

# **Curriculum Vitae**

## **Tingfen Yan**

### Contact information

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### Education

**1996-1999. Ph. D.** Northeast Forestry University (NFU), China.

Major: Molecular Ecology

Thesis: Study on Molecular Ecology of *Rhodiola sachalinensis* using allozyme and RAPD (Random Amplification of Polymorphic DNA) methods

**1993-1996. M.S.** NFU, China

Major: Genetic Ecology

**1987-1991. B.S.** NFU, China

Major: Forestry

### Professional experience

**2004.5-present.** Postdoctoral Research Associate at the Oak Ridge National laboratory (ORNL), TN, USA. Cloning whole genomic genes of *Shewanella oneidensis* for phage display purpose and characterization of dps mutant of *S. oneidensis* using microarray and physiological assay, functional genes and 16s rDNA clone libraries, rolling circle amplification (RCA) and functional gene microarray for marine sediment samples.

**2000- 2004.** Visiting Research Scholar at Michigan State University, USA. All research was performed at ORNL. Clone libraries of bacterial community for ground water samples, establishing the whole genomic microarray for *S. oneidensis*, *Nitrosomonas europaea* and *Rhodopseudomonas palustic*, and global gene expression for *N. europaea* under starvation conditions using microarray and real-time PCR methods.

**1999-2000.** Visiting Professor at the University of Tokyo, Japan. Isolation of mRNA, screening functional genes for controlling the pigments of strawberry fruit, and establishing cDNA library for Strawberries.

**1999-2000.** Associate Professor, (NFU), China.

**1999 -1997.** Lecturer, NFU, China

**1997 -1991.** Research Associate, NFU, China

### Professional societies

American Society for Microbiology

American Association for the Advancement of Science

## **Professional skills and techniques**

1. hands-on experience on construction of whole genomic microarray; microarray hybridization and microarray data analyzing using programs such as ARRAYSTAT, IMAGE and GENESPRING.
2. Microbial genome manipulation using cloning and mutagenesis approaches (Gene knockout).
3. Real-time PCR
4. Construction of clone library of functional genes for environmental samples.
5. DNA sequencing
6. Rolling Circle Amplification (RCA)
7. Functional Gene Array (FGA) for microbial community structure analysis.
8. Statistic analysis for community clone library and FGA data

## **Peer-reviewed publications (selected) (in Total: 25)**

1. Gentile M., **Yan T.**, Tiquia S., Fields MW., Nyman J., Zhou J and Criddle C. Stability in a Denitrifying Fluidized Bed Reactor. *Microb. Ecol.* **2006**. online, DOI:10.1007/s00248-006-9024-1
2. **Yan, T.**, Ye, Q., Zhou, J. and Zhang, C. L. Novel Functional Genes for Methanotrophs in Sediments Associated with Gas-Hydrates and Hydrocarbon-Seeps in the Gulf of Mexico. *FEMS Microbiology Ecology* **2006**. 57:251-9
3. Wei\*, X., **Yan\***, T., Hommes, N. G., Liu, X., Wu, L., McAlvin, C., Klotz, M. G., Sayavedra-Soto, L. A. Zhou, J. and Arp D. J.. Transcript profiles of *Nitrosomonas europaea* during growth and deprivation of ammonia and carbonate. *FEMS Microbiology letters* **2006**. 257: 76-83  
**Note:** \* Equal contribution to the paper.
4. Fields, W.M., Bagwell, C.E., Carroll, L.S., **Yan, T.**, Liu, X., Watson, B.D., Jardine, M.P., Criddle, C.S., Hazen, T.C., Zhou, J. Phylogenetic and functional biomarkers as indicators of bacterial community responses to mixed-waste contamination. *Environ. Sci. Technol.* **2006**. 40: 2601-2607
5. Brown, S. D., Martin, M., Deshpande, S., Seal, S., Huang, K., Alm, E., Yang, Y., Wu, Liyou, **Yan, T.**, Liu, X., Arkin, A., Chourey, K., Zhou, J. and Thompson, D. K., Cellular response of *Shewanella oneidensis* to strontium stress. *Appl. Environ. Microbiol.* **2006**. 72: 890-900.
6. Leaphart, AB., Thompson, DK., Huang, K., Alm, E., Wan, X., Arkin, A., Brown, SD., Wu, L., **Yan, T.**, Liu, X., Wickham, GS., Zhou, J. Transcriptome Profiling of *Shewanella oneidensis* Gene Expression following Exposure to Acidic and Alkaline pH *J. Bacteriol.* **2006** 188: 1633-1642
7. Wu, W., Gu, B., Fields, W. M., Gentile, M., Ku, Y., Yan H., Tiauias S., **Yan T.**, Nyman, J., Zhou, J., Phillip, J., Criddle C. Uranium (VI) reduction by denitrifying biomass. *Bioremediation Journal*. 2005. 9: 49-61.
8. Fields, W.M., **Yan, T.**, Rhee, S., Carroll, L.S., Jardine, M.P., Watson, B.D., Criddle, C.S., Zhou, J. Impacts on microbial communities and cultivable isolates from groundwater contaminated with high levels of nitric acid-uranium waste. *FEMS Microbiology Ecology*. **2005**. 53(3): 417-428.
9. Liu, Y., Gao, W., Wang, Y., Wu, L., Liu, X., **Yan, T.**, Alm, E., Arkin, A., Thompson, K.D., Fields, W.M., Zhou, J. Transcriptome analysis of *Shewanella oneidensis* MR-1 in response to elevated salt conditions. *J. Bacteriol.* **2005**. 187: 2501-2507.
10. Oda, Y., Samanta, S. K., Rey, F. E., Wu, ., Liu, X., **Yan, T.**, Zhou, J., Harwood, C. S. Functional genomic analysis of three nitrogenase isozymes in the photosynthetic bacterium *Rhodospseudomonas palustris*. *J. Bacteriol.* **2005** 187: 7784-7794.

11. Wan, X., VerBerkmoes, C.N., McCue, L., Stanek, D., Connelly, H., Hauser, J.L., Wu, L., Liu, X., **Yan, T.**, Leaphart, A., Hettich, L.R., Zhou, J., Thompson, K.D. Transcriptomic and Proteomic Characterization of the Fur Modulon in the Metal-Reducing Bacterium *Shewanella oneidensis*. *J. Bacteriol.* **2004**. 186: 8385-8400
12. Gao, H., Wang, Y., Liu, X., **Yan, T.**, Wu, L., Alm, E., Arkin, A., Thompson, K.D., Zhou, J. Global Transcriptome Analysis of the Heat Shock Response of *Shewanella oneidensis*. *J. Bacteriol.* **2004**. 186: 7796-7803
13. Palumbo, A. V., Schryver, J. C., Fields, M. W., Bagwell, C. E., Zhou, J.-Z., **Yan, T.**, Liu, X., Brandt, C. C. Coupling of Functional Gene Diversity and Geochemical Data from Environmental Samples. *Appl. Environ. Microbiol.* **2004**. 70: 6525-6534
14. **Yan T**, Fields W.M., Wu L., Zu Y., Tiedjie J. and Zhou J. Molecular diversity and characterization of nitrite reductase gene fragments ( nirK and nirS ) from nitrate- and uranium-contaminated groundwater. *Environmental Microbiology.* **2003**. 5(1) 13-20
15. **Yan T.**, Zu Y., Yan X., Zhou F. Genetic Structure of Endangered *Rhodiola Sachlinensis*. *Conservation Genetics.* **2003**. 4(2) 213-218.
16. Zhou F., **Yan T.**, Wang Q., Yan X. and Zu Y. Study on The Relation Between Morphodifferentiation and living Environment of *Rhodiola sachalinensis*. *Bulletin of Botanical Research.* **2001**, 21(1) 90-96.
17. Zhou F., **Yan T.**, Gu H and Zhang W. Research contents and methods of genetic ecology, *Journal of Northeast Forestry University.* **2000**, 28(6) 78-82.
18. **Yan T.**, Xiufeng Yan and Yuangang Zu. A primarily discuss on the Adaptive mechanism at different altitude level of *Rhodiola sachalinensis* population. *Bulletin of Botany Research*, **1999**, 19(2): 202-206.
19. **Yan T.**, Fujun Zhou, Xiufeng Yan and Yuangang Zu. Genetic diversity and population differentiation of *Rhodiola sachalinensis*. *Bulletin of Botany Research*, **1999**, 19(2): 189-194.
20. Yuangang Zu, Hengqing Zhang, **Yan T.**, and Xiaoying Yuan.. Allozyme analysis on natural population for *Pinus koraiensis*. *Bulletin of Botanical Research*, **1999**. 19(1): 75- 78.
21. **Yan T.**, Peitong Cong, Xinghua Liu and Yuangang Zu. Effect analysis of Environment factors on plant niche breadth. *Journal of Northeast Forestry University*, **1999**. 27(1): 36- 38.
22. Peitong Cong, **Yan T.**, Fujun Zhou, Xinghua Liu and Yuangang Zu. The study on Ecological niche overlap relations of several populations on *Leymus* community in northeast plain. *Bulletin of Botanical Research*, **1999**. 19(2): 213-219.
23. Yuangang Zu, **Yan T.**, and Fujun Zhou. A preliminary study on genetic variation and endangered mechanism of *Rhodiola sachalinensis* natural population. *Bulletin of Botany Research*, **1998**, 18(3): 304-310.
24. Fuchen Shi, **Yan T.** and Yuangang Zu. Characteristics of reproductive biology for *Larix* originating in Japan. *Journal of Forestry Research*, **1998**, 9(1): 51- 53.
25. Fuchen Shi, Yuangang Zu and **Yan T.** Effect of closing hillsides afforestation on population diversity. *Journal of Forestry Research*, **1998**, 9(1): 31-33.

## **Book chapters**

1. **Yan T.**, Xiufeng Yan ,Fujun Zhou and Yuangang Zu. **1999**. Research on the distribution and differentiation of RAPD polymorphic fragment for *Rhodiola sachalinensis*. In: Zu Yuangang, Sun Mei and Kang Le edit. The application, Method and theory of Molecular Ecology, 167-176. Beijing: China Higher Education Press and Springer-Verlag Heidelberg, 1999.
2. Zijun Mao, **Yan T.**, Fujun Zhou and Yuangang Zu. **1999**. A comparative study on *Larix sibirica* Ldb. and *L. sukaczewii* Dii. by the method of allozyme analysis. In: Zu Yuangang, Sun Mei and Kang Le edit. The application, Method and theory of Molecular Ecology, 217-225. Beijing: China Higher Education Press and Springer-Verlag Heidelberg, **1999**.
3. Yuangang Zu, **Yan T.**, and Jinghua Yu. 1999. Formation and Development of Molecular Ecology. In: Zu Yuangang, Sun Mei and Kang Le edit. The application, Method and theory of Molecular Ecology, 1-16. China Higher Education Press Beijing and Springer-Verlag Heidelberg, **1999**.
4. Shaoquan Nie, Fuchen Shi, Bing Sun and **Yan T.** The development and utilization of Birch resources and birch sap of heilongjiang province, China. In: Minoru Terazawa, Christopher A. McLeod and Yutaka Tamai eds. Tree sap. Hokkaido University press, **1995**.

## **Manuscripts in preparation**

1. **Tingfen Yan**, Matthew Fields, Anthony V. Palumbo, and James M. Tiedje, Jizhong Zhou. Diversity of amoA and pmoA in Low pH, Metal Contaminated Groundwater.
2. Wensui Luo, Jizhong Zhou, Wei-min Wu, **Tingfen Yan**, Craig S. Criddle, Philip Jardine, and Baohua Gu. Electron Donor Effects on Bioreduction Rates of Uranium and Microbial Community under Varying Bicarbonate and Sulfate Conditions (**submitted to AEM**).
3. **Tingfen Yan**, Terry J. Gentry, Christopher Schadt, David B. Watson, and Jizhong Zhou. Shifts in Groundwater Microbial Community Structure along Contaminant-Gradients at the DOE ERSP-Field Research Center in Oak Ridge of Tennessee.

## **Abstracts**

**2006**. American Society for Microbiology, 106<sup>th</sup> General Meeting, Orlando, Florida.

1. \*Shifts in groundwater microbial community structure along contaminant-gradients at the DOE ERSP-field research center in Oak Ridge, TN
2. \*Microbial community structure of the Gulf of Mexico gas hydrates and hydrocarbon seeps revealed by functional gene microarray and clone libraries.
3. Microbial diversity and functional characteristics in metal- and radionuclide-contaminated soils at Savannah River sites, South Carolina, USA.
4. Deletion of a predicted sensory box gene in *Shewanella oneidensis* MR-1 causes pleiotrophic phenotypes.
5. Global analysis of iron response and fur modulon *Shewanella oneidensis* MR-1.

6. Transcriptome and computational analysis of the regulatory role of the fur gene in the H<sub>2</sub>O<sub>2</sub> stress response of *Shewanella oneidensis*.

7. Global analysis of H<sub>2</sub>O<sub>2</sub>-induced stress response of *Shewanella oneidensis* MR-1 and the identification of a dual function oxyR.

8. Transcriptomic characterization of the *Arca* regulon in the metal-reducing bacterium *Shewanella oneidensis*.

**2005.** American Society for Microbiology, 104th General Meeting, Atlanta, Georgia.

1. \*Novel functional genes for methanotrophs in gas-hydrate and hydrocarbon-seep environments in the Gulf of Mexico

2. Bacterial diversity associated with metal-contamination at the DOE Savannah River site, South Carolina, USA.

3. Identification of different relationships between contaminated groundwater samples based upon extensive geochemical data or multiple gene sequences from microbial communities.

4. A transcriptome perspective of *Shewanella oneidensis* MR-1 cells adapted to hypoosmotic stress.

5. The identification of a hypothetical ORF in *Shewanella oneidensis* MR-1 involved in the transition between aerobic and anaerobic growth.

6. Identification and characterization of several novel genes implicated in metal reduction pathway of *Shewanella oneidensis*.

**2004.** American Society for Microbiology, 104th General Meeting, New Orleans, Louisiana.

1. Diversity of Nitrite Reductase Gene Fragments in Marine Sediments Associated with Gas Hydrates in the Gulf of Mexico.

3. Functional Analysis of the *Nitrosomonas europaea nirK* Mutant using a Genomic Microarray

2. Gene Expression Profiles of *Rhodospseudomonas palustris* Nitrogenases by Whole Genome Microarray.

**2003.** American Society for Microbiology, 103th General Meeting, Washington DC.

1. \*Gene Expression Profiles of *Nitrosomonas europaea* under Starvation.
  2. Heat Shock Response in *Shewanella oneidensis*.
  3. Microarray Expression Profiling of *Shewanella oneidensis* MR-1 during Anaerobic Growth with different electron Acceptors.
  4. Whole Genome Microarray –Based Transcription Profiling of H<sub>2</sub>O<sub>2</sub>-Induced Stress Response of *Shewanella oneidensis*.
  5. DNA to Phenotype: Functional Annotation of a Conserved Hypothetical Protein in *Shewanella oneidensis*.
  6. Molecular Characterization of a Fluidized Bed reactor Designed for denitrification of treated Groundwater Contaminated with High Levels of Nitrate, Uranium, and Heavy Metals.
- 2002.** American Society for Microbiology, 102th General Meeting, Salt Lake City, Utah
1. \*The Diversity of Nitrite Reductase Genes ( *nirS* and *nirK* ) from Bacterial Communities and Isolates in Nitrate- and Uranium-Contaminated Groundwater
- 2001.** 9<sup>th</sup> International Conference on Microbial Genomes, Catlinburg, TN
1. \*The Diversity of Nitrite Reductase Genes ( *nirS* and *nirK* ) from Bacterial Communities in Groundwater Contaminated with Nitrate, Uranium and Heavy Metals
- Note:** \* I presented

## **References**

1. Anthony V. Palumbo, palumboav@ornl.gov, 865-576-8002, Oak Ridge National Laboratory.
2. Matthew W. Fields, FieldsMW@MUOhio.edu, 513-529-5434. Department of Microbiology, Miami University (Ohio USA).
3. Dorothea K. Thompson, dthomps@purdue.edu, 765-496-8301, Purdue University
4. Chuanlun Zhang, zhang@srel.edu, 803-725-5299, Savannah River Ecology Laboratory and Marine Sciences Department, University of Georgia.

## **Statement of Research Interests**

Based on my previous research experience and my own research interests, I would like to perform research in molecular microbial ecology using integrated approaches of molecular biology, bacterial isolation and characterization, and metagenomic methods.

**First of all**, I am not only interested in monitoring changes of composition, structure and dynamics for microbial communities from contaminated ground water and sediments at DNA level using **functional gene microarray (FGA)** method, but also interested in observing those changes at RNA level using FGA, because the results can reflect the metabolically active microbial communities. microarray is a powerful and high throughput system that allows the analysis of thousands and thousands of genes at the same time. DNA from environmental samples has been successfully used for FGA analysis combined with whole genome amplification. However, because of the difficulties of getting high quality RNA, successful amplification and labeling etc, it is big challenge to perform FGA analysis at RNA level for environmental samples,

**Secondly**, it is of my interests to explore if certain microorganism or functional genes could be related to special environment using metagenomic library combined with other genomics tool and bacterial isolation.

Based on 16s rDNA clone library data for FRC watershed sample contaminated with U and Nitrate at Y-12 in ORNL, we found out that many of the detected dominant bacteria in several sites appear to be novel organisms that may play as yet unidentified roles in the attenuation of contaminants at the FRC. Culture-independent metagenomic library combined with other genomics tool and physiological characterization of isolates is necessary to determine their potential for contaminant remediation.

**Moreover**, I am very interested in monitoring the effects of global warming to natural microbial communities.

Global warming would threat the life on the earth. Microorganisms are central players in Earth's climatic, geological, geochemical, and biological evolution. Studies on the changes of structure, composition and function of microbial communities would reveal and provide the baseline for the consequences of global warming.

The above research interests will allow me to achieve a goal in understanding how microorganisms are interacted with each other, with their environment and geochemistry cycling aspect, providing fundamental information for bioremediation and other studies in the natural environmental communities.