

## 岡田 典弘 (Okada, Norihiro)

Professor Emeritus: Tokyo Institute of Technology, Japan

Professor: National Cheng Kung University (Taiwan)

Principal Investigator :Foundation for Advancement of International Science (FAIS)



### EDUCATION

- The University of Tokyo (Department of Agriculture), BSc., 1973
- Graduate School of Pharmaceutical Sciences, The University of Tokyo, PhD., 1978

### PROFESSIONAL POSITIONS

- National Institutes of Health, USA, Post-Doctoral Fellow (1978-1979)
- University of Tsukuba, Assistant Professor (1979-1987), Associate Professor (1987-1992)
- Tokyo Institute of Technology, Professor (1992-2013)
- Foundation for Advancement of International Science (FAIS), Principal Investigator (2013-present)
- National Cheng Kung University (Taiwan), Research Professor (2012-present)
- Nagahama Institute of Bio-Science and Technology, Visiting Professor (2012-present)
- Kitasato University, Visiting Professor (2013-present)

### RESEARCH INTERESTS

- Structure and function of SINEs (1979-present)
- Phylogenetic usage of retroposons (1993- present)
- Experimental study on the amplification mechanism of SINEs (1986- present)
- Study on the speciation mechanism of cichlid fishes (1996- present)
- Study on the phylogeny of generation of mammals (2004- present)
- Study on the mechanism of generation of mammalian brain (2007- present)

### HONORS & AWARDS

- Fellows of American Association for the Advancement of Science (2001)
- Kimura Prize of the Japanese Evolution Society (2003)
- Kihara Prize of the Genetics Society of Japan (2006)
- Fujiwara Prize (2006)
- Medal with Purple Ribbon (2007)
- TORAY Prize for Science and Technology (2011)

### REPRESENTATIVE PUBLICATIONS

1. Nikaïdo M (27 coauthors) **Okada, N.** Coelacanth genomes reveal signatures for evolutionary transition from water to land. *Genome Res.* 1, October (2013)
2. Nishihara H, Maruyama S, **Okada N.** Retroposon analysis and recent geological data suggest near-simultaneous divergence of the three superorders of mammals. *Proc Natl Acad Sci USA.* Mar 31; 106(13):5235-40 (2009)
3. Seehausen O, Terai Y, Magalhaes I.S, Carleton K.L, Mrosso H.D.J, Miyagi R, Sluijs V.I, Schneider M.V, Maan M, Tachida H, Imai H, **Okada N.** Speciation through sensory drive in cichlid fish. *Nature*, 455(7213) 620-6 (2008)
4. Sasaki T, Nishihara H, Hirakawa M, Fujimura K, Tanaka M, Kokubo N, Kimura-Yoshida C, Matsuo I, Sumiyama K, Saitou N, Shimogori T, **Okada N.** Possible involvement of SINEs in mammalian-specific brain formation. *Proc Natl Acad Sci USA.* 105(11), 4220-5 (2008)
5. Piskurek O, **Okada N.** Poxviruses as possible vectors for horizontal transfer of retroposons from reptiles to mammals. *Proc Natl Acad Sci USA.* 104(29):12046-51 (2007)
6. Ichianagi K, Nakajima R, Kajikawa M, **Okada N.** Novel retrotransposon analysis reveals multiple mobility pathways dictated by hosts. *Genome Res.* Jan;17(1):33-41 (2007)

11. Terai Y, Seehausen O, Sasaki T, Takahashi K, Mizoiri S, Sugawara T, Sato T, Watanabe M, Konijnendijk N, Mrosso HD, Tachida H, Imai H, Shichida Y, **Okada N**. Divergent Selection on Opsins Drives Incipient Speciation in Lake Victoria Cichlids. *PLoS Biol.* 5;4(12):e433 (2006)
12. Nishihara H, Hasegawa M, **Okada N**. Pegasoferae, an unexpected mammalian clade revealed by tracking ancient retroposon insertions. *Proc Natl Acad Sci USA.* 103(26), 9929-9934 (2006)
13. Nishihara H, Smit AF, **Okada N**. Functional noncoding sequences derived from SINEs in the mammalian genome. *Genome Res.* 22 (2006)
14. Sugawara T, Terai Y, Imai H, Turner G F, Koblmuller S, Sturmbauer C, Shichida Y, and **Okada N**. Parallelism of amino acid changes at the RH1 affecting spectral sensitivity among deep-water cichlids from Lakes Tanganyika and Malawi. *Proc. Natl. Acad. Sci. USA* 102, 5448-5453 (2005)
15. Terai Y, Morikawa N, Kawakami K, and **Okada N**. The complexity of alternative splicing of hageromo mRNA is increased in an explosively speciated lineage in East African cichlids. *Proc. Natl. Acad. Sci. U S A.* 28, 12798-12803 (2003)
16. Terai Y, Mayer W E, Klein J, Tichy H, and **Okada N**. The effect of selection on a long wavelength-sensitive (LWS) opsin gene of Lake Victoria cichlid fishes. *Proc. Natl. Acad. Sci. USA.* 99, 15501-15506 (2002)
17. Kajikawa M, and **Okada N**. LINEs Mobilize SINEs in the Eel through a Shared 3' Sequence. *CELL* 111, 433-444 (2002)
18. Ogiwara I, Miya M, Ohshima K, and **Okada N**. V-SINEs: a new superfamily of vertebrate SINEs that are widespread in vertebrate genomes and retain a strongly conserved segment within each repetitive unit. *Genome Res.* 12, 316-324 (2002)
19. Nikaido M, Matsuno F, Hamilton H, Brownell R L Jr., Cao Y, Ding W, Zuoyan Z, Shedlock A M, Fordyce R E, Hasegawa M, and **Okada N**. Retroposon analysis of major cetacean lineages: the monophyly of toothed whales and the paraphyly of river dolphins. *Proc. Natl. Acad. Sci. USA.* 98, 7384-7389 (2001)

## **Fighting fish (*Betta splendens*) provides an excellent platform for investigating the neurogenomic state of aggression.**

### **Abstract**

Aggressive behavior is prevalently observed in many animal species and it finally contributes to the animal's survival and fitness. To get insight about how fighting experience interacts with information in the genome to modulate brain activity, we newly generated RNA-sequencing data from brains of fighting fish (*Betta splendens*) and performed transcriptome analysis of their fighting processes. Their typical fight continues for more than 60 mins, long enough for the state to be neurogenomically distinct, finally to yield the outcome of a loser and a winner. Massive changes of the brain transcriptome were observed, and the analysis of differential expression of genes (DEGs) exhibited the specific pattern of each neurogenomic state of fighting (i.e. "Before fighting", "During fighting", "After fighting"). When the time for "During fighting" was divided into two stages, i.e. early (20 mins) and late stages (60 mins), each stage can be characterized as the specific expression of several-tens immediate early genes (IEGs). Interestingly, the neurogenomic state of each opponent in a pair is becoming very similar to each other in a later stage of fighting, whereas that of the earlier stage is not differentiated to each other, suggesting that opponents in a pair are becoming to think very similarly to each other or to adapt to the same fighting circumstance during the process. The neurogenomic states of the loser and winner are almost the same just after the outcome of fighting and are differentiated after 30mins of the outcome, suggesting that the decision making for the end of the fight does not reflect to the global expression pattern of transcriptome. Our systems biological method using weighted gene co-expression analysis (WGCNA) essentially supports DEGs data and several modules correlate very well with the expression of "After fighting" and "Time". This is the first report, to our knowledge, in that a distinct neurogenomic state of "During fighting" is precisely characterized. Such neurogenomic state potentially includes the procedure of opponents' mutual assessment about their fighting ability, mediating transition from neurogenomic state of "Before fighting" to that of "After fighting". The fighting fish thus provides an excellent platform for investigating the neurogenomic state of aggression given its remarkable fighting characteristics in terms of its fighting spirit and duration.