

CURRICULUM VITAE (brevis)

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EDUCATION AND POSTDOCTORAL STUDIES

- **Biology Diploma (MS)**. University Babes-Bolyai of Cluj, Romania, 1988.
- **PhD**. University of Texas Southwestern Medical Ctr. Dallas, Texas, August 1997. *Advisor: Philip S. Perlman.*
- **Postdoctoral Scholar**, Woods Hole Oceanographical Institution, Woods Hole, Massachusetts (1997-1999).
- **Postdoctoral Fellow**, The Salk Institute for Biological Sciences, La Jolla, California (1999-2000).

PROFESSIONAL APPOINTMENTS

- **Systems Genetics Group Leader and Senior Staff Scientist** (present), Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN (at ORNL since 2007).
- **Joint Associate Professor** (2010-present), Microbiology Dept., University of Tennessee Knoxville.
- **Faculty Member** (2008-present), Genome Sciences and Technology Graduate Program, UTK/ORNL.
- **Visiting Scholar** (2006-2007), Pharmacology Department, University of California San Diego.
- **Bioinformatics Staff Scientist** (2000-2006), Diversa Corporation, San Diego.

SELECTED PUBLICATIONS (out of 52, in chronological order)

1. Padgett, R.A., **Podar, M.**, Boulanger, S.C. and Perlman, P.S. (1994). The stereochemical course of group II intron self-splicing. *Science*, **266**, 1685-1688.
2. **Podar, M.**, Perlman, P.S. and Padgett, R.A. (1995). Stereochemical selectivity of group II intron splicing, reverse splicing and hydrolysis reactions. *Molecular and Cellular Biology*, **15**, 4466-4478.
3. **Podar, M.**, Zhou, J., Zhang, M., Franzen, J. S., Perlman, P.S. and Peebles, C.L. (1998). Domain 5 binds near a highly conserved dinucleotide in the joiner linking domains 2 and 3 of a group II intron. *RNA*, **4**, 151-166.
4. **Podar, M.**, Chu, V. T., Pyle, A.M. and Perlman, P.S. (1998). Group II intron splicing *in vivo* by first step hydrolysis. *Nature*, **391**, 915-918.
5. **Podar, M.**, Perlman, P.S. and Padgett, R.A. (1998). The two steps of group II introns splicing are mechanistically distinguishable. *RNA*, **4**, 890-900.
6. **Podar, M.**, Haddock, SHD., Sogin, M. and Harbison, G.R. (2001) A molecular phylogenetic framework for phylum Ctenophora. *Molecular Phylogenetics and Evolution*, **21**, 218-230.
7. Waters, E, Hohn, M.J., Ahel, I., Graham, D.E., Adams, M.D., Barnstead, M., Beeson, K.Y., Bibbs, L., Bolanos, R., Keller, M., Kretz, K., Lin, X., Mathur, E., Ni, J., **Podar, M.**, Richardson, T., Sutton, G.G., Simon, M., Söll, D., Stetter, K.O., Short, J. and Noordewier, M. (2003). The genome of *Nanoarchaeum equitans*: Insights into early archaeal evolution and derived parasitism. *Proc. Natl. Acad. Sci. U.S.A.* **100**, 12984-12988.
8. Tringe, S.G., Mering, C., Kobayashi, A., Salamov, A.A., Chen, K., Chang, H.W., **Podar, M.**, Short, J.M., Mathur, E.J., Detter, J.C., Bork, P., Hugenholtz, P. and Rubin, E.M. (2005) Comparative metagenomics of microbial communities. *Science*, **308**: 554-557.
9. Giovannoni, S., Tripp, J., Givan, S., **Podar, M.**, Vergin, K., Bibbs, L., Eads, J., Richardson, T., Noordewier, M., Rappé, M., Short, J. and Mathur, E. (2005). Genome Streamlining in a Cosmopolitan Oceanic Bacterium. *Science*, **309**: 1242-1245.
10. **Podar, M.**, Abulencia, C., Wachter, M., Hutchinson, D., Zengler, K, Garcia, J., Hausser, L and Keller, M. (2007). Targeted access to the genomes of low abundance organisms in complex microbial communities. *Applied and Environmental Microbiology*, **73**:3205-3214.
11. **Podar, M.** and Reysenbach, A.L. (2006). New opportunities revealed by biotechnological explorations of extremophiles. *Current Opinions in Biotechnology*, **17**:1-6.
12. **Podar, M.** (2007) Two component systems in microbial communities: Approaches and resources for generating and analyzing metagenomic data sets. *Methods in Enzymology*, **422**, 32-46.
13. Warnecke, F., Luginbühl, P., Ivanova, N., Ghassemian, M., Richardson, T.H., Stege, J., Djordjevic, G., Aboushadi, N., Sorek, R., Tringe, S., **Podar, M.**, Martin, H.G., Kunin, V., Dalevi, D., Madejska, J., Kirton, E., Platt, D., Szeto, E.,

- Salamov, A., Barry, K., Mikhailova, N., Kyrpides, N., Matson, E., Ottesen, E., Zhang, X., McHardy, A., Hernández, M., Murillo, C., Acosta, C., Rigoutsos, I., Tamayo, G., Green, B., Chang, C., Rubin, E., Mathur, E., Robertson, D., Hugenholtz, P. and Leadbetter, J.R. (2007). Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. **Nature**, **450**, 560-565.
14. **Podar M**, Wall MA, Makarova KS, Koonin EV. (2008). The prokaryotic V4R domain is the likely ancestor of a key component of the eukaryotic vesicle transport system. **Biology Direct**, **3**, 2.
 15. **Podar M**, Anderson I, Makarova KS, Elkins JG, Ivanova N, Wall M, Lykidis A, Mavrommatis K, Sun H, Hudson ME, Chen W, Deciu C, Hutchison D, Eads JR, Anderson A, Fernandes F, Szeto E, Lapidus A, Kyrpides NC, Saier MH Jr, Richardson PM, Rachel R, Huber H, Eisen JA, Koonin EV, Keller M, Stetter KO. (2008). A genomic analysis of the archaeal system *Ignicoccus hospitalis*-*Nanoarchaeum equitans*. **Genome Biol.** 10;9 (11):R158
 16. Elkins, J. G., **Podar, M.**, D. E. Graham, K. S. Makarova, Y. Wolf, L. Randau, B. P. Hedlund, C. Brochier, V. Kunin, I. Anderson, A. Lapidus, E. Goltsman, K. Berry, E. V. Koonin, P. Hugenholtz, N. Kyrpides, G. Wanner, P. Richardson, M. Keller, and K. O. Stetter. 2008. A korarchaeal genome reveals new insights into the evolution of the Archaea. **Proc. Natl. Acad. Sci. USA.**, **105**:8102-8107.
 17. Sukharnikov LO, Cantwell BJ, **Podar M**, Zhulin IB. (2011). Cellulases: ambiguous nonhomologous enzymes in a genomic perspective. **Trends Biotechnol.** **29**:473-9.
 18. Giannone RJ, Huber H, Karpinets T, Heimerl T, Küper U, Rachel R, Keller M, Hettich RL, **Podar M.** (2011). Proteomic Characterization of Cellular and Molecular Processes that Enable the *Nanoarchaeum equitans*-*Ignicoccus hospitalis* Relationship. **PLoS One.** 2011;**6**(8):e22942.
 19. Griffen AL, Beall CJ, Campbell JH, Firestone ND, Kumar P, Yang ZK, **Podar M** and Leys EJ. (2012). Distinct and Complex Bacterial Profiles in Human Periodontitis and Health Revealed by 16S Pyrosequencing. **ISME J.**, **6**:1176-85
 20. Flores GE, Shakya M, Meneghin J, Yang ZK, Seewald JS, Wheat CG, **Podar M** and Reysenbach AL. (2012) Inter-field Variability in the Microbial Communities of Hydrothermal Vent Deposits from a Back-Arc Basin. **Geobiology**, **10**:333-46..
 21. James H. Campbell JH, Foster CM, Vishnivetskaya T, Campbell AG, Yang ZK, Wymore A, Palumbo AV, Chesler EJ and **Podar M.** (2012). Host Genetic and Environmental Effects on Mouse Intestinal Microbiota. **ISME J.** **6**:2033-44.
 22. The Human Microbiome Research Consortium (Methe B.A. et al.)(2012). A framework for Human Microbiome Research. **Nature**, **486**:215-21.
 23. The Human Microbiome Research Consortium (Huttenhower, C. et al)(2012). Structure, function and diversity of the healthy human microbiome. **Nature**, **486**:207-14.
 24. Zhou Y, Gao H, Mihindukulasuriya KA, Rosa PS, Wylie KM, Vishnivetskaya T, **Podar M**, Warner B, Tarr PI, Nelson DE, Fortenberry JD, Holland MJ, Burr SE, Shannon WD, Sodergren E, Weinstock GM. (2013) Biogeography of the ecosystems of the healthy human body. **Genome Biol.** **14**:R1. [Epub ahead of print].
 25. Shakya M, Quince C, Campbell JH, Yang ZK, Schadt CW and **Podar M** (2013). Comparative metagenomic and rRNA microbial diversity characterization using Archaeal and Bacterial synthetic communities. **Environ Microbiol.** *in press*.

SYNERGISTIC ACTIVITIES

- JGI Community Sequencing Proposals review panels (2008-2010, 2012)
- NASA Exobiology review panels (2009-2011; panel chair in 2011)
- NIH review panels on human microbiome research for NHGRI, NIGMS, NIDCR (2008-2011)
- DOE-OBBER review panels (2010, 2012).
- Editorial Boards: Standards in Genomic Sciences, Applied and Environmental Microbiology, Biology Direct.

FUNDING

- 1R01HG004857-01A1, National Institutes of Health / National Human Genome Research Institute (Sep.2009-Aug.2012): *Targeted genomic characterization of uncultured bacteria from the human microbiota*. Principal Investigator.
- 1R56DE021567-01, National Institutes of Health / National Institute for Dental and Cranial Research (Sep.2010-Sep.2012): *Targeted metagenomics of the microbiome in adult and pediatric periodontitis*. Principal Investigator (PD: E. Leys, Ohio State University).
- DOE-DE-SC0006654, Department of Energy (Sep 2011-Aug 2014); *From genomes to metabolomes: Understanding mechanisms of symbiosis and cell-cell signaling using the archaeal system Ignicoccus-Nanoarchaeum*. Principal Investigator. (co-I: R. Hettich, ORNL; V. Copie, Montana State University; B. Bothner, Montana State University).
- 201REY307, National Science Foundation (Sep 2011-Aug 2015); *Enhancing expertise in archaeal taxonomy: Classical and molecular-based monographic research of the Nanoarchaeota*. Co-investigator. (PD: A.L. Reysenbach, Portland State University).