

## Additional Information of our paper

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Title: The dynamics, causes, and impacts of mammalian evolutionary rates revealed by the analyses of capybara draft genome sequences

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### Abstract

Capybara (*Hydrochoerus hydrochaeri*) is an extant rodent species with the highest body weight. The draft genome of capybara was sequenced and the estimated genome size was 2.6 Gbp. Although the body size of capybara is about 60 times that of guinea pig, comparative analyses revealed that the neutral evolutionary rates of the two species were not substantially different. However, analyses of 39 genomes revealed very heterogeneous evolutionary rates. The highest evolutionary rate, 8.5 times higher than the human rate, was found in the Cricetidae-Muridae common ancestor after the divergence of Spalacidae. Muridae, the family with the highest number of species among mammals, emerged after the rate acceleration. Factors responsible for the evolutionary rate heterogeneity was investigated through correlations between the evolutionary rate and longevity, gestation length, litter frequency, litter size, body weight, generation interval, age at maturity, and taxonomic order. The regression analysis of these factors showed that the model with three factors (taxonomic order, generation interval and litter size) had the highest predictive power ( $R^2 = 0.74$ ). These three factors determine the number of meiosis per unit time. We also conducted transcriptome analysis, and found that the evolutionary rate dynamics affects the evolution of gene expression patterns.

Note: Abstract in Journal website has one error in line 3: 2.7 should be 2.6 (shown in red).

Dr. Isaac Babarinde



Professor Naruya Saitou





Capybara individual (male) “Rai” when he was alive; died in March 2015. This photo was provided by Izu Shaboten Park.

In spring of 2015, Dr. Wen-Hsiung Li, Director of Academia Sinica Biodiversity Research Center at that time, visited NIG Saitou Laboratory. We discussed about evolutionary rate heterogeneity among mammals. Because body size was considered to be negatively correlated with the evolutionary rate of the species, we got interested in capybara that has the largest body size among the extant rodents. Saitou remembered capybaras in hot spring in Izu Shaboten Park in Sizuoka prefecture, and phoned that park immediately. Fortunately, one individual named Rai passed away one week ago, and they promised Saitou to dig that body up.

Saitou and Dr. Babarinde, who was at that time Ph.D. student in Saitou Laboratory, visited Izu Shaboten Park and received small muscle piece of Rai. Dr. Babarinde extracted Rai’s DNA in Saitou Lab, and that was used for draft genome sequencing conducted in Professor Ituro Inoue’s Human Genetics Laboratory at National Institute of Genetics, using Next Generation Sequencer MiSeq. It took us more than four years to complete data analysis, and finally our paper was published in *Genome Biology and Evolution*. Coincidentally, Dr. Wen-Hsiung Li handled our paper as associate editor of this journal. This is the first report of de novo genome sequencing from our laboratory. Please look at our paper about our findings.

### **Future perspectives**

We are interested in genomic regions responsible for morphological characters among diverse mammals. For example, capybara’s tail is vestigial as in hominoids. We hope to find these parallelism in morphology from genome sequence comparison.