Anolis Newsletter VII

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Anolis Newsletter
VII

Edited by
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Collaborative research projects on *Anolis* lizards in Cuba

We have been collaborating with Dr. Antonio Cádiz (Havana University until 2016, and Queens College at the present) and Dr. Luis M. Díaz (the National Museum and Natural History of Cuba) since 2009 to investigate the ecological and evolutionary aspects of *Anolis* lizards in Cuba. Our researches have conducted under the collaboration agreements between Tohoku University and Havana University (2010-2016), and between Tohoku University and the National Museum and Natural History of Cuba (2017-). Our Japanese members have conducted fieldwork throughout Cuba every September since 2010. Herein, we would like to describe the focus of our ongoing research.

**Evolution of thermal adaptation in Anolis lizards in Cuba**

We hypothesize that ancestral *Anolis* species of Cuba might have inhabited forest interiors, where dense canopy cover limits direct sunlight, allowing ambient air temperatures to remain relatively cool. However, some *Anolis* species, such as *A. sagrei* and *A. porcatus*, inhabit open habitats and human-developed areas where direct sunlight leads to much higher air and substrate temperatures. We estimate that the evolution of *Anolis* from shade-adapted, interior-forest species to open-habitat species has occurred at five independent times in Cuba (Kanamori et al. manuscript under preparation).

We are currently examining the genetic factors responsible for facilitating the evolution to different thermal environments, particularly from cool-shaded habitat to hot-open habitat. In one of our previous studies (Akashi et al. 2016), we detected a differentially expressed gene associated with circadian regulation, *Nrld1*, which exhibits opposite expression patterns in the cool-adapted *A. allogus* and the hot-adapted *A. sagrei*. In that study, we also focused on heat avoidance behavior and the sensor genes that might be responsible for that behavior. We showed that temperatures triggering behavioral and TRPA1 responses are significantly lower in the shade-dwelling species *A. allogus* than in the sun-dwelling species *A. homolechis* and *A. sagrei*. Similarly, the TRPV1 and TRPM3 genes are believed to be involved in acute noxious heat sensing (Vandewauw et al. 2018; Nature, 662-666). Therefore, we are planning to examine the sequence evolution and thermal sensitivity of TRPV1 and TRPM3 as well as TRPA1 genes.
Based on previous results, we are now pursuing the following lines of research:

(1) Using coding sequences determined with RNA-seq, we are attempting to detect positively selected genes in *Anolis* lineages to determine which species have evolved from exploiting cool-shaded habitats to hot-open habitats (Kanamori et al. in prep.).

(2) We are comparing the gene expression and genomic sequences between forest and semi-desert populations of *Anolis* to detect candidate genes associated with adaptation to hot and dry habitats (Ishii et al. manuscript under preparation). Our focus is on *A. homolechis*, which usually inhabits forest edges. However, in eastern Cuba, we found a population of *A. homolechis* living in semi-arid areas where the annual average temperature is 5° higher than nearby forest habitats.

(3) Because thermal environments differ among populations even within a species, we plan to compare whole-genome sequences among *Anolis* populations living in different thermal habitats to detect gene sequences related to thermal regulation. At present, whole genome sequences of only a few species (e.g., *A. carolinensis*) have been reported (e.g., Tollis et al. 2018; Genome Biology and Evolution, 10:489-506). We are attempting to determine whole genome sequences for several Cuban species using Chromium systems.

Adaptation to hot-open habitat might be related to invasion ability. *A. carolinensis* and *A. sagrei* (both species native to Cuba) are known to be invasive, and both species have exerted significant negative impacts on habitats in regions where they have been introduced. *A. carolinensis* evolved from within a clade of *A. procaucus*, which also inhabits open-hot habitats. However, *A. procaucus* and *A. sagrei* might have evolved from ancestral species that inhabited cool-shaded habitats. Thus, we hypothesize that the ability to exploit hot-open environments might be related to the evolution of invasiveness, and therefore, we are searching a genomic basis that could facilitate both adaptation to hot-open habitat and invasiveness.

**Phylogeny of Cuban Anolis lizards**

Cádiz et al. (2013) constructed a phylogeny using 13 trunk-ground species from 34 locations throughout Cuba and analyzed factors affecting species differences in genetic variation within species (Cádiz et al. 2018). We estimated that there are 33 species belonging to more than 219 populations. Our results provide the most comprehensive sampling of Cuban *Anolis* species to date.

**Literature published by the project**

**Thermal adaptation**


**Development of hind limb**

**Phylogeny and diversity**

**Invasion by Anolis carolinensis**