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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

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

GENOME-WIDE APPROACHES TO ELUCIDATE EVOLUTION OF SEX DETERMINATION SYSTEMS AND SEX DETERMINING GENES IN FISH

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Fish show a great variety of sex determination mechanisms ranging from pure environmental (ESD) to pure genetic (GSD) with high variability of sex chromosome differentiation. Curiously, this variability does not follow any obvious phylogenetic pattern with transitions within closely related genera or even within species. To better understand the biological significance of sex determination diversity and the mechanisms driving sex chromosome evolution we attempted to decipher the molecular basis of the primary sex determination mechanisms and the structure and genetic organization of sex chromosomes across a broad diversity (>40 species) of ray-finned fishes (Actinopterygii) and one cartilaginous fish (Chondrichthyes). On the one hand, we analysed a broad collection of species that represent major branches of the fish tree of life, and on the other hand, we focused on closely related species within some branches of the phylogenetic tree (Esociformes, Danioids, Poeciliids, Pangasiidae). We used a large array of genomics approaches including, restriction site-associated DNA (RAD) sequencing, pool-sequencing, transcriptomics and *de novo* whole genome sequencing to characterize sex determination systems, delineate sex-specific chromosomal regions and identify candidate sex determining genes. These strategies led to the identification of many XX/XY or ZZ/ZW simple monofactorial systems but also species with more complex sex-determination systems including species with a mix of GSD and ESD and species with potential polygenic systems. Sex-biased markers and whole genome sequences delineated the extent of recombination suppression showing a wide range of sex-chromosome differentiation. Finally, novel master sex determination gene candidates were also identified in some species.