

Genetic mechanism of brain-gonad axis regulating sex differentiation in sex-biased zebrafish families

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Global warming

Changes in the ecobiology of animal species

Particularly in those with phenotypic sexual plasticity

Changes in population dynamics

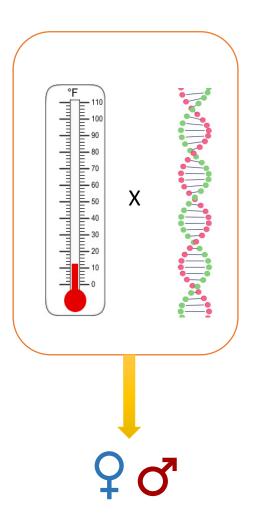
Increase the risk of extinction

 Phenotypic sexual plasticity in response to environmental conditions leads to skewed sex ratio, which can affect population dynamics and loss of biodiversity

 The hypothalamic-pituitary-gonadal axis is a well-known neuronal reproductive axis in vertebrates that triggers reproduction by activating the endocrine machinery

 The brain is a key factor that combines environmental stimuli with physiological responses to direct gonadal fate in animal species whose sex determination is influenced by the environment • Zebrafish (*Danio rerio*) is an excellent research model to study the mechanism of sex determination and differentiation and the effect of environmental factors on sexual fate in vertebrates

- Sex in zebrafish is determined by interaction between genetic and environmental factors ($G \times E$) and sex ratio in this model is family-specific
- Temperature is one of the most important environmental factors that influences sex determination in zebrafish and other species with G×E sex determination mechanism



Objectives

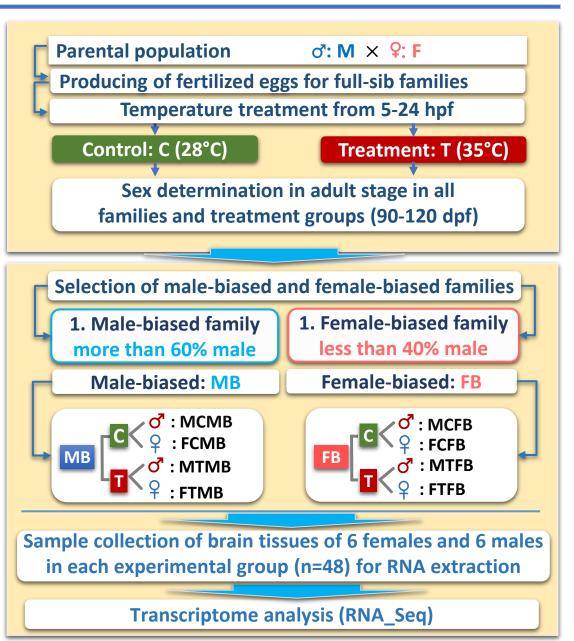
- Understanding the mechanisms underlying G×E in thermosensitive species, is of fundamental research importance for the conservation of natural populations and livestock species under rapid climate changes
- The zebrafish brain exhibits sex-specific differences at hormonal and transcriptional levels and is highly plastic even after sexual maturity
- > The main goal of this study was:
- to investigate the genetic mechanism underlying phenotypic sexual plasticity in the model animal zebrafish using transcriptome profiling
- to gain new insights into the regulatory mechanism of the brain-gonadal axis on sex ratio disequilibrium in response to elevated temperature



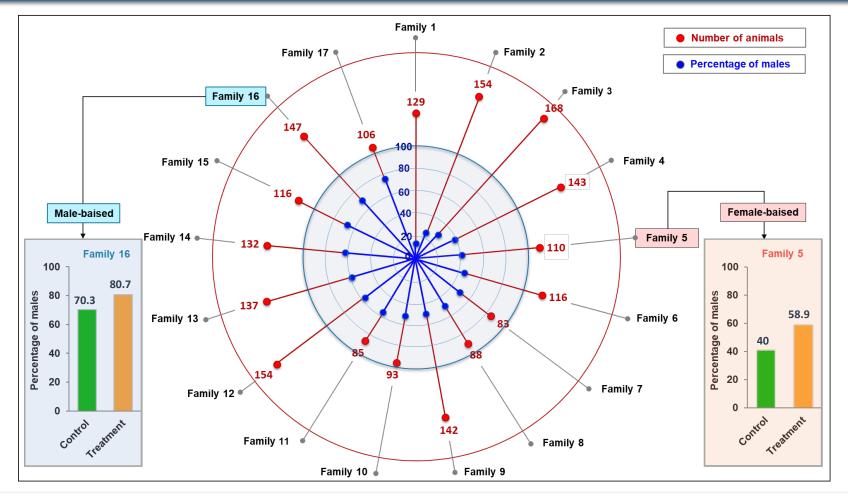
Materials and Methods

• 17 full-sib zebrafish families were produced and exposed into two different temperature incubations: 1) control group at a constant temperature of 28°C, 2) high incubation temperature group (treatment) at 35°C from 5 to 24 hpf

- One male-biased and one female-biased family in the adult stage were selected for transcriptome analysis (RNA_Seq)
- The brain tissue samples of 48 animals were collected for RNA_Seq analysis (24 samples in each sex-biased family)



Sex ratio of different zebrafish families and the selected sex-biased families for RNA_Seq



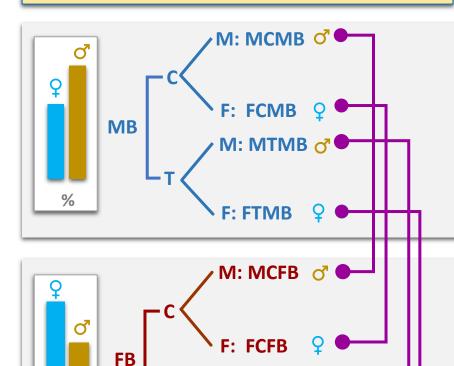
Two sex-biased families with a significant difference in sex ratio were selected for RNA_Seq: a male-biased (family 16) and a female-biased (family 5)

Strategy developed for comparative RNA_Seq analysis of different experimental groups

Male-biased vs. Female-biased family in each sex type (Strategy 1)

experimental groups (n=8)

Males vs. Females in each family type (Strategy 2)



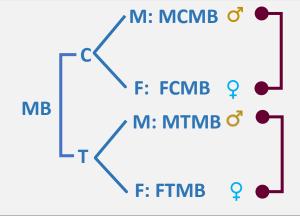
M: MTFB

Male Control Male-Biased

Female Control Male-biased

Male Treat Male-biased

Female Treat Male-biased

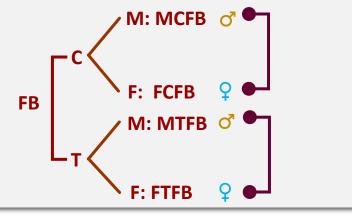


Male control Female-biased

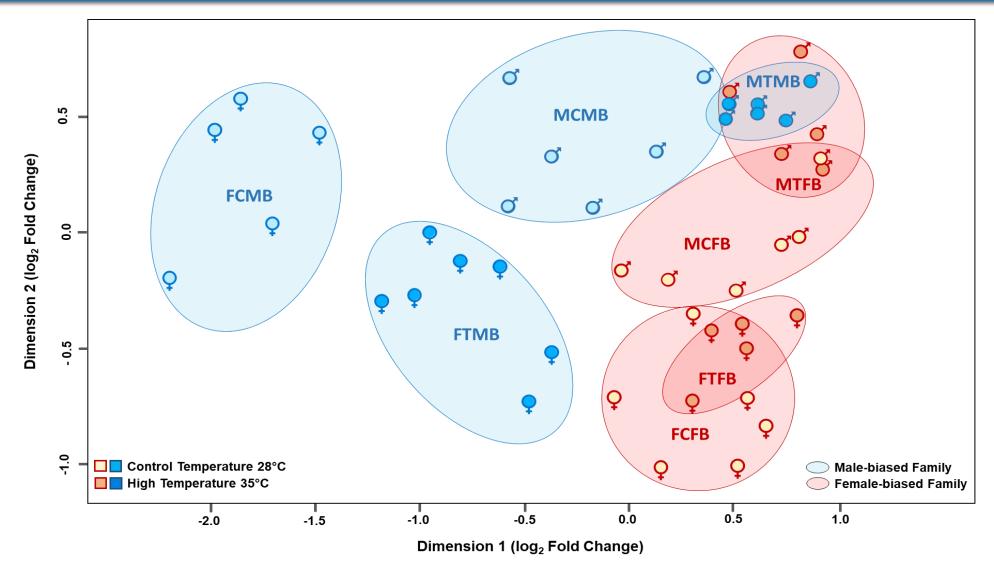
Female Control Female-biased

Male Treat Female-biased

Female Treat Female-biased



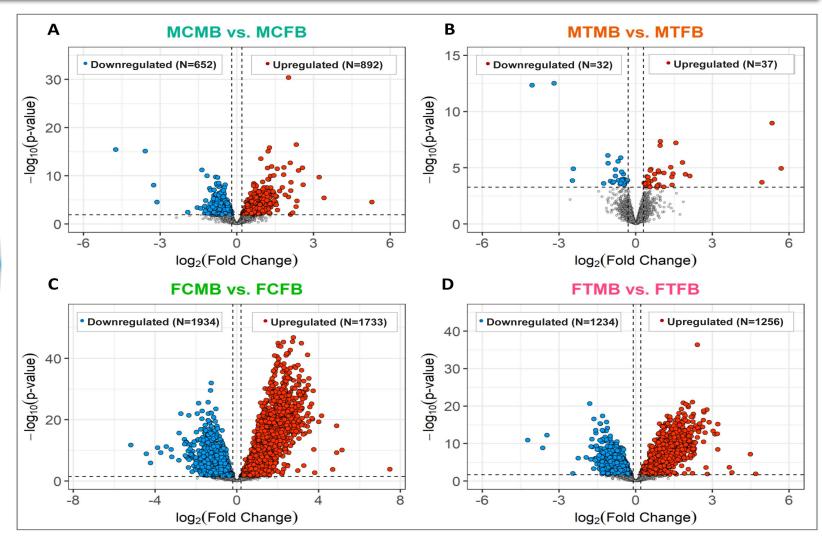
Multidimensional scaling of overall transcriptome profiles in individual samples



Differentially expressed genes (DEGs) comparing male-biased versus female-biased family (Strategy 1)

 a total of 1,544 DEGs in the control group and 69 DEGs in the treatment group in the male brains

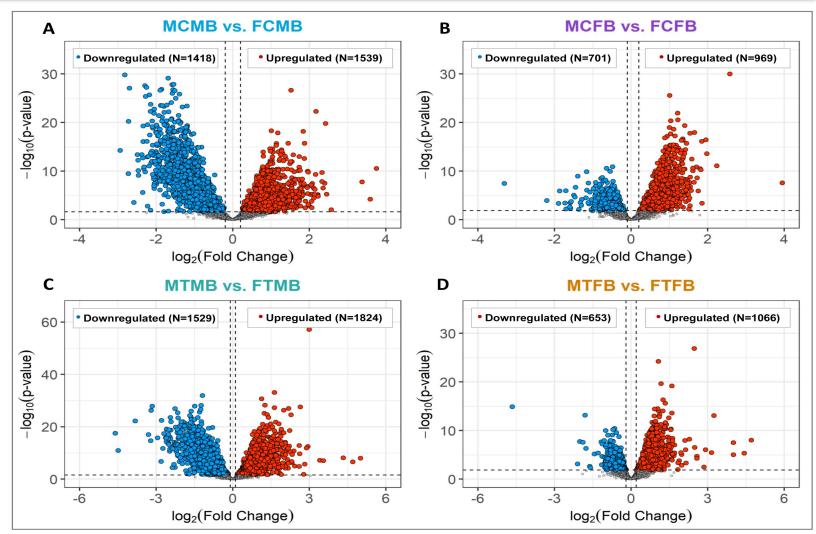
a total of 3,667 DEGs in the control group and 2,490 DEGs in the treatment group in the female brains



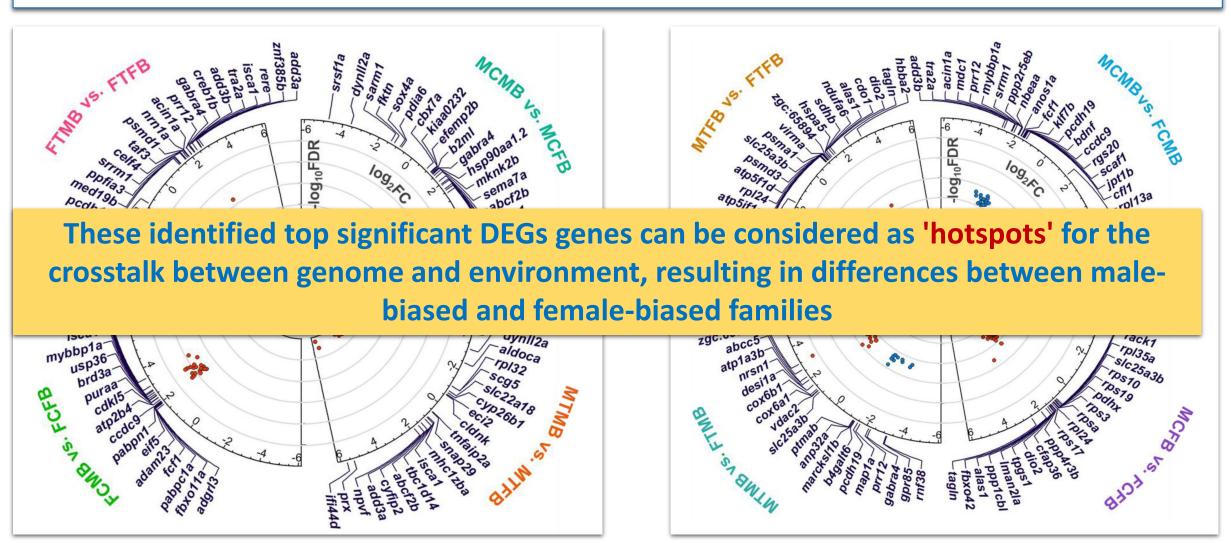
Differentially expressed genes (DEGs) comparing brain of males versus females within sex-biased families (Strategy 2)

a total of 2,957 and 1,670
 DEGs in the male-biased
 and female-biased
 families, respectively, in
 the control group

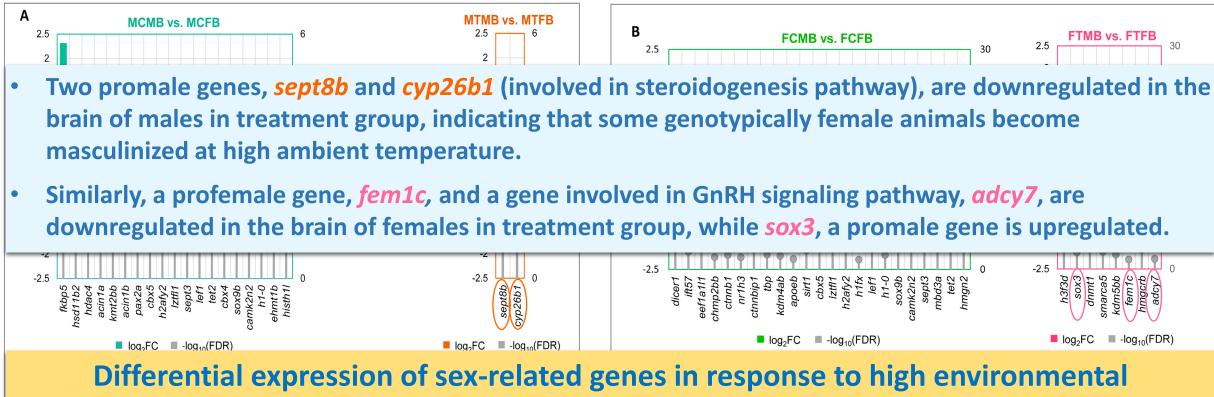
a total of 3,353 and 1,719
 DEGs in the male-biased and female-biased families, respectively, in the treatment group



Top significant differentially expressed genes (DEGs) in sex-biased zebrafish families



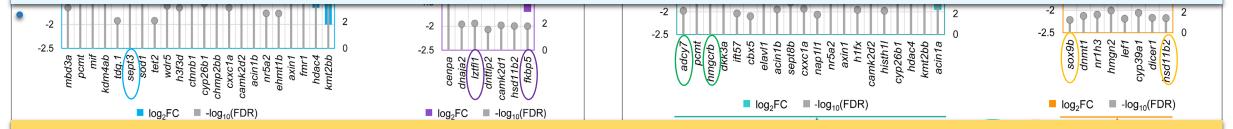
Unique identified reproduction-related genes between sex-biased zebrafish families



Differential expression of sex-related genes in response to high environmental temperature can affect the phenotypic sexual dimorphism, resulting in sex-reversed females (masculinized) and females with expressing a male-like transcriptome

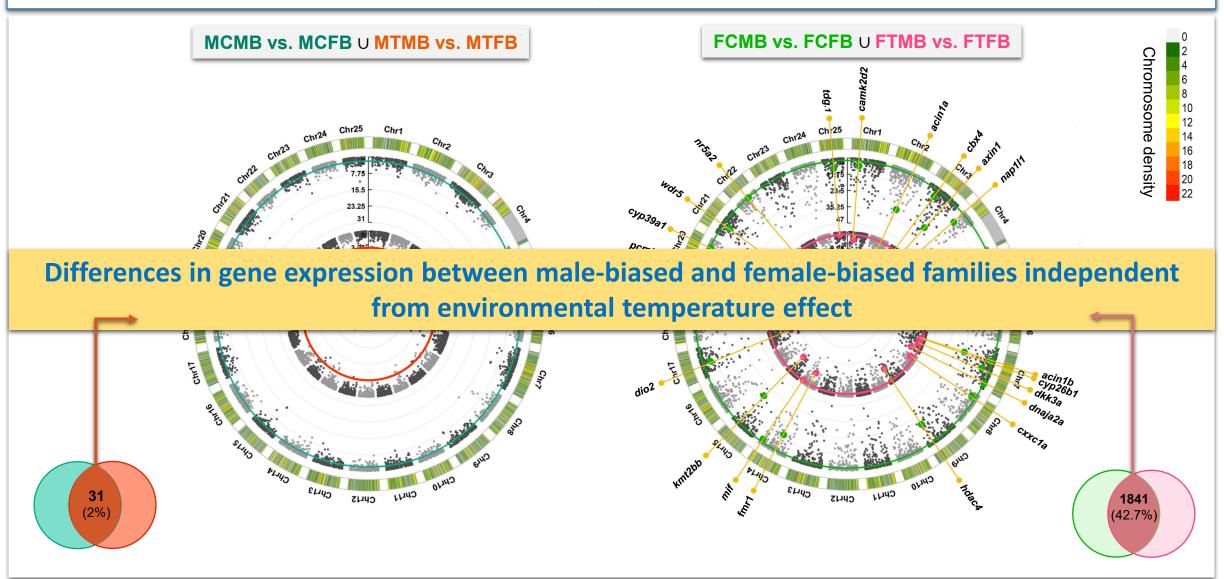
Unique identified reproduction-related genes within sex-biased zebrafish families

- Many promale genes such as *sept3* (spermatogenesis gene), *adcy7* (GnRH signaling pathway gene), *dkk3a* (testicular differentiation gene) were upregulated in male-biased family.
- By contrast, several promale genes were downregulated in female-biased family such as fkbp5 (a steroid hormone biosynthesis gene), lztfl1 (involved in spermatogenesis and testicular differentiation, and hsd11b2 (a gene involved in steroidogenesis pathway), while sox9b (a gene for ovary development) was upregulated in this family.

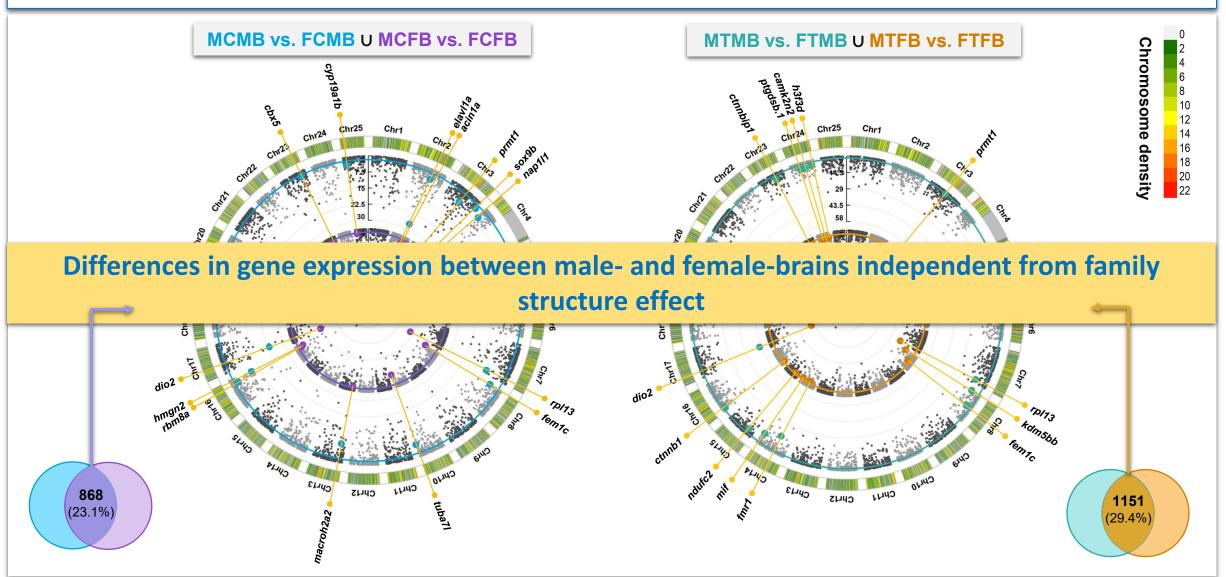


The identified family-specific reproduction-related genes can influence the trends of sex determination pathways towards maleness or femaleness

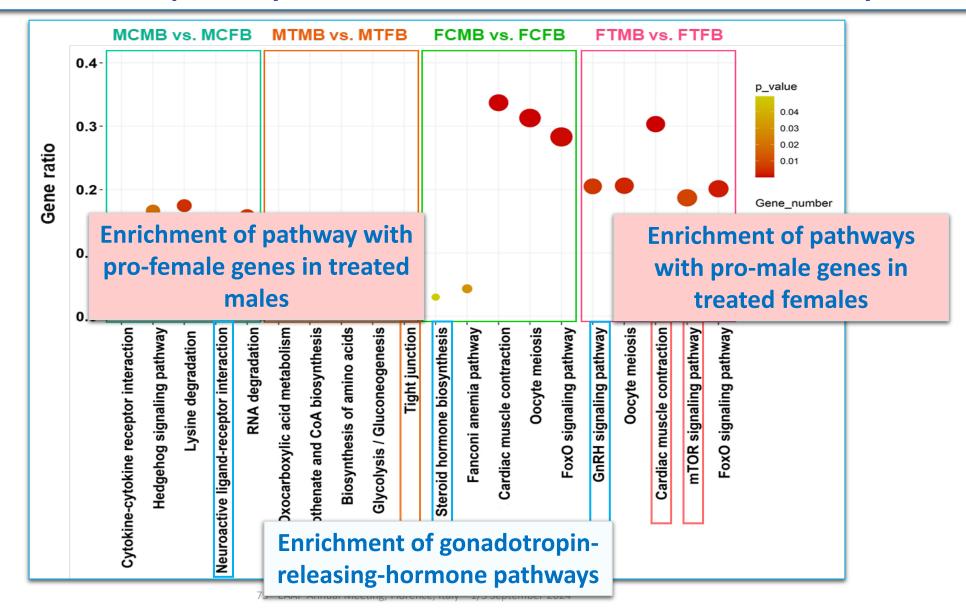
Common identified reproduction-related genes between sex-biased zebrafish families



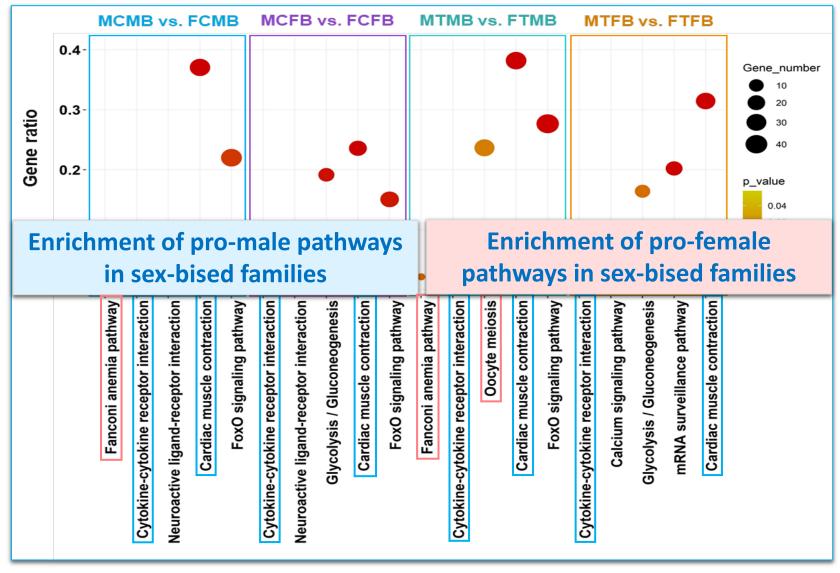
Common identified reproduction-related genes within sex-biased zebrafish families



Enriched KEGG pathways in male-biased versus female-biased family



Enriched KEGG pathways in brain of males versus females within sex-biased families



➤ Our study provides new insights into the importance of the brain-gonadal axis as a transducer of environmental stimuli that cause skewed sex ratio and generate sexbiased families in model animal, the zebrafish

➤ A highly skewed sex ratio may have a detrimental effect on the viability of populations and can lead to a greater risk of extinct in animal species with G×E sex-determining system under rapid global warming

➤ Our findings lead us to conclude that the effect of high ambient temperature in sexbiased zebrafish families can affect the phenotypic sexual dimorphism, resulting in sexreversed females (masculinized) and females with ovaries expressing a male-like transcriptome Dr. Shahrbanou Hosseini

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