

Attempts at Repeated Cell Re-Constitution as Integral Developmental Dynamics of Cell Proliferation in Oncogenesis

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Abstract

Performance re-characterization of pathway definition constitutes the defining elements of patterned response of the injured integral cell that individually defines the nature of biology of the cell clone and of the specific transformation event in oncogenesis. Determining parameters concern the patterns of response in the face of ongoing oncogenesis in terms that elusively create an autonomous response as systems biology pathways. It is within the further cooperative patterns of single cell integrity that oncogenesis defines a determined focality of response in terms that overall defines the primal proliferation and scatter of cells as induced by hepatocyte growth factor/MET activation.

Introduction

Integral participation of ongoing hepatocyte-growth factor/MET formulation includes a cascade evolutionary series of step-phases that further conform to the dimensions of proliferation and survival of cells, including epithelial cells. Binding of HGF to MET receptor initiates a whole spectrum of cell signaling driving malignancies and invasion and indicates poor clinical outcome [1]. The mesenchymal origin of HGF is tantamount identity for the increasingly involved participation of dual and also multiple incremental processes that developmentally allow the identification of neoplastic interactivities. Activating mutants of beta-catenin are oncogenic, but inhibiting this pathway facilitates hepatocellular recurrence following targeted therapy of the primary neoplasm [2].

The further conformational binding of HGF with the kinase domain of MET includes the activation of cascade events within the increasingly complex nature of oncogenesis. Human papillomavirus-negative oropharyngeal carcinomas enhance fibroblast-induced support of tumor invasion through microenvironmental release of HGF and IL-6 [3]. Primal attachment and also detachment dynamics of ligand-receptor binding allows a largely permissive nature for binding that is originally cooperative coordination in terms of collaborative instances in cell growth and cell scatter. Within such dimensions there emerges the overall characterization of index factors that specifically characterize the primal transformation step event in oncogenesis. Epidermal growth factor receptor tyrosine kinase inhibitor-resistant tumors together with c-Met inhibitors are likely to be most effective in combination with continued EGFR TKI therapy [4].

Collaborative Attempts

Dual and parallel collaboration is further towards the emergence of integral stimulus/response in a manner that specifically conforms to

the origin of autonomous malignant transformation as dictated by systems of incomplete recognition dynamics of paracrine stimulation in large measure. The expression of HGF and c-Met is significantly increased in the presence of H.pylori infection in gastric dysplasia and carcinoma [5]. It is towards the identification of biologic markers in cancer therapeutics that there is involved also paracrine/autocrine stimulation of mesenchymal and vascular endothelial cell proliferation. Over-expression of c-Met is a common molecular finding in squamous cell carcinoma of the head and neck [6].

Evolutionary Attempts

The evolutionary implications of oncogenesis are permissive in terms arising primarily as system biologic pathways of integral cells. A combined approach that targets neoplastic cells by chemotherapy while inhibiting pathways mediating stromal-tumor interactions may constitute a novel therapeutic strategy to improve prognosis in pancreatic carcinoma [7].

In this sense, oncogenesis is reflected participation of incremental cell proliferation within the pathway formulations for such specific proliferation increments. HGF/MET is a novel substrate for the non-receptor tyrosine kinase FER and modulates ovarian cancer cell invasiveness in a ligand independent manner [8]. It is within the integral cell as reflected especially in phosphorylation/dephosphorylation events that there is defined a susceptibility trait for further paracrine/autocrine stimulation of cascade initiation and maintenance. Serum HGF may prove useful in predicting tumor response and progression-free survival in patients with advanced non-small-cell lung cancer [9].

The whole integral characterization of pathways of conformational identity is central to the system biology of oncogenesis as defined by the predominant agonistic cast for further cell growth and

proliferation. The functional heterogeneity of pancreatic stellate cells with regard to HGF-mediated tumor-stroma interactions indicates that inhibition of the HGF pathway in Pancreatic ductal adenocarcinoma may have different therapeutic effects in different subsets of patients [10]. In terms of metastatic spread, the vascularization of such systems within integral cells is further defined as the nature of oncogenesis as specification of the increasing and integral cell proliferation. MET gene exon 14 alterations and MET gene amplification play a critical role in cancer origin [11].

It is highly significant to view structural and functional coordinates as indices of oncogenic origin and maintenance, as simply delineated by increasing cell proliferation. C-Met/HGF pathway has potential as a prognostic, or predictive biomarker in cervical cancer [12].

Patterns of Re-Constitution

The parameters for incremental system pathway progression are viewed within the biologic character for further change. The HGF/c-MET pathway plays a role in neutrophil recruitment and function and c-MET inhibition co-treatment may improve response to cancer immunotherapy in settings beyond c-Met-dependent tumors [13]. The supporting systems for incremental change are permissive within the framework constitution of such biologic systems in further definition of delineated overall coefficients for cell integrity. It is the declining participation for autonomous proliferative rates of such cells that allows for biologic dimensions of autonomous cell pathway activation and subsequent permissive hyper-response to ligand-receptor interactivity. Simultaneous inhibition of HGF and MET is required to overcome resistance to MET inhibitors in MET-amplified non-small-cell lung cancer cells [14].

The dual and further multiple co-existence of paracrine and autocrine stimulation pathways is chief character to the dimensions for further integral cell proliferation as seen in specific cell-scatter patterns. The further inhibiting and participating overall integral nature of the transformation event is characteristic parameter pattern evolution as systems biology. An important mechanism is stimulation of the c-MET RTK; this facilitates cell survival by boosting DNA damage repair pathways and also by escaping cell cycle arrest, as in BRCA-mutated gastric carcinomas [15].

Paracrine/Autocrine Events

Parametric discovery for paracrine mesenchymal dominance is a chief identifying attribute that is reflected as cell integral systems that permit the evolutionary nature and history of developmental biology. HGF, acting through the c-Met receptor, is the key polarity-inducing morphogen which acts to activate beta1-integrin-dependent adhesion; derived signals can thus influence morphogenesis in epithelial cells by controlling activation and localisation of cell polarity pathways [16]. It is in terms of the specificity of developmental processes that oncogenesis is derivative integral participation in increasing cell proliferation and cell scatter. Targeting both the HGF/c-Met and Hedgehog pathways, simultaneously, may overcome the resistance to the single-inhibitor treatment and lead to more potent antitumor effect in pancreatic cancer [17].

Indeed, the superficial characterization of interactive paracrine/autocrine events permits the potential for maintenance spread of malignant cells and the establishment of multiple focal metastatic deposits as may be well-characterized by systems biology. Potential determination of cell growth dynamics is chief coordination pathway

effect in the dominant phenotype character of incremental integral cell proliferation. HGF induces invasiveness of breast cancer cells via the PI3K/Akt and p38 MAPK signaling pathways to up-regulate the expression of COX2 [18]. In such a series of promotional events, the further dimensions of emergence of a malignant cell clonality is simply a response on the part of mesenchymal cells to autonomous epithelial cell malignancy in terms that re-define the systems of biologic nature. Natural product-derived inhibitors known as “fourth generation inhibitors” constitute over 60% of anticancer drugs [19]. The participation of cell injury within conceptual non-healing of a wound is significant in terms that delineate boundaries of compound nature. The full definition of oncogenic processes is significant in the identification of proliferating cells in terms of specific infiltrating nature to such proliferating malignant cells. The MET proto-oncogene plays a crucial role throughout lung oncogenesis, unbalancing proliferation/apoptosis signaling and influencing the epithelial-mesenchymal transition and the invasive phenotype [20].

Substantiation of the Integral Transformation Event

Necessary substantiation for biologic systems for progression allows the boundary definitions for further conformational participation of the mesenchymal cell elements within the integrity character for further adaptive change in oncogenesis.

It is towards the definition of the integral transformational event that singular dynamics of the single cell clone in malignancy evolves as development of increasing proliferation rates and infiltrative behavior as systems biology events in malignant transformation. RNA in situ hybridisation is a valid platform for testing predictive biomarkers for patient selection [21].

Overall macroscopic entities of malignancy definition are dimensions for cooperative involvement in pathway specification within terms of referential progression of the malignant transformation event. It is significant to re-establish the formulated patterns for cooperative dimensions within a series of promotional reconstitution of developmental characterization. MiRNAs can effectively regulate gene expression and function as gene therapy; their identification for c-Met regulation and study of related mechanisms are of critical importance [22]. The promotion of pathway cascades allows particular definitions of oncogenesis to emerge as dynamics of an initial cell response; autonomous inhibitory biology systems may be viewed as being well-delineated morphologically, and also genetically, in terms of mutability and impaired DNA repair systems. The “compact” conformation of the MET extracellular domain is important and relevant to HGF/Scatter factor binding and signaling [23].

Dimensional coordinative parameters, therefore, are re-constituted within patterns of fixed character nature and as exhibited by the dysfunctional characterization of the mitotic cell cycle. In such terms the evolutionary determination of identifiable definitions for cell growth linked to cell survival pathways includes the defining cluster events as integral survival of apparatus and conformation of the integral cell processes.

Conclusion

The definition of cell integrity is fundamental to a concept of destabilization of such cell in defining the single transformation event in oncogenesis. Such formulation is best identified as parameter patterns of evolutionary nature that permit emergent pathways of

possible partial and aberrant biology systems of conformation and adaptation.

The system patterns in such malignant transformation include the dynamics of DNA repair processes as subsequent events to a cell injury that permeates within the paracrine/autocrine pattern formulation. Such formulation re-defines repeated cycles of oncogenic transformation that promotes the emergence of propensity for further change. The degrees of formulation are well-characterized by dysfunctional response of the individually integral cell in terms of re-constituted identity and performance dynamics.

Further dimensions of re-constitution are best defined within the developmental nature of systems biology, as originally projected in terms of evolutionary dynamics of cell replacement and reappraisal of malignant transformation event constitution.

References

1. Parikh PK, Ghate (2017) "Recent advances in the discovery of small molecule c-Met Kinase inhibitors". *Eur J Med Chem* 17: 223-234.
2. Liang Y, Feng Y, Zong M, Wei X, Lee J, et al. (2017) "Beta-Catenin deficiency in hepatocytes aggravates hepatocarcinogenesis driven by oncogenic beta-catenin and MET". *Hepatology*.
3. Bolt R, Foran B, Murdoch C, Lambert DW, Thomas S, et al. (2018) "HPV-negative, but not HPV-positive, oropharyngeal carcinomas induce fibroblasts to support tumor invasion through micro-environmental release of HGF and IL-6". *Carcinogenesis* 39: 170-179.
4. Wu YL, Soo RA, Locatelli G, Stamberger U, Scaglietti G, et al. (2017) "Does c-Met remain a rational target for therapy in patients with EGFR TKI-resistant non-small cell lung cancer?". *Cancer Treat Rev* 61: 70-81.
5. Xie C, Yang Z, Hu Y, Cao X, Chen J, et al. (2017) "Expression of c-Met and hepatocyte growth factor in various gastric pathologies and its association with *Helicobacter pylori* infection". *Oncol Lett* 14: 6151-6155.
6. Szturz P, Budikova M, Vermorken JB, Horova I, Raymond E et al. (2017) "Prognostic value of c-MET in head and neck cancer: a systematic review and meta-analysis of aggregate data". *Oral Oncol* 74: 68-76.
7. Pothula SP, Xu Z, Goldstein D, Merrett N, Pirola RC, et al. (2017) "Targeting the HGF/c-MET pathway: stromal remodelling in pancreatic cancer". *Oncotarget* 8: 76722-76739.
8. Fan G, Nicholas N (2017) "FER mediated HGF-independent regulation of HGFR/MET activates RAC1-PAK1 pathway to potentiate metastasis in ovarian cancer". *Small GTPases* 3: 1-5.
9. Tsuji T, Sakamori Y, Ozase H, Yagi Y, Ajimizu H, et al. (2017) "Clinical impact of high serum hepatocyte growth factor in advanced non-small cell lung cancer". *Oncotarget* 8: 71805-71816.
10. Tjomsland V, Aasrum M, Christoffersen T, Gladhaug IP (2017) "Functional heterogeneity in tumor-derived human pancreatic stellate cells: differential expression of HGF and implications for mitogenic signaling and migration in pancreatic cancer cells". *Oncotarget* 8: 71672-71684.
11. Mo HN, Liu P (2017) "Targeting MET in cancer therapy" *Chronic Dis Transl Med* 3: 148-153.
12. Boromand N, Hasanzaden M, ShahidSales S, Ferazestanian M, Gharib M, et al. (2017) "Clinical and prognostic value of the C-Met/HGF signaling pathway in cervical cancer". *J Cell Physiol* 233: 4490-4496.
13. Glodde N, Bald T, van den Boom-Konijnenber D, Nakamura K, O'Donnell JS, et al. (2017) "Reactive neutrophil responses dependent on the receptor tyrosine kinase c-MET limit cancer immunotherapy". *Immunity* 47: 789-802.
14. Owusu BY, Thomas S, Venukadasula P, Han Z, Janetka JW, et al. (2017) "Targeting the tumor-promoting microenvironment in MET-amplified NSCLC cells with a novel inhibitor of pro-HGF activation" *Oncotarget* 8: 63014-63025.
15. Mihailidou C, Karamouzis MV, Schizas D, Papavassiliou AG (2017) "Co-targeting c-MET and DNA double strand breaks (DSBs): therapeutic strategies in BRCA-mutated gastric carcinomas". *Biochimie* 142: 135-143.
16. Datta A, Sandilands E, Rostov KE, Bryand DM (2017) "Fibroblast-derived HGF drives acinar lung cancer cell polarisation through integrin-dependent RhoA-ROCK1 inhibition". *Cell Signal* 40: 91-96.
17. Rucki AA, Xiao Q, Muth S, Chen J, Che X, et al. (2017) "Dual inhibition of Hedgehog and c-Met pathways for pancreatic cancer treatment". *Mol Cancer Ther* 16: 2399-2409.
18. Kuang W, Deng Q, Deng C, Li W, Shu S, (2017) "Hepatocyte growth factor induces breast cancer cell invasion via the PI3K/Akt and p38 MAPK signaling pathways to up-regulate the expression of COX2". *Am J Transl Res* 9: 3816-3826.
19. Aliebrahimi S, Montasser Kouhsari S, Ostad SN, Arab SS, Karami L (2017) "Identification of phytochemicals targeting c-Met kinase domain using consensus docking and molecular dynamics simulation studies". *Cell Biochem Biophys*.
20. Pilotto S, Carbognin L, Karachaliou N, Ma PC, Rosell R, et al. (2017) "Tracking MET de-addiction in lung cancer: a road towards the oncogenic target" *Cancer Treat Rev* 60: 1-11.
21. Schmid E, Klotz M, Steiner-Hahn K, Konen T, Frisk AL, et al. (2017) "Detection of MET mRNA in gastric cancer in situ. Comparison with immunohistochemistry and sandwich immunoassays". *Biotech Histochem* 92: 425-435.
22. Liu H, Li SR, Si Q (2017) "Regulation of miRNAs on c-met protein expression in ovarian cancer and its implication". *Eur Rev Med Pharmacol Sci* 21: 3353-3359.
23. DiCara DM, Chirgadze DY, Pope AR, Karatt-Vellatt A, Winter A, et al. (2017) "Characterization and structural determination of a new anti-MET function-blocking antibody with binding epitope distinct from the ligand binding domain". *Sci Rep* 7: 9000.

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