

# Micro-evolution of sex determination mechanisms and sex determining genes in the cavefish Astyanax mexicanus

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#### ► To cite this version:

Boudjema Imarazene, Amaury Herpin, Romain Feron, John H Postlethwait, Manfred Schartl, et al.. Micro-evolution of sex determination mechanisms and sex determining genes in the cavefish Astyanax mexicanus. 8. International Symposium on the Biology of Vertebrate Sex Determination, Apr 2018, Kona (Hawaii), United States. hal-02734624

## HAL Id: hal-02734624 https://hal.inrae.fr/hal-02734624

Submitted on 2 Jun2020

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# EIGHTH INTERNATIONAL SYMPOSIUM ON THE BIOLOGY OF VERTEBRATE SEX DETERMINATION



# April 16-20, 2018 KONA, HAWAII

#### EIGHTH INTERNATIONAL SYMPOSIUM ON THE BIOLOGY OF VERTEBRATE SEX DETERMINATION

### 16-20, APRIL 2018

### King Kamehameha's Kona Beach Hotel

#### Kailua-Kona, Hawaii

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**Cover:** Statue of Ardhanarishvara, the half-male, half-female form of Shiva, India 11<sup>th</sup> century A.D.

## MICRO-EVOLUTION OF SEX DETERMINATION MECHANISMS AND SEX DETERMINING GENES IN THE CAVEFISH, ASTYANAX MEXICANUS.

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Vertebrates display remarkable diversity of sex determining (SD) mechanisms, ranging from environmental to genetic sex determination (ESD and GSD). In teleosts, sex determination (SD) mechanisms include both environmental and genetic regulation and are extremely diverse, changeable, and labile. In addition, many sex-determining (SD) genes have been already found in this group of vertebrates, showing that SD genes can be extremely variable even between closely related species. Hence, teleost fish have emerged as interesting models to study the macroevolution of SD mechanisms within vertebrates. The cavefish Astyanax mexicanus belongs to the Characiform group. Different populations of Astvanax have been described, including pigmented riverdwelling and several depigmented blind cave populations. These populations are still inter-fertile and cave populations are known to have evolved from a surface ancestral population less than 100,000 years ago. In addition these Astyanax populations can be also reared under laboratory conditions quite easily and are amenable to genetic manipulations. Altogether, this makes surface and cave populations a particularly interesting evolutionary genetic model system for comparative and microevolution studies. We thus initiated studies on the microevolution of SD and SD genes in the cavefish Astyanax mexicanus, and used restriction site-associated DNA (RAD) sequencing and pool-sequencing approaches to identify sex-biased molecular markers in both cavefish originating from the Pachón cave and surface fish populations. Our first results led to the identification of a candidate master SD gene that potentially triggers SD in both morphs. Despite this conservation of a strict GSD and the same master SD gene in both populations, our results also reveal a quick evolutionary transition between a polygenic SD system in surface population and a simple monofactorial system in the Pachón cave population.