

BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors in the order listed on the Sample Form.

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| NAME Zhenyu Jia | POSITION TITLE Project Scientist III | | |
|--|---|---------|--|
| EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.) | | | |
| INSTITUTION AND LOCATION | DEGREE (if applicable) | YEAR(S) | FIELD OF STUDY |
| Wuhan University, Wuhan, China | B.S. | 06/98 | Biochemistry |
| University of California, Riverside, Riverside, CA | M.S. | 12/05 | Statistics |
| University of California, Riverside, Riverside, CA | Ph.D. | 12/06 | Genetics, Genomics and Bioinformatics |

Personal Statement

I have a Ph.D. in Genetics, Genomics and Bioinformatics. Over the past 5 years, my major interest is development of improved diagnostic and prognostic tests for prostate and other cancers through development of methods for the analysis of multigene signature of heterogeneous diseases. I will serve as the Principal Investigator for the proposed project which aims to identify methylation signature in tumor-associated stroma in comparison to normal stroma for prostate cancer.

A. Positions and Honors.

Position and Employment

2006-2007 Postdoctoral Scholar, Botany and Plant Science, University of California, Riverside

2007-2008 Specialist, Pathology and Laboratory Medicine, University of California, Irvine

2008-present Project Scientist, Pathology and Laboratory Medicine, University of California, Irvine

Other Experience and Professional Memberships

1999-2001 Research Assistant, Institute of Biophysics, CAS, China

2002-2006 Research Assistant, University of California, Riverside

2006 Teaching Assistant, University of California, Riverside

2004-2007 Statistical Consulting, University of California, Riverside

2007-present Statistical Consulting, University of California, Irvine; Proveri Inc.; Biostatistics Shared Resource, UCI.

2006-present Member, American Statistical Association (ASA); American Association for Cancer Research (AACR)

2009-present Conference Program Committee, EvoStar (EvoBIO); International Association for Pattern Recognition (ICPR)

2010-present Editorial Board Member, Journal of Data Mining in Genomics & Proteomics

Honors

1994-1997 Outstanding Undergraduate Scholarship, Wuhan University, Wuhan, China

1997-1998 Tong-yi Fellowship, Wuhan University, Wuhan, China
 1998-1999 Excellent Graduate Student Scholarship, CAS, China
 2002-2003 Dean's Fellowship, University of California, Riverside
 2003 Ecology and Evolution Summer Fellowship, University of
 California, Riverside
 2008 International conference travel award, EvoStar 08 in Naples, Italy
 2008-2009 Faculty Career Development Award, University of California, Irvine
 2009 Travel Award, EVOSTAR 09 In Tubingen Germany
 2009 Scholarship, AACR Cancer Biostatistics Workshop, Sonoma, CA
 2012 Bridging Fund award (Co-PI), UCI Chao Family Comprehensive
 Cancer Center

B. Selected Peer-reviewed Publications (* Corresponding author; ¹ Co-First author).

1. Jia, Z. and Xu, S. Clustering expressed genes on the basis of their association with a quantitative phenotype. *Genetical Research*, 86:193-207 (2005). PMID: 16454859
2. Xu, S. and Jia, Z. Genome-wide Analysis of Epistatic Effects for Quantitative Traits in Barley. *Genetics*, 175:1955-1963 (2007). PMID: 17277367
3. Jia, Z. and Xu, S. Mapping Quantitative Trait Loci for Expression Abundance. *Genetics*, 176:611-623 (2007). PMID: 17339210
4. Jia, Z.* and Xu, S. Bayesian Mixture Model Analysis for Detecting Differentially Expressed Genes. *The International Journal of Plant Genomics*, Volume 2008, Article ID 892927, 12 pages (2008). PMID: 18431446
5. Jia, Z.*, Tang, S., Mercola, D. and Xu, S. Detection of Quantitative Trait Associated Genes Using Cluster Analysis. *EvoBIO 2008, Lecture Notes in Computer Science 4973, E. Marchiori and J.H. Moore (Eds.)*, 83-94 (2008). PMID: 19738934
6. Jia, Z.*, Wang, Y., Koziol, J., McClelland, M. and Mercola, D. A New Bi-Model Classifier for Predicting Outcomes of Prostate Cancer Patients. *in JSM Proceedings, Biometrics Section. Denver, CO: American Statistical Association* (2008).
7. Arora, S., Wang, Y., Jia, Z., Vardar-Sengul, S., Munawar, A., Doctor, K., Birrer, M., McClelland, M., Adamson, E. and Mercola, D. Egr1 Regulates the Coordinated Expression of Numerous EGF Receptor Target Genes as identified by ChIP on chip of Prostate Cancer Cells. *Genome Biology*, 9:R166 (2008). PMID: 19032775, PMCID: PMC2614498
8. Koziol, J., Feng, A., Jia, Z., Wang, Y., Goodison, S., McClelland, M. and Mercola, D. The Wisdom of the Commons: Ensemble Tree Classifiers for Prostate Cancer Prognosis. *Bioinformatics*, 25:54-60 (2009). PMID: 18628288, PMCID: PMC2638928
9. Jia, Z.*, Wang, Y., Ye, K., Li, Q., Tang, S., Xu, S. and Mercola, D. Association Study between Gene Expression and Multiple Relevant Phenotypes with Cluster Analysis. *EvoBIO 2009, Lecture Notes in Computer Science 5483, C. Pizzuti, M.D. Ritchie, and M. Giacobini (Eds.)*, 1-12 (2009). PMID: 19655036, PMCID: PMC2719899
10. Koziol, J. and Jia, Z.* The Concordance Index C and the Mann-Whitney Parameter $\Pr[X>Y]$ with Randomly Censored Data. *Biometrical Journal*, 51:467-474 (2009). PMID: 19588452
11. Cheng, C., Bettahi, I., Cruz-Fisher, M., Pal, S., Jain, P., Jia, Z., Holmgren, J., Harandi, A. and de la Maza, L. Effective vaccination against *Chlamydia trachomatis* using the major outer membrane protein adjuvanted with CpG oligodeoxynucleotide coupled to the nontoxic B subunit of cholera toxin. *Vaccine*, 27:6239-6246 (2009). PMID: 19686693

12. Cao, J.N., Gollapudi, S., Sharman, E.H., Jia, Z., Gupta, S. Age-related Alterations of Gene Expression Patterns in Human CD8+ T cells. *Aging Cell*, 9:19-31 (2010). PMID: 19878143
13. Ye, K., Jia, Z., Wang, Y., Flicek, P., Apweiler, R. Mining Unique-m Substrings from Genomes. *Journal of Proteomics & Bioinformatics*, 3:99-103 (2010).
14. Xia, X.¹, Jia, Z.¹, Porwollik, S., Long, F., Hömme, C., Ye, K., Müller-Tidow, C., McClelland, M., Wang, Y. Evaluating Oligonucleotide Properties for DNA Microarray Probe Design. *Nucleic Acids Research*, 38:11 e121 (2010). PMID: 20236987
15. Wang, Y.¹, Xia, X.¹, Jia, Z.¹, Sawyers, A., Yao, H., Wang-Rodriquez, J., Mercola, D., McClelland, M. In silico estimates of tissue components in surgical samples based on expression profiling data. *Cancer Research*, 70:6448-6455 (2010). PMID: 20663908
16. Basu, A., Banerjee, H., Rojas, H., Martinez, S., Roy, S., Jia, Z., Lilly, M., De León, M., Casiano, C. Differential Expression of Peroxiredoxins in Prostate Cancer: Consistent Upregulation of PRDX3 and PRDX4. *The Prostate*, 71:755-765 (2010). PMID: 21031435
17. Jia, Z.¹, Wang, Y.¹, Sawyers, A., Yao, H., Rahmatpanah, F., Xia, X., Xu, Q., Pio, R., Turan, T., Koziol, J., Goodison, S., Carpenter, P., Wang-Rodriquez, J., Simoneau, A., Meyskens, F., Sutton, M., Lernhardt, W., Beach, T., Monforte, J., McClelland, M., Mercola, D. Diagnosis of Prostate Cancer Using Differentially Expressed Genes in Stroma. *Cancer Research*, 71:2476-2487 (2011). PMID: 21459804
18. Chen, X.¹, Xu, S.¹, Wang, Y., McClelland, M., Jia, Z.*¹, Mercola, D.* Identification of Biomarkers for Prostate Cancer Prognosis Using a Novel Two-Step Cluster Analysis. *Pattern Recognition in Bioinformatics, Lecture Notes in Computer Science 7036*:63-74 (2011).
19. Jia, Z.*¹, Rahmatpanah, F., Chen, X., Lernhardt, W., Wang, Y., Xia, X., Sawyers, A., Sutton, M., McClelland, M.*¹, Mercola, D.*¹ Expression changes in the stroma of prostate cancer predict subsequent relapse. *PLoS ONE*, 7(8): e41371 (2012). PMID: 22870216
20. Chen, X., Xu, S., McClelland, M., Rahmatpanah, F., Sawyers, A., Jia, Z.*¹, Mercola, D.*¹ An Accurate Prostate Cancer Prognosticator Using a Seven-Gene Signature Plus Gleason Score and Taking Cell Type Heterogeneity into Account. *PLoS ONE*, 7(9): e45178 (2012). PMID: 23028830
21. Lee, C., Zhang, Q., Zi, X., Dash, A., Soares, M., Rahmatpanah, F., Jia, Z., McClelland, M., Mercola, D. TGF- β mediated DNA methylation in prostate cancer. *Transl Androl Urol*, 1(2): 78-88 (2012).
22. Rahmatpanah, F., Jia, Z.*¹, Chen, X., Jones, F., McClelland, M. and Mercola, D. (2012) Expression of HER2 in Breast Cancer Promotes a Massive Reorganization of Gene Activity and Suggests a Role for Epigenetic Regulation. *J Data Mining Genomics Proteomics*, 3:e102.
23. Pio, R., Jia, Z., Baron, V.T., Mercola, D., UCI NCI SPECS consortium of the Strategic Partners for the Evaluation of Cancer Signatures, Prostate Cancer, Early Growth Response 3 (Egr3) Is Highly Over-Expressed in Non-Relapsing Prostate Cancer but Not in Relapsing Prostate Cancer. *PLoS ONE* 8(1): e54096 (2013).
24. Jia, Z.*¹, Wang, Y., Hu, Y., McLaren, C., Yu, Y., Ye, K., Xia, X., Koziol, J., Lernhardt, W., McClelland, M., Mercola, D. A Sample Selection Strategy to Boost the Statistical Power of Signature Detection in Cancer Expression Profile Studies. *Anti-Cancer Agents in Medicinal Chemistry*, 13: 203-211 (2013). PMID: 22934703

C. Support

ONGOING RESEARCH SUPPORT

RFA-CA-09-017 MERCOLA AND LEE (PI) 07/01/10-06/30/15

THE EARLY DETECTION RESEARCH NETWORK

THE PROSTATE CANCER TUMOR MICROENVIRONMENT EXHIBITS DIFFERENTIALLY EXPRESSED GENE CHANGES THAT CAN BE USED FOR DIAGNOSIS WITHOUT TUMOR CELLS.

ROLE: PRINCIPAL BIOSTATISTICIAN

DEPARTMENT OF DEFENSE PROSTATE CANCER RESEARCH PROGRAM

IDEA DEVELOPMENT AWARD MERCOLA (PI) 01/01/13-12/31/15

UNIQUE METHYLOME PROFILES IN TUMOR ASSOCIATED STROMA FOR DETECTION OF PROSTATE CANCER

THE PROSTATE CANCER TUMOR MICROENVIRONMENT EXHIBITS UNIQUE EPIGENETIC PROFILES THAT CAN BE USED FOR DISEASE DIAGNOSIS.