Wei Dai

Current Position: Research Assistant Professor, Honorary Assistant Professor,

Department of Clinical Oncology, The University of Hong Kong

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Research Interest

My research interest mainly lies in two areas 1) application and development of bioinformatics tools for integration of genomics and epigenomics data with clinical data to identify biomarkers and therapeutics targets in cancers for precision medicine, 2) further understanding the genetic basis and molecular mechanisms for metastasis and drug resistance using next-generation sequencing approaches. Recently, more and more studies have been focused on immunotherapy in various cancers, so I am also interested in deciphering the cancer immunogenomics, particularly for the virus-associated cancers, such as nasopharyngeal carcinoma.

Education

2008-2011 PhD. Cancer Bioinformatics, Imperial College London, UK

2003-2004 MSc. Bioinformatics, Manchester University, UK

<u>1997-2002</u> Bachelor Degree of Medicine, First Class Equivalent, School of Medical Informatics, China Medical University, China

Awards

 British Association of Cancer Research (BACR) Gordon Hamilton-Fairley Young Investigator Award in 2011 (http://conference.ncri.org.uk/past-conferences/2011-awards/)

Work Experience

2016 until now Research Assistant Professor, Honorary Assistant Professor, Department of Clinical Oncology, the University of Hong Kong

- Use of whole-exome sequencing approach to identify the somatic mutations associated with metastasis in ESCC
- Use of next-generation sequencing approach to understand the genetic basis and molecular changes in NPC

2013-2016 Post-doctoral Fellow, Department of Clinical Oncology, the University of Hong Kong

- Investigation of genome-wide methylation and genomic changes in both NPC and ESCC to identify novel biomarkers for diagnosis and prognosis, as well as the therapeutic targets
- Use of whole-exome sequencing approach to understand the genetic basis and molecular changes in NPC

2011 - 2013 Research Associate, Epigenetics Section, Department of Surgery and Cancer, Imperial College London

 Epigenetic regulation of the Wnt signalling pathways and relevant biological mechanisms contributing to tumour relapse and chemosensitivity in ovarian cancer

2008 - 2011 Research Assistant, Epigenetics Section Department of Oncology, Faculty of Medicine, Imperial College London

• Identification of DNA methylation biomarker associated with cancer relapse and drug resistance in ovarian cancer, and microarray data management and analysis

2004 Work placement, AstraZeneca, Alderley Park, UK

 Development of a novel tool for pharmacokinetic data integration in new drug development using Visual Basic Application in Microsoft Excel

Teaching and Mentoring Experience

- Problem-based learning for MBBS II Cardiovascular System Block, 2016
- Problem-based learning for MBBS II Head and Neck and Nervous System, 2018
- Master of Philosophy (MPhil): Chi Shan Candy Lam, 09/2017-09/2019; Larry Chow, 09/2018-09/2020

Guest Lecture

- Epigenetics applied to drug resistance in ovarian cancer. Imperial College London.
 2012
- Microarray data clustering and classification. Imperial College London. 2012

Invited Talks

- NPC Gordon Research Conference (2018, Hong Kong), Genetic Susceptibility in NPC.
- 17th International Symposium on EBV and Associated Diseases (2016, Switzerland). Whole-Exome Sequencing Identifies Genetic Susceptibility Locus Associated with Familial Nasopharyngeal Carcinoma.
- NPC Gordon Research Conference (2016, Hong Kong). Methylation Biomarkers in NPC.
- Advanced Study Institute (ASI) in Hong Kong for nasopharyngeal carcinoma (2014, Hong Kong). Methylome Study in Nasopharyngeal Carcinoma

Conference

- <u>Dai W.</u>, Ko J.M.Y., Ng H.Y., Zheng H. and Lung M.L., Elucidation of Genetic Susceptibility in Nasopharyngeal Carcinoma by Next Generation Sequencing., 109th American Association for Cancer Research. Chicago, Illinois, USA, April 14-18, 2018.
- Deng M., Cheung A.K.L., <u>Dai W</u>. and Lung M.L., Functional and molecular analysis of the loss-of-function somatic mutations in two NF-κB pathway inhibitors: NFKBIA and CYLD in nasopharyngeal carcinoma., Gordon Research Conference on Nasopharyngeal Carcinoma. Hong Kong, June 24-29, 2018.
- Leong M.L., Cheung A.K.L., <u>Dai W.</u>, Tsao G.S.W. and Lung M.L., EBV-associated Histone Modifications in the Regulation of DNA Damage Repair Members Resulting in Cisplatin Resistance in Nasopharyngeal Carcinoma., Gordon Research Conference on Nasopharyngeal Carcinoma. Hong Kong, June 24-29, 2018.
- Guo C., Ko J.M.Y., <u>Dai W.</u>, Law S.Y.K., Lo A. and Lung M.L., Genomic characterization of mutation hotspots related to chemotherapy responses in esophageal squamous cell carcinoma with archived formalin-fixed paraffin-embedded tissues., 109th American Association for Cancer Research. Chicago, Illinois, USA, April 14-18, 2018.
- Ko J.M.Y., Tsang H.K., <u>Dai W.</u>, CHOI S.S.A., LEONG M.L., Ngan K.C.R., Kwong D.L.W., Cheng A., Lee W.M.A., Ng W.T., Tung S., Lee V.H.F., Lam K.O., Chan K.C. and Lung M.L., Blood telomere length associates with NPC risk and survival., Gordon Research Conference on Nasopharyngeal Carcinoma. Hong Kong, June 24-29, 2018.
- Lung M.L., <u>Dai W.</u>, ZHENG H., Ko J.M.Y., Sham P.C., Yang W., Cherny S.S., Ngan R.K.C., Kwong D.L.W., Ng W.T., Chiang A.K.S. and Lee W.M.A., Elucidating the Genetic Basis for Early-age Onset Nasopharyngeal Carcinoma in Hong Kong, Health Research Symposium 2017, Hong Kong, June 16, 2017.
- CHAI W.Y., Cheung A.K.L., <u>Dai W.</u>, Ko J.M.Y. and Lung M.L., Functional Analysis of a Basement Membrane Protein, Nidogen-2 (NID2), in Nasopharyngeal Carcinoma and Esophageal Squamous Cell Carcinoma, 24th Asia Pacific Cancer Conference, Coex, Seoul, Korea. June 22-24, 2017.
- Deng M., Lung M.L., Cheung A.K.L., <u>Dai W.</u>, Chan K.C. and ZHENG H., Functional and Molecular Analysis of the Loss-of-Function Somatic Mutations in Two NF-KB Pathway Inhibitors, 24th Asia Pacific Cancer Conference, Coex, Seoul, Korea. June 22-24, 2017.
- Leong M.L., Cheung A.K.L., <u>Dai W.</u>, Tsao G.S.W. and Lung M.L., EBV-associated Histone Modifications in the Regulation of DNA Damage Repair Members in Nasopharyngeal Carcinoma., The 76th Annual Meeting of the Japanese Cancer Association, Tokyo, Japan. Sept 28-30, 2017
- Chai W.Y., Cheung A.K.L., <u>Dai W.</u>, Ko J.M.Y. and Lung M.L., Functional analysis of a basement membrane protein, Nidogen-2 (NID2) in NPC and ESCC, Sydney Cancer Conference, Australia, September 2016.
- Cheung A.K.L., <u>Dai W.</u>, LEONG M.L., Tsao G.S.W. and Lung M.L., EBV infection suppresses the DNA repair mechanisms in nasopharyngeal epithelial cells via reduction of the H3K4m33 mark, 107th American Association for Cancer Research. 2016.
- Zheng H., <u>Dai W.</u>, Cheung A.K.L., Ko J.M.Y., KAN P.Q.R., Wong W.Y., Leong M.L., Deng M., Kwong D.L.W., Lee W.M.A., Ng W.T., Ngan R.K.C., Yau C.C., Tung S., Lee V.H.F., Lam K.O., Au K.H., Cheng H.C., Yiu H.H.Y. and Lung M.L., Whole-exome sequencing identifies multiple loss-of-function mutations in the

NFkB pathways regulators in NPC, 107th American Association for Cancer Research. 2016.

- <u>Dai W</u>., Methylation Biomarkers in Nasopharyngeal Carcinoma, NPC Gordon Research Conference. 2016
- <u>Dai W.</u>, Tang C., ZHENG H., Cheung A.K.L., Ko J.M.Y., Wong W.Y., Sham P.C. and Lung M.L., Whole-exome sequencing identifies genetic susceptibility locus associated with familial nasopharyngeal carcinoma, 17th International Symposium on EBV and Associated Diseases. Zurich, Switzerland. Aug 8-12, 2016.
- <u>Dai W.</u>, Cheung A.K.L., Ko J.M.Y., Cheng Y., ZHENG H., Kwong D.L.W., Ngan R., Ng W.T., Lee A.W.M., Yau C.C. and Lung M.L., Aberrant methylation at chromosome 6p as novel biomarkers for diagnosis and prognosis of nasopharyngeal carcinoma, 106th American Association of Cancer Research. Philadelphia, Pennsylvania, USA. 2015.
- Zheng H., <u>Dai W.</u>, Tang S.M., Cheung A.K.L., Ko J.M.Y., Sham P.C. and Lung M.L., Unraveling the genetic basis of nasopharyngeal carcinoma using next-generation sequencing approaches, 106th American Association of Cancer Research. Philadelphia, Pennsylvania, USA. 2015.
- Ko J.M.Y., <u>Dai W.</u>, Kwong D.L.W., Ng W.T., Lee A.W.M., Ngan R.C., Yau C.C., Tung S. and Lung M.L., The genetic susceptibility and prognostic role of TERT-CLPTM1L and dnes in DNA damage pathways in NPC, 7th International NPC Biannual Meeting. Yogyakarta, Indonesia. 2015.
- <u>Dai W.</u>, Zheng H., Tang S.M., Sham P.C., Ko J.M.Y., Cheung A.K.L. and Lung M.L., Using Next-generation Whole-Exome Sequencing Approaches to Elucidate the Genetic Basis for Nasopharyngeal Carcinoma, Gorden Research Conference Genomic Instability. 2014.
- Ko J.M.Y., <u>Dai W.</u>, Wong E.H.W., Kwong D.L.W., Ng W.T., Lee A., Ngan R.K.C., Yau C.C., Tung S. and Lung M.L., Case-control association studies of DNA damage repair genes associated with genetic susceptibility of nasopharyngeal carcinoma, Gordon Research Conference Genomic Instability. 2014.
- Lung M.L., Ko J.M.Y., <u>Dai W.</u>, Wong H.W.E., Kwong D.L.W., Ng W.T., Lee A., Ngan R.K., Yau C.C. and Tung S., Adverse effects if TERT-CLPTM1L and double-strand breaks repair contribute to risk for NPC, 105th AACR. 2014.
- Yang X., <u>Dai W.</u>, Szeto C.Y.Y., Cheng Y., Kwong D.L.W. and Lung M.L., Epigenetic markers for early detection of NPC, 18th postgraduate symposium HKU. 2013
- <u>Dai W</u>, Brown R. 30 Years of Wnt Conference (2012, Netherland). Frizzled Receptor 4 (FZD4) and Dishevelled 1 (DVL1) in High Grade Serous (HGS) Ovarian Tumour Progression
- <u>Dai</u> W, Brown R. NCRI Cancer Conference. Systematic CpG Islands Methylation Profiling of Key Signalling Pathways and Their Prognostic Value for Epithelial Ovarian Cancer. Liverpool, UK. 2011
- <u>Dai W</u>, Brown R. Hallmark of Cancer-British Association of Cancer Research 50th Anniversary conference. Evaluation of Prognostic DNA Methylation Biomarkers in Ovarian Cancer, Edinburgh, UK, 2010
- <u>Dai W</u>, Brown R. Mathematical and Statistical Aspects of Molecular Biology (MSAMB). Implementation of methylation linear discriminant analysis (MLDA) on CpG Island microarray data of ovarian cancer. London, UK, 2009

Membership

Member of American Association for Cancer Research since 2014

- Member of British Association for Cancer Research since 2009
- Member of European Association for Cancer Research since 2009

Computer Skills

Java Intermediate (Sun Certified Java Programmer and Developer)

Perl Intermediate

R Advanced (R package developer)

SPSS Advanced

MySQL Advanced (Certified MySQL 5 database administrator)

Shell scripts Advanced

Publications (*co-first author)

- 1. Lin W, Yip YL, Jia L, Deng W, Zheng H, <u>Dai W</u>, Ko JM, Chung GTY, Yip KY, Lee SD, Kwang SH, Zhang J, Liu T, Chan JYW, Kwong DLW, Lee VHF, Nicholls JM, Busson P, Liu X, Chiang AK, Hui KF, Kwok H, T. CS, Cheung YC, Chan CK, Li B, Cheung ALM, Hau PM, Zhou Y, Tsang CM, Middeldorp J, Chen H, Lung ML, Tsao SW: Establishment and characterization of new tumor xenografts and cancer cell lines from EBV-positive nasopharyngeal carcinoma. *Nat Commun* 2018, Accepted.
- 2. Ko JM, Tsang KH, <u>Dai W</u>, Choi SSA, Leong MM, Ngan RK, Kwong DL, Cheng A, Lee AW, Ng WT, Tung S, Lee VH, Lam KO, Chan CK, Lung ML: Leukocyte telomere length associates with nasopharyngeal carcinoma risk and survival in Hong Kong Chinese. *Int J Cancer* 2018.
- 3. Chai AWY, Cheung AKL, <u>Dai W</u>, Ko JMY, Lee NPY, Chan KT, Law SY, Lung ML: Elevated levels of serum nidogen-2 in esophageal squamous cell carcinoma. *Cancer Biomark* 2018, 21(3):583-590.
- 4. <u>Dai W</u>, Ko JMY, Choi SSA, Yu Z, Ning L, Zheng H, Gopalan V, Chan KT, Lee NP, Chan KW, Law SY, Lam AK, Lung ML: Whole-exome sequencing reveals critical genes underlying metastasis in oesophageal squamous cell carcinoma. *J Pathol* 2017, 242(4):500-510.
- 5. Chatterjee J*, <u>Dai W*</u>, Aziz NHA, Teo PY, Wahba J, Phelps DL, Maine CJ, Whilding LM, Dina R, Trevisan G, Flower KJ, George AJT, Ghaem-Maghami S: Clinical Use of Programmed Cell Death-1 and Its Ligand Expression as Discriminatory and Predictive Markers in Ovarian Cancer. *Clin Cancer Res* 2017, 23(13):3453-3460.
- 6. Zheng H*, <u>Dai W*</u>, Cheung AK*, Ko JM, Kan R, Wong BW, Leong MM, Deng M, Kwok TC, Chan JY, Kwong DL, Lee AW, Ng WT, Ngan RK, Yau CC, Tung S, Lee VH, Lam KO, Kwan CK, Li WS, Yau S, Chan KW, Lung ML: Whole-exome sequencing identifies multiple loss-of-function mutations of NF-kappaB pathway regulators in nasopharyngeal carcinoma. *Proc Natl Acad Sci U S A* 2016, 113(40):11283-11288.
- 7. Ng HY, Ko JM, Yu VZ, Ip JC, <u>Dai W</u>, Cal S, Lung ML: DESC1, a novel tumor suppressor, sensitizes cells to apoptosis by downregulating the EGFR/AKT pathway in esophageal squamous cell carcinoma. *Int J Cancer* 2016, 138(12):2940-2951.
- 8. <u>Dai W*</u>, Zheng H*, Cheung AK, Tang CS, Ko JM, Wong BW, Leong MM, Sham PC, Cheung F, Kwong DL, Ngan RK, Ng WT, Yau CC, Pan J, Peng X, Tung S, Zhang Z, Ji M, Chiang AK, Lee AW, Lee VH, Lam KO, Au KH,

- Cheng HC, Yiu HH, Lung ML: Whole-exome sequencing identifies MST1R as a genetic susceptibility gene in nasopharyngeal carcinoma. *Proc Natl Acad Sci U S A* 2016, 113(12):3317-3322.
- 9. <u>Dai W</u>, Zheng H, Cheung AK, Lung ML: Genetic and epigenetic landscape of nasopharyngeal carcinoma. *Chin Clin Oncol* 2016, 5(2):16.
- 10. Chai AW, Cheung AK, <u>Dai W</u>, Ko JM, Ip JC, Chan KW, Kwong DL, Ng WT, Lee AW, Ngan RK, Yau CC, Tung SY, Lee VH, Lam AK, Pillai S, Law S, Lung ML: Metastasis-suppressing NID2, an epigenetically-silenced gene, in the pathogenesis of nasopharyngeal carcinoma and esophageal squamous cell carcinoma. *Oncotarget* 2016, 7(48):78859-78871.
- 11. Yu VZ, Wong VC, <u>Dai W</u>, Ko JM, Lam AK, Chan KW, Samant RS, Lung HL, Shuen WH, Law S, Chan YP, Lee NP, Tong DK, Law TT, Lee VH, Lung ML: Nuclear Localization of DNAJB6 Is Associated With Survival of Patients With Esophageal Cancer and Reduces AKT Signaling and Proliferation of Cancer Cells. *Gastroenterology* 2015, 149(7):1825-1836 e1825.
- 12. Yang X, <u>Dai W</u>, Kwong DL, Szeto CY, Wong EH, Ng WT, Lee AW, Ngan RK, Yau CC, Tung SY, Lung ML: Epigenetic markers for noninvasive early detection of nasopharyngeal carcinoma by methylation-sensitive high resolution melting. *Int J Cancer* 2015, 136(4):E127-135.
- 13. Shenker NS, Flower KJ, Wilhelm-Benartzi CS, <u>Dai W</u>, Bell E, Gore E, El Bahrawy M, Weaver G, Brown R, Flanagan JM: Transcriptional implications of intragenic DNA methylation in the oestrogen receptor alpha gene in breast cancer cells and tissues. *BMC Cancer* 2015, 15:337.
- 14. Kan R, Shuen WH, Lung HL, Cheung AK, <u>Dai W</u>, Kwong DL, Ng WT, Lee AW, Yau CC, Ngan RK, Tung SY, Lung ML: NF-kappaB p65 Subunit Is Modulated by Latent Transforming Growth Factor-beta Binding Protein 2 (LTBP2) in Nasopharyngeal Carcinoma HONE1 and HK1 Cells. *PLoS One* 2015, 10(5):e0127239.
- 15. <u>Dai W</u>, Cheung AK, Ko JM, Cheng Y, Zheng H, Ngan RK, Ng WT, Lee AW, Yau CC, Lee VH, Lung ML: Comparative methylome analysis in solid tumors reveals aberrant methylation at chromosome 6p in nasopharyngeal carcinoma. *Cancer Med* 2015, 4(7):1079-1090.
- 16. Yee Ko JM, <u>Dai W</u>, Wun Wong EH, Kwong D, Tong Ng W, Lee A, Kai Cheong Ngan R, Chung Yau C, Tung S, Li Lung M: Multigene pathway-based analyses identify nasopharyngeal carcinoma risk associations for cumulative adverse effects of TERT-CLPTM1L and DNA double-strand breaks repair. *Int J Cancer* 2014, 135(7):1634-1645.
- 17. Lung ML, Cheung AK, Ko JM, Lung HL, Cheng Y, <u>Dai W</u>: The interplay of host genetic factors and Epstein-Barr virus in the development of nasopharyngeal carcinoma. *Chin J Cancer* 2014, 33(11):556-568.
- 18. Zeller C, <u>Dai W</u>, Curry E, Siddiq A, Walley A, Masrour N, Kitsou-Mylona I, Anderson G, Ghaem-Maghami S, Brown R, El-Bahrawy M: The DNA methylomes of serous borderline tumors reveal subgroups with malignant- or benign-like profiles. *Am J Pathol* 2013, 182(3):668-677.
- 19. <u>Dai W</u>, Zeller C, Masrour N, Siddiqui N, Paul J, Brown R: Promoter CpG island methylation of genes in key cancer pathways associates with clinical outcome in high-grade serous ovarian cancer. *Clin Cancer Res* 2013, 19(20):5788-5797.
- 20. Zeller C, <u>Dai W</u>, Steele NL, Siddiq A, Walley AJ, Wilhelm-Benartzi CS, Rizzo S, van der Zee A, Plumb JA, Brown R: Candidate DNA methylation

- drivers of acquired cisplatin resistance in ovarian cancer identified by methylome and expression profiling. *Oncogene* 2012, 31(42):4567-4576.
- 21. Sriraksa R, Zeller C, El-Bahrawy MA, <u>Dai W</u>, Daduang J, Jearanaikoon P, Chau-In S, Brown R, Limpaiboon T: CpG-island methylation study of liver fluke-related cholangiocarcinoma. *Br J Cancer* 2011, 104(8):1313-1318.
- 22. Rizzo S, Hersey JM, Mellor P, <u>Dai W</u>, Santos-Silva A, Liber D, Luk L, Titley I, Carden CP, Box G, Hudson DL, Kaye SB, Brown R: Ovarian cancer stem cell-like side populations are enriched following chemotherapy and overexpress EZH2. *Mol Cancer Ther* 2011, 10(2):325-335.
- 23. <u>Dai W</u>, Teodoridis JM, Zeller C, Graham J, Hersey J, Flanagan JM, Stronach E, Millan DW, Siddiqui N, Paul J, Brown R: Systematic CpG islands methylation profiling of genes in the wnt pathway in epithelial ovarian cancer identifies biomarkers of progression-free survival. *Clin Cancer Res* 2011, 17(12):4052-4062.
- 24. <u>Dai W</u>, Teodoridis JM, Graham J, Zeller C, Huang TH, Yan P, Vass JK, Brown R, Paul J: Methylation Linear Discriminant Analysis (MLDA) for identifying differentially methylated CpG islands. *BMC Bioinformatics* 2008, 9:337.

Paper review

Paper review for International Journal of Cancer and Plos One

• (2017) *PLOS ONE* 2016 Reviewer and Editorial Board Thank You. PLoS ONE 12(3): e0174259.

Grants

- General Research Fund. The Research Grant Council. Genomic and Functional Study by Targeting MST1R and Its Related Chromosome 3p21.3 Region Associated with Genetic Susceptibility in Nasopharyngeal Carcinoma. Principal investigator, HK \$956,853, 1 Jan 2019-31 December 2021
- General Research Fund. The Research Grant Council. Functional characterization of Epstein-Barr virus long non-coding RNA (lnc-BARTs) in nasopharyngeal carcinoma. Co-investigator, HK972,000, 1 Jan 2019-31 December 2021
- *Health Medical Research Fund*. Clinical application of enumeration and genomic characterization for non-invasive detection and real-time monitoring of circulating tumor cells for esophageal carcinoma. **Co-investigator**, HK \$1,199,732, 1 June 2018-31 May 2020
- **SK** Yee Medical Foundation Grant. Non-invasive real-time monitoring and next-generation sequencing of circulating tumor cells for improved personalized treatment of metastatic colorectal cancer patients. Co-Investigator, HK \$1,610,107, March 2018-Feb 2019
- *Platform Technology Grant*. The University Research Committee. Establishing platform technology for use of circulating tumor cells for cancer diagnosis and drug testing. **Co-Investigator**, HK \$1,000,000, 30 June 2017-29 June 2019

Software

Dai W; Paul J; Brown R. Methylation Linear Discriminant Analysis (MLDA).
 Version: 2.0. CRAN, R project (Jun 2008).