red, increasing; blue, decreasing). B, quantitative levels of protein (from a) and matching pTyr sites (from 2a) on the same protein. Rows represent values in log2 scale relative to t = 0a minute. Onset of color in the heatmaps represents changes greater than approximately 1.4-fold from the mean (red, increasing; blue, decreasing) to emphasize uniformity in protein expression values compared with pTyr values. Plotted pTyr values are also quantitatively normalized to the protein expression levels. See Supplementary Table S6 for details. C, selected examples of corresponding protein and pTyr levels from B. Columns are shaded to group identical timepoint samples that are spatially distinct. Mean value ± SEM is plotted.
resection and a step-wise signaling response. In fact, the pTyr sites within the identified temporal clusters appear to correlate with progressive stages of ischemic stress (Fig. 1E and Supplementary Fig. S4 and Supplementary Table S3). For example, physical stresses from wounding, hypoxia, and osmotic shock result in the immediate activation of response pathways to promote tissue repair and regeneration. This activity is consistent with the observed rapid hyperphosphorylation of p38 MAPKs (i.e., MAPK12, MAPK13, MAPK14) through oxidative stress-sensing ASK1 and osmosensing OSM (34, 35). Activation of these pathways can in turn trigger signaling programs necessary for the production of proinflammatory cytokines and tissue repair (36). This immediate signaling cluster also included increased phosphorylation of PRKCD, a known substrate of a caspase-3 during apoptosis, was observed across all ovarian tumors. Lack of perfusion leads to cellular dehydration, shrinkage, and distortion. Accordingly,
phosphorylation decreases on EPHA2, EPHA4, EPHB2, PARD3, PKP4, and TNS3 agree with physiologic changes in loss of cell–cell and ECM contacts (31–33). Collectively, the directionality and timing of several phosphorylation sites are consistent with the physiologic stages of severe ischemia.

Of note, the core pTyr ischemia signature described overlaps with functional pathways known to be relevant in the signaling of cancer cells such as adhesion, migration, and proliferation (37, 38). Importantly, in many cases the pTyr sites annotated are directly implicated in regulating protein function, for example, 17 of 22 pTyr sites in the core ischemia signature (Fig. 1F) have been shown experimentally to directly modulate protein kinase activity and function. As such, these are not uncharacterized phosphorylation events but rather functionally relevant pTyr sites with probable signaling consequences. Moreover, although phosphorylation changes of greater than 2-fold were detected during the ischemia time-course (20%–28% and 25%–48% of peptides in ovarian and colon tumors respectively; Supplementary Tables S2 and S4) and often used to prioritize biologically significant signaling changes, the magnitude of change does not always correlate with signaling significance. In fact, modest changes to phosphorylation levels may correspond to meaningful biologic results as demonstrated in the context of MEK, K-RasG12D, or EGFRVIII, where slight changes to the signaling activity have profound effects on viability and oncogenicity (39–41). As such, the subset of pTyr sites with seemingly insignificant variations may still in fact push signaling networks away from a fine-tuned steady state (42).

It is important to emphasize that the extensive list of ischemia-regulated pTyr sites in ovarian and colon tumors (Fig. 4C and Supplementary Fig. S9) spans a multitude of pathways and processes and are not limited to obvious stress response pathway proteins (i.e., p38 MAPKs). Although it is tempting to speculate that tumors with strong driver signaling (i.e., HER2 overexpression) could still generate pTyr signatures that overshadow ischemia-induced signatures, this is conceptually unlikely for at least two reasons. First, oncogenic signaling mutations do not always exhibit enhanced levels of phosphorylation, but can instead present persistent, minor increases to achieve oncogenic network states (40, 41). Second, strong pTyr signaling would likely impinge on the nodes and pathways affected by ischemia (i.e., proliferation, migration, adhesion, etc.) preventing definite attribution of the source. Thus, it will not be feasible for future pTyr experiments to simply exclude a set of ‘ischemia susceptible’ proteins and derive a quantitatively reliable dataset because the boundaries of susceptible and stable pTyr sites are not entirely clear, appear to be patient specific, and cannot be predicted a priori based on our current knowledge.

The use of surgically excised tumors in this study was paramount to recapitulate a typical biospecimen collection scenario; however, an unexpected caveat of this analysis was the realization that pTyr tumor heterogeneity exists even on a relatively proximal scale. Spatial heterogeneity of tyrosine phosphorylation may have significant impact on clinical decisions. As alluded to in Fig. 2C, monitoring of therapeutic efficacy in preclinical or clinical trials is often examined by measuring phosphorylation levels on kinases and other signaling targets. However, using pTyr as a diagnostic proxy in human specimens could pose challenging, as inadequate assessment of clinically relevant pTyr sites is possible depending on the extent of tumor spatial heterogeneity and breadth of sampling. Ideally, this variation should be acknowledged and accounted for in current and future studies to allow appropriate interpretation of pTyr levels in human tumor specimens (e.g., multiple, spatially distinct pre- and posttherapy biopsies when evaluating drug efficacy.)

A concurrent CPTAC study of the ischemia-driven effects on serine/threonine phosphorylation in tumor samples revealed complementary insights (21). Although examination of the same ovarian tumor specimens used here suggested that serine/threonine phosphorylation might be less susceptible to ischemia, perturbations were observed in approximately 6% of the approximately 9,000 pSer/pThr sites measured (based on those sites overlapping in at least 3 samples), with the majority of these sites concentrated in stress signaling pathways. This result is in contrast with this study, where perturbations were observed in 62% of 217 sites measured in ovarian tumors (based on those sites overlapping in at least 3 samples) and approximately 44% of 57 sites measured across both ovarian and colon tumors (overlap in at least three samples). These differences are likely attributable to the highly regulated nature of pTyr sites compared with pSer/pThr sites, and may be indicative of the biologic relevance of the regulated phosphorylation sites measured in both studies.

In summary, immediate freezing of human tumor specimens is necessary to minimize postresection artifacts that could confound identification of physiologic pTyr signaling networks. Intratumoral phosphorylation heterogeneity suggests that performing single biopsies of primary tumors or metastases, as is usual clinical practice, may provide erroneous or incomplete profiles of signaling systems in tumors. These data suggest that multiple biopsies, immediately flash frozen, may be necessary to accurately assess the signaling characteristics of human tumors.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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