Speaker information

General Information

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Speaker information

Recent Publications

1. G. Anuraga, J. Lang, D. T. M. Xuan, H. D. K. Ta, J. Z. Jiang, Z. Sun, S. Dey, S. Kumar, A. Singh, G. Kajla, W. J. Wang and C. Y. Wang, "Integrated bioinformatics approaches to investigate alterations in transcriptomic profiles of monkeypox infected human cell line model," J Infect Public Health, vol. 17, no. 1, pp. 60-69, 2024.
2. C. Y. Li, G. Anuraga, C. P. Chang, T. Y. Weng, H. P. Hsu, H. D. K. Ta, P. F. Su, P. H. Chiu, S. J. Yang, F. W. Chen, P. H. Ye, C. Y. Wang and M. D. Lai, "Repurposing nitric oxide donating drugs in cancer therapy through immune modulation," J Exp Clin Cancer Res, vol. 42, no. 1, pp. 22, 2023.
3. C. Y. Wang, D. T. M. Xuan, P. H. Ye, C. Y. Li, G. Anuraga, H. D. K. Ta, M. D. Lai and H. P. Hsu, "Synergistic suppressive effects on triple-negative breast cancer by the combination of JTC-801 and sodium oxamate," Am J Cancer Res, vol. 13, no. 10, pp. 4661-4677, 2023.
4. D. T. M. Xuan, I. J. Yeh, C. C. Wu, C. Y. Su, H. L. Liu, C. C. Chiao, S. C. Ku, J. Z. Jiang, Z. Sun, H. D. K. Ta, G. Anuraga, C. Y. Wang and M. C. Yen, "Comparison of Transcriptomic Signatures between Monkeypox-Infected Monkey and Human Cell Lines," J Immunol Res, vol. 2022, pp. 3883822, 2022.
5. O. M. Gbenedio, C. Bonnans, D. Grun, C. Y. Wang, A. J. Hatch, M. R. Mahoney, D. Barras, M. Matli, Y. Miao, K. C. Garcia, S. Tejpar, M. Delorenzi, A. P. Venook, A. B. Nixon, R. S. Warren, J. P. Roose and P. Depeille, "RasGRP1 is a potential biomarker to stratify anti-EGFR therapy response in colorectal cancer," JCI Insight, vol. 5, 2019.
6. C. Hagerling, H. Gonzalez, K. Salari, C. Y. Wang, C. Lin, I. Robles, M. van Gogh, A. Dejmek, K. Jirström and Z. Werb, "Immune effector monocyte-neutrophil cooperation induced by the primary tumor prevents metastatic progression of breast cancer," Proc Natl Acad Sci U S A, vol. 116, no. 43, pp. 21704-21714, 2019.
7. P. Shahi, C. Y. Wang, D. A. Lawson, E. M. Slorach, A. Lu, Y. Yu, M. D. Lai, H. Gonzalez Velozo and Z. Werb, "ZNF503/Zpo2 drives aggressive breast cancer progression by down-regulation of GATA3 expression," Proc Natl Acad Sci U S A, vol. 114, no. 12, pp. 3169-3174, 2017.
8. P. Shahi, C. Y. Wang, J. Chou, C. Hagerling, H. Gonzalez Velozo, A. Ruderisch, Y. Yu, M. D. Lai and Z. Werb, "GATA3 targets semaphorin 3B in mammary epithelial cells to suppress breast cancer progression and metastasis," Oncogene, vol. 36, no. 40, pp. 5567-5575, 2017.
9. P. Depeille, L. M. Henricks, R. A. van de Ven, E. Lemmens, C. Y. Wang, M. Matli, Z. Werb, K. M. Haigis, D. Donner, R. Warren and J. P. Roose, "RasGRP1 opposes proliferative EGFR-SOS1-Ras signals and restricts intestinal epithelial cell growth," Nat Cell Biol, vol. 17, no. 6, pp. 804-815, 2015.
10. D. A. Lawson, N. R. Bhakta, K. Kessenbrock, K. D. Prummel, Y. Yu, K. Takai, A. Zhou, H. Eyob, S. Balakrishnan, C. Y. Wang, P. Yaswen, A. Goga and Z. Werb, "Single-cell analysis reveals a stem-cell program in human metastatic breast cancer cells," Nature, vol. 526, no. 7571, pp. 131-135, 2015.

Speaker information

Speech Topic and Abstract

Title:
The application of multi-omics in medical research

Abstract:
Recent advances across diverse branches of medical research, especially in oncology and infectious disease control, underscore the transformative potential of multi-omics and single-cell technologies. Despite considerable progress in cancer therapeutics, mortality rates associated with various cancers continue to present significant clinical challenges, emphasizing the urgent need for more personalized and efficacious therapeutic strategies. Innovations such as immune checkpoint-related therapies have demonstrated substantial promise by effectively modulating immune system activity to combat malignancies. Concurrently, the application of high-throughput sequencing has illuminated the profound heterogeneity of tumors, reinforcing the imperative for novel target identification and the adoption of precision medicine approaches. Single-cell RNA sequencing (scRNA-seq) and associated technologies have become indispensable in exploring cellular composition and intra-tumor heterogeneity within the tumor microenvironment (TME). These methodologies afford a detailed view of cellular dynamics and interactions, which are pivotal for advancing the precision of cancer diagnostics and the development of targeted therapies. in the context of cancer research, the repurposing of nitric oxide-donating drugs, traditionally utilized for cardiovascular diseases, has been explored for cancer therapy through immune modulation. Experiments in immunocompetent mouse models have demonstrated that these drugs significantly inhibit tumor growth by modulating immune responses, notably enhancing the activity of CD8+ T cells and altering macrophage profiles within the TME. Moreover, in the context of infectious diseases, the re-emergence of monkeypox has catalyzed the deployment of these high-throughput technologies to investigate the viral impact at the cellular level. Detailed analyses using Multi-omics have revealed critical insights into immune responses and cellular interactions within infected cell lines, elucidating significant pathways influenced by the virus, including Toll-like receptor and tumor necrosis factor-α-related signaling pathways. This compilation of research underscores the extensive applicability of multi-omics and single-cell technologies in advancing our comprehension of complex biological systems and improving therapeutic strategies. These methodologies not only deepen our understanding of disease mechanisms but also pave the way for the development of personalized treatment approaches, thereby significantly contributing to the advancement of precision medicine and more effective treatment modalities.

Keywords: Multi-Omics, Bioinformatics, Tumor Microenvironment, Precision Medicine, Infectious Disease.