



OPEN ACCESS

EDITED AND REVIEWED BY
Claire Perks,
University of Bristol, United Kingdom

*CORRESPONDENCE

Rick Francis Thorne
✉ rickfthorne@gmail.com
Yang Mi
✉ miyang198@126.com

SPECIALTY SECTION

This article was submitted to
Cancer Endocrinology,
a section of the journal
Frontiers in Endocrinology

RECEIVED 18 December 2022

ACCEPTED 27 December 2022

PUBLISHED 12 January 2023

CITATION

Bukhari I, Zhang Y, Thorne RF and Mi Y
(2023) Editorial: Complexity of tumor
microenvironment: A major culprit in
cancer development, volume II
Front. Endocrinol. 13:1126778.
doi: 10.3389/fendo.2022.1126778

COPYRIGHT

© 2023 Bukhari, Zhang, Thorne and Mi.
This is an open-access article
distributed under the terms of the
[Creative Commons Attribution License
\(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution or
reproduction in other forums is
permitted, provided the original
author(s) and the copyright owner(s)
are credited and that the original
publication in this journal is cited, in
accordance with accepted academic
practice. No use, distribution or
reproduction is permitted which does
not comply with these terms.

Editorial: Complexity of tumor microenvironment: A major culprit in cancer development, volume II

Ihtisham Bukhari^{1,2}, Yuanwei Zhang³, Rick Francis Thorne^{2,4*}
and Yang Mi^{1*}

¹Henan Key Laboratory of Helicobacter pylori, Microbiota and Gastrointestinal Cancers, Marshall Medical Research Center, Fifth Affiliated Hospital of Zhengzhou University, Zhengzhou, China,

²Translational Research Institute, Henan Provincial and Zhengzhou City Key Laboratory of Non-coding RNA and Cancer Metabolism, Henan International Joint Laboratory of Non-coding RNA and Metabolism in Cancer, Henan Provincial People's Hospital, Academy of Medical Sciences, Zhengzhou University, Zhengzhou, Henan, China, ³School of Life Sciences, University of Science and Technology of China, Hefei, Anhui, China, ⁴School of Environmental and Life Sciences, University of Newcastle, Callaghan, NSW, Australia

KEYWORDS

tumor microenvironment, immunotherapy, cancer management, survival and prognosis, cancer biomarkers

Editorial on the Research Topic

Complexity of tumor microenvironment: A major culprit in cancer development, volume II

The tumor microenvironment (TME) consists of tumor cells along with various immune, stromal, and endothelial cells, along with extracellular matrix components (1–3). Notably, complex interactions and material exchanges between the tumor microenvironment and its surroundings support tumor growth and progression (4, 5). Thus, a proper understanding of the TME requires a thorough study of its components and interactions (5, 6) with such information being essential for defining the underlying mechanisms of cancer development and progressing anti-cancer therapies for routine clinical use (7–10).

Various factors have been associated with cancer development and progression including recent research highlights concerning the metabolic (11–13) and other molecular factors (14–16). Notably, it has been well-established that metabolism and infiltrating cells in the TME represent attractive prognostic markers across a range of cancer types (17, 18). Additionally, recent work has also better delineated the role of lncRNAs and miRNAs, particularly their essential contribution in the TME as mediators of cancer progression and drug resistance (19–22). Indeed, such information has helped popularize the notion of using RNA-based targeting in future cancer management strategies (23–25).

Other recent advances in cancer therapeutic approaches have shifted the focus back toward the immunotherapy (26, 27). Surprisingly, the routine clinical introduction of

cell-based immunotherapy has completely resketched the treatment landscape of the cancer management (28–30). Genetically modified immune cells such as CAR-T cells have produced incredible responses in some solid tumors (31–33). These immune cells have enhanced functional ability and protection from negative signals from immune checkpoints and the hostile tumor microenvironment (34). However, more therapeutic precision is still required to target tumors accurately. Moreover, multiplexed precision genome editing with pros and cons has become a highly flexible and modular toolkit for specifically addressing the challenges of precision interventions (35–37). Towards better functionality, genome editing tools like CRISPR/Cas9 and TALENs have made it possible to create additional genetic modifications in immune cells (36, 38, 39). Such methods have also been modified for better efficiency and safety in the therapeutic applications (40, 41) although off-target and other hidden effects of genome editing are major concerns for their widespread routine use in clinics. Thus, more comprehensive studies related to the genetic modifications of immune and cancer cells are required to gain sufficient confidence for application as standard cancer therapy.

For the current research topic, we aimed to collect research studies on the advancements in the tumor microenvironment and its roles in cancer regulation and clinical applications. After an extensive selection and peer review, only four articles were selected exploring new dimensions in this research field.

Firstly, [Catellani et al.](#) reviewed the role of lncRNAs and miRNAs in regulating growth hormones and insulin-like growth factor, both of which are crucial for biological processes including cellular proliferation, differentiation, and angiogenesis of various cancers including pituitary adenomas, osteosarcomas, and colorectal cancer. [Wu et al.](#) studied the clinical and biological importance of glucocorticoid receptors (GR) in adrenocortical carcinoma (ACC) patients. Their extensive analyses showed that GR positively correlates with higher cortisol levels, immune function, and poorer survival in ACC patients. This work advances GR as a potential ACC biomarker for use in prognostic and therapeutic settings although further work is required to obtain enough confidence before being used clinically. [Ruan et al.](#), analyzed a cohort of 5221 mixed cancer patients to define the relationship between inflammation and insulin resistance markers. Among the studied markers, the CRP-TyG index (CTI) was revealed as an indicator of poor prognosis that could be considered for treatment stratifications in multiple cancer types. Lastly, it is well documented that the E3-ubiquitin ligase TRIM21 (Tripartite Motif Containing-21) acts in dual capacities as

either a tumor suppressor or promotor, altering metabolic and inflammatory pathways in different cancers. To shed further light on TRIM21, [Chen et al.](#) reviewed the participation of TRIM21 in cancer development, cancer-associated immune responses and potential roles in cancer immunity and therapeutics. Considering that TRIM21 appears to display dual roles in cancer development, some caution is required if this enzyme is to be considered as a therapeutic target.

Conclusion and prospects

Although thousands of potential cancer biomarkers have been suggested, very few are currently used confidently in clinics for diagnostic, prognostic, and therapeutic applications. The role of the TME in cancer progression is being increasingly appreciated and therefore further focus is required to better understand its unique cellular and extracellular composition and function. In turn, more wholistic knowledge of the TME is expected to help translate basic research into more effective outcomes, rewriting clinical guidelines to include new biomarkers, therapeutic targets and treatment approaches.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

References

- Talaat IM, Kim B. A brief glimpse of a tangled web in a small world: Tumor microenvironment. *Front Med (Lausanne)* (2022) 9:1002715. doi: 10.3389/fmed.2022.1002715
- Galmiche A, Rak J, Roumenina LT, Saidak Z. Coagulum and the tumor microenvironment: an actionable interplay. *Trends Cancer* (2022) 8:369–83. doi: 10.1016/j.trecan.2021.12.008
- Mao X, Xu J, Wang W, Liang C, Hua J, Liu J, et al. Crosstalk between cancer-associated fibroblasts and immune cells in the tumor microenvironment: new findings and future perspectives. *Mol Cancer* (2021) 20:131. doi: 10.1186/s12943-021-01428-1
- Dubey S, Ghosh S, Goswami D, Ghatak D, De R. Immunometabolic attributes and mitochondria-associated signaling of tumor-associated macrophages in tumor microenvironment modulate cancer progression. *Biochem Pharmacol* (2022) 208:115369. doi: 10.1016/j.bcp.2022.115369
- Zhao C, Liu S, Gao F, Zou Y, Ren Z, Yu Z. The role of tumor microenvironment reprogramming in primary liver cancer chemotherapy resistance. *Front Oncol* (2022) 12:1008902. doi: 10.3389/fonc.2022.1008902
- Bukhari I, Zhang Y, Thorne RF, Mi Y. Editorial: Complexity of tumor microenvironment: A major culprit in cancer development. *Front Endocrinol (Lausanne)* (2022) 13:1059885. doi: 10.3389/fendo.2022.1059885
- Xiao J, Liu Z, Wang J, Zhang S, Zhang Y. Identification of cuprotosis-mediated subtypes, the development of a prognosis model, and influence immune microenvironment in hepatocellular carcinoma. *Front Oncol* (2022) 12:941211. doi: 10.3389/fonc.2022.941211
- Zhuang Z, Gao C. Development of a clinical prognostic model for metabolism-related genes in squamous lung cancer and correlation analysis of immune microenvironment. *BioMed Res Int* (2022) 2022:6962056. doi: 10.1155/2022/6962056
- Zhang Y, Kong X, Xin S, Bi L, Sun X. Discovery of lipid metabolism-related genes for predicting tumor immune microenvironment status and prognosis in prostate cancer. *J Oncol* (2022) 2022:8227806. doi: 10.1155/2022/8227806
- Mucileanu A, Chira R, Mircea PA. PD-1/PD-L1 expression in pancreatic cancer and its implication in novel therapies. *Med Pharm Rep* (2021) 94:402–10. doi: 10.15386/MPR-2116
- Zhang X, Zhao L, Zhang H, Zhang Y, Ju H, Wang X, et al. The immunosuppressive microenvironment and immunotherapy in human glioblastoma. *Front Immunol* (2022) 13:1003651. doi: 10.3389/fimmu.2022.1003651
- Kang S, Kang BH. Structure, function, and inhibitors of the mitochondrial chaperone TRAP1. *J Med Chem* (2022) 65(24):16155–16172. doi: 10.1021/acs.jmedchem.2c01633
- Heuser C, Renner K, Kreutz M, Gattinoni L. Targeting lactate metabolism for cancer immunotherapy - a matter of precision. *Semin Cancer Biol* (2022) 88:32–45. doi: 10.1016/j.semcancer.2022.12.001
- Akhmetova DA, Kozlov VV, Gulyaeva LF. New insight into the role of AhR in lung carcinogenesis. *Biochem (Mosc)* (2022) 87:1219–25. doi: 10.1134/S0006297922110013
- An C, Pipia I, Ruiz AS, Arguelles I, An M, Wase S, et al. The molecular link between obesity and genomic instability in cancer development. *Cancer Lett* (2022) 555:216035. doi: 10.1016/j.canlet.2022.216035
- Saman H, Raza A, Patil K, Uddin S, Crnogorac-Jurcevic T. Non-invasive biomarkers for early lung cancer detection. *Cancers (Basel)* (2022) 14:5782. doi: 10.3390/cancers14235782
- Huang De, Alexander PB, Li QJ, Wang XF. GABAergic signaling beyond synapses: an emerging target for cancer therapy. *Trends Cell Biol* (2022) S0962-8924(22):00195-7. doi: 10.1016/j.tcb.2022.08.004
- Kocher F, Puccini A, Untergasser G, Martowicz A, Zimmer K, Pircher A, et al. Multi-omic characterization of pancreatic ductal adenocarcinoma relates CXCR4 mRNA expression levels to potential clinical targets. *Clin Cancer Res* (2022) 28(22):4957–4967. doi: 10.1158/1078-0432.CCR-22-0275
- Bukhari I, Khan MR, Hussain MA, Thorne RF, Yu Y, Zhang B, et al. PINTology: A short history of the lncRNA LINC-PINT in different diseases. *Wiley Interdiscip Rev RNA* (2022) 13(4):e1705. doi: 10.1002/wrna.1705
- Tang Y, Feng H, Zhang L, Qu C, Li J, Deng X, et al. A novel prognostic model for cutaneous melanoma based on an immune-related gene signature and clinical variables. *Sci Rep* (2022) 12:20374. doi: 10.1038/s41598-022-23475-4
- Rajtmajerova M, Trailin A, Liska V, Hemminki K, Ambrozkiwicz F. Long non-coding RNA and microRNA interplay in colorectal cancer and their effect on the tumor microenvironment. *Cancers (Basel)* (2022) 14:5450. doi: 10.3390/cancers14215450
- Chen L, Deng J. Role of non-coding RNA in immune microenvironment and anticancer therapy of gastric cancer. *J Mol Med (Berl)* (2022) 100:1703–19. doi: 10.1007/s00109-022-02264-6
- Alshahrani SH, Ibrahim YS, Jalil AT, Altoum AA, Achmad H, Zabibah RS, et al. Metabolic reprogramming by miRNAs in the tumor microenvironment: Focused on immunometabolism. *Front Oncol* (2022) 12:1042196. doi: 10.3389/fonc.2022.1042196
- Chen J, Song YW, Liang GZ, Zhang ZJ, Wen XF, Li RB, et al. A novel m7G-related gene signature predicts the prognosis of colon cancer. *Cancers (Basel)* (2022) 14:5527. doi: 10.3390/cancers14225527
- Sun B, Sherrin M, Roy R. Unscheduled epigenetic modifications cause genome instability and sterility through aberrant r-loops following starvation. *Nucleic Acids Res* (2022) 50:11093. doi: 10.1093/nar/gkac1155
- Yang Y, Huang J, Liu M, Qiu Y, Chen Q, Zhao T, et al. Emerging sonodynamic therapy-based nanomedicines for cancer immunotherapy. *Adv Sci (Weinh)* (2022) 27:e2204365. doi: 10.1002/adv.202204365
- Fan X, Wang K, Lu Q, Lu Y, Sun J. Cell-based drug delivery systems participate in the cancer immunity cycle for improved cancer immunotherapy. *Small* (2022):e2205166. doi: 10.1002/smll.202205166
- Liu L, Qu Y, Cheng L, Yoon CW, He P, Monther A, et al. Engineering chimeric antigen receptor T cells for solid tumour therapy. *Clin Transl Med* (2022) 12:e1141. doi: 10.1002/ctm2.1141
- Smole A. Cancer immunotherapy with CAR T cells: well-trodden paths and journey along lesser-known routes. *Radiol Oncol* (2022) 56:409–19. doi: 10.2478/raon-2022-0049
- Gajon JA, Juarez-Flores A, De Leon Rodriguez SG, Aguilar Flores C, Mantilla A, Fuentes-Panana EM, et al. Immunotherapy options for acral melanoma, a fast-growing but neglected malignancy. *Arch Med Res* (2022) 53:794–806. doi: 10.1016/j.arcmed.2022.11.008
- Muhammad N, Wang R, Li W, Zhang Z, Chang Y, Hu Y, et al. A novel TanCAR targeting IL13Ralpha2 and EphA2 for enhanced glioblastoma therapy. *Mol Ther Oncolytics* (2022) 24:729–41. doi: 10.1016/j.omto.2022.02.012
- Rao P, Furst L, Meyran D, Mayoh C, Neeson PJ, Terry R, et al. Advances in CAR T cell immunotherapy for paediatric brain tumours. *Front Oncol* (2022) 12:873722. doi: 10.3389/fonc.2022.873722
- Chen Q, Lu L, Ma W. Efficacy, safety, and challenges of CAR T-cells in the treatment of solid tumors. *Cancers (Basel)* (2022) 14:5983. doi: 10.3390/cancers14235983
- Qin C, Wang J, Du Y, Xu T. Immunosuppressive environment in response to androgen deprivation treatment in prostate cancer. *Front Endocrinol (Lausanne)* (2022) 13:1055826. doi: 10.3389/fendo.2022.1055826
- Yang X, Garner LI, Zvyagin IV, Paley MA, Komech EA, Jude KM, et al. Autoimmunity-associated T cell receptors recognize HLA-B*27-bound peptides. *Nature*. (2022) 612(7941):771–777. doi: 10.1038/s41586-022-05501-7
- Biederstadt A, Manzar GS, Daher M. Multiplexed engineering and precision gene editing in cellular immunotherapy. *Front Immunol* (2022) 13:1063303. doi: 10.3389/fimmu.2022.1063303
- Wu X, Matosevic S. Gene-edited and CAR-NK cells: Opportunities and challenges with engineering of NK cells for immunotherapy. *Mol Ther Oncolytics* (2022) 27:224–38. doi: 10.1016/j.omto.2022.10.011
- Wei Y, Zhao Z, Ma X. Description of CRISPR-Cas9 development and its prospects in human papillomavirus-driven cancer treatment. *Front Immunol* (2022) 13:1037124. doi: 10.3389/fimmu.2022.1037124
- Lin Y, Wilk U, Pohmerer J, Horterer E, Hohn M, Luo X, et al. Folate receptor-mediated delivery of Cas9 RNP for enhanced immune checkpoint disruption in cancer cells. *Small* (2022) 18:e2205318. doi: 10.1002/smll.202205318
- Mamun MMA, Bukhari I. Fast-track and integration-free method of genome editing by CRISPR/Cas9 in murine pluripotent stem cells. *Front Cell Dev Biol* (2022) 10:819906. doi: 10.3389/fcell.2022.819906
- Bhat AA, Nisar S, Mukherjee S, Saha N, Yarravarapu N, Lone SN, et al. Integration of CRISPR/Cas9 with artificial intelligence for improved cancer therapeutics. *J Transl Med* (2022) 20:534. doi: 10.1186/s12967-022-03765-1