



MOLECULAR DIAGNOSTICS

Genetics of Disease Susceptibility



Principal Investigator

Professor Nelson Tang



Team Members

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Research Progress Summary



Research Directions

1. Genetics of complex traits: to identify prevalent genetic variants causing common diseases in Han Chinese;
2. Statistical genetics and computational statistical analysis of big genetic and biological datasets;
3. Analysis of variation of the transcriptome using the latest technology of next-generation sequencing.



Research into Genetics of Disease Susceptibility (GDS)

The mission of the GDS laboratory is to identify disease predisposition genes for common diseases, also known as complex traits. The research group is involved in the development of various analysis methods and wet laboratory validation of the results generated from such analysis. The team also participates in international consortiums in studies of healthy ageing (including bone

and other phenotypes), breast cancer, and genetic susceptibility to adolescent idiopathic scoliosis and tuberculosis. With the advance in sequencing and other technology, the team acquires biological data in an unprecedented volume nowadays. The analysis and statistic method become limiting factors in handling such a huge volume of data.



Research and Scholarship

Academic Editorship

| Member's Name | Details | |
|---------------|------------------------|-----------------------------------|
| | Role | Journal |
| Nelson Tang | Editorial Board Member | Frontiers in Genetic Disorders |
| | | Frontiers in Pediatrics |
| | | Journal of Pediatric Biochemistry |
| | | Genes |

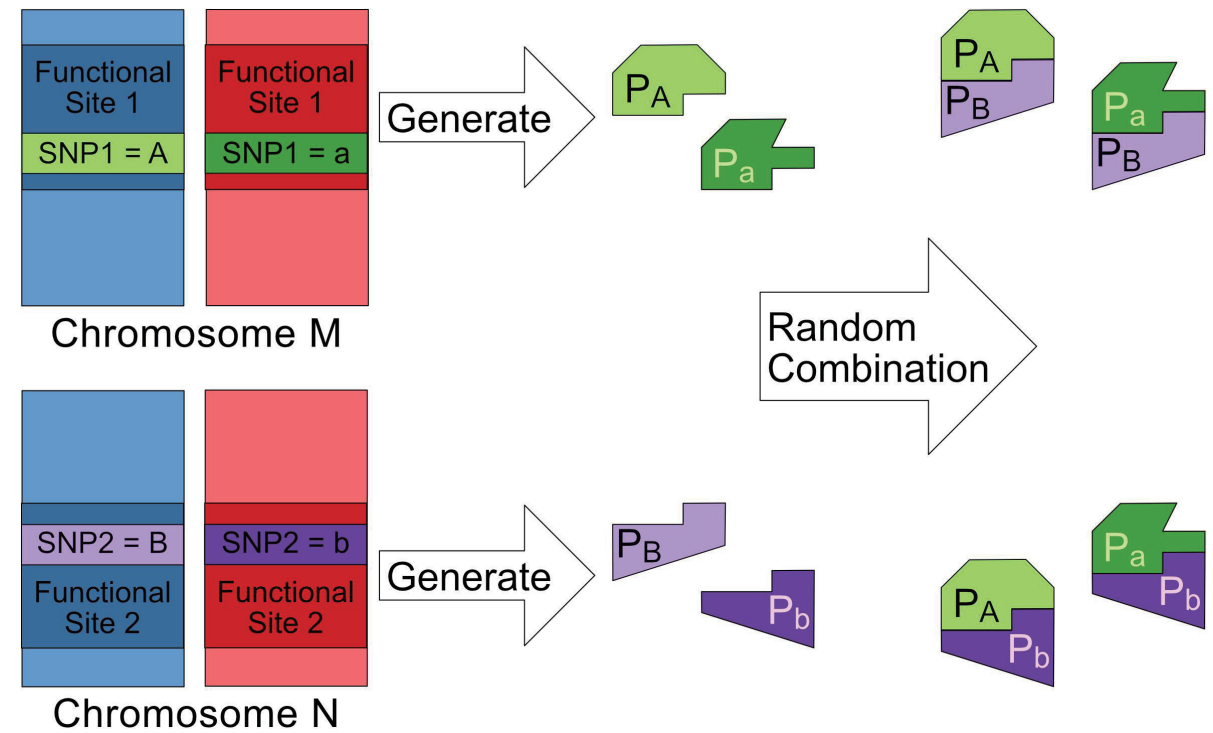
Reviewer of Journal / Conference

| Member's Name | Details | |
|---------------|----------|--|
| | Role | Journal / Conference |
| Nelson Tang | Reviewer | Hong Kong Medical Journal |
| | | Metabolic Brain Disease |
| | | Frontiers |
| | | Scientific Reports |
| | | Journal of Genetics and Genomics |
| | | Nephrology |
| | | Journal of Leukocyte Biology |
| | | Genetic Epidemiology |
| | | The 51 st Union World Conference on Lung Health |
| | | Journal of Biomolecular Structure & Dynamics |

Grants and Consultancy

| Name | Project Title | Funding Source | Start Date (dd/mm/yyyy) | End Date (dd/mm/yyyy) | Amount (HK\$) |
|-------------|--|---|-------------------------|-----------------------|---------------|
| Nelson Tang | Investigating the Key Factors Regulating Healthy Ageing in Chinese Longevity Family Cohort | Ministry of Science and Technology of China | 01/01/2020 | 31/12/2022 | RMB 876,000 |

| Name | Project Title | Funding Source | Start Date (dd/mm/yyyy) | End Date (dd/mm/yyyy) | Amount (HK\$) |
|-------------|---|---|-------------------------|-----------------------|---------------|
| Nelson Tang | Establishment Hong Kong Branch of CAS Center for Excellence in Animal Evolution and Genetics | The Chinese University of Hong Kong – Vice-Chancellor’s One-off Discretionary Fund | 01/06/2020 | 31/05/2023 | 12,000,000 |
| | Pilot Study on the Changes of Transcriptome for Neuro-navigated Repetitive Transcranial Magnetic Stimulation (rTMS) in the Management of Depression in Major Neurocognitive Disorders | The Chinese University of Hong Kong Research Committee – Direct Grants | 29/06/2020 | 28/06/2021 | 40,400 |
| | Expression and Functional Characterization of LBX1 in Adolescent Idiopathic Scoliosis | The National Natural Science Foundation of China – Research Grant Council Joint Research Scheme | 01/01/2017 | 31/12/2020 | 1,045,271 |
| | Prediction of Clinical Outcomes by Determining the Kinetics of Serum Proadrenomedullin, Procalcitonin, and C-Reactive Protein in Adult Patients with Bloodstream Infections | The Chinese University of Hong Kong Research Committee – Direct Grants | 30/06/2019 | 29/06/2020 | 149,775 |



Long term research in the analysis of gene-gene interaction by Professor Tang and his team confirmed the effect of such biomolecular interaction hypothesis.

Source: <https://www.frontiersin.org/articles/10.3389/fgene.2020.01003/full>

Publications

A. Journal Papers

- Lee KY, Leung KS, Ma SL, So HC, Huang D, Tang NLS, Wong MH. Genome-wide search for SNP interactions in GWAS data: Algorithm, feasibility, replication using schizophrenia datasets. *Frontiers in Genetics*. 2020;11. doi:10.3389/fgene.2020.01003.
- Ma SL, Tang NLS, Lam LCW. Promoter methylation and gene expression of Pin1 is associated to the risk on Alzheimer’s disease in southern Chinese. *medRxiv*. Published online August 25, 2020:2020.08.23.20172403. doi:10.1101/2020.08.23.20172403. (In press)
- Ji L, Tang NLS, Xu Z, Xu J. Genes regulate blood pressure, but “environments” cause hypertension. *Frontiers in Genetics*. 2020;11. doi:10.3389/fgene.2020.580443. (Editorial)
- Yeo W, Lau TKH, Kwok CCH, Lai KT, Chan VTC, Li L, Chan V, Wong A, Soo WMT, Yeung EWM, Wong KH, Tang NLS, Suen JJS, Mo FKF. NEPA efficacy and tolerability during (neo)adjuvant breast cancer chemotherapy with cyclophosphamide and doxorubicin. *BMJ Supportive and Palliative Care*. Published online 2020. doi:10.1136/bmjspcare-2019-002037. (Epub ahead of print)
- Yeo W, Lau TK, Li L, Lai T, Pang E, Cheung M, Chan VT, Wong A, Soo WM, Yeung VT, Tse T, Lam DC, Yeung EW, Ng KP, Tang NL, Tong M, Suen JJ, Mo FK. A randomized study of olanzapine-containing versus standard antiemetic regimens for the prevention of chemotherapy-induced nausea and vomiting in Chinese breast cancer patients. *Breast*. Published online 2020. doi:10.1016/j.breast.2020.01.005.
- Tang NLS, Hui J, Huang D, Tang MF, Wang X, Wu J, Chan IHS, Leung TF. Reference intervals of spot urine copper excretion in preschool children and potential application in pre-symptomatic screening of Wilson disease. *Pathology*. 2020;52(4):439-446. doi:10.1016/j.pathol.2020.02.003.
- Ji L, Wu D, Xie H, Yao B, Chen Y, Irwin DM, Huang D, Xu J, Tang NLS, Zhang Y. Ambient temperature is a strong selective factor influencing human development and immunity. *Genomics, Proteomics and Bioinformatics*. Published online 2020. doi:10.1016/j.gpb.2019.11.009. (In press)

| | Disease Associated Complex | | Disease Associated Complex |
|-----|----------------------------|-----|----------------------------|
| (1) | $P_A P_B$ (Dominant) | (5) | $P_A P_B$ (Recessive) |
| (2) | $P_A P_b$ (Dominant) | (6) | $P_A P_b$ (Recessive) |
| (3) | $P_a P_B$ (Dominant) | (7) | $P_a P_B$ (Recessive) |
| (4) | $P_a P_b$ (Dominant) | (8) | $P_a P_b$ (Recessive) |

As a consequence, the search space of possible interaction pattern is now reduced from hundreds to these 8 biologically plausible patterns. This reduction made the search for gene-gene interaction became a feasible task.

Source: <https://www.frontiersin.org/articles/10.3389/fgene.2020.01003/full>