



Contribution ID: 164

Type: Talk

An AI-Supported Large Scale Morphological Study: The Medaka Inbred Kiyosu–Karlsruhe Repository

Abstract

Genotype–phenotype associations are fundamental to biomedical research, providing insights into hereditary diseases, developmental biology, and the function of organoids. The medaka fish (*Oryzias latipes*) is a powerful model organism due to its natural genetic diversity and tolerance to inbreeding. The Medaka Inbred Kiyosu–Karlsruhe (MIKK) panel, comprising 80 fully sequenced isogenic inbred lines, offers a unique resource for systematic mapping of genetic variation to phenotypic traits.

We present the phenotype data repository MIKK-P, a comprehensive resource that integrates tomographic, morphological, and morphometric data for the MIKK panel. Using a high-throughput X-ray microtomography platform, we generated high-resolution 3D images of 900 medaka specimens. To convert these tomographic data into quantitative traits, we applied AI-supported methods, enabling the automatic segmentation of organs and landmark detection. From these morphological results, we derived a wide range of morphometric measurements, including organ volumes, distances, angles, and ratios. The repository supports phenotypic characterization at multiple levels: across the entire population, within individual lines, and in comparative analyses between line pairs or groups. The interactive platform provides open access to these data, supporting the exploration of morphometric variability and the design of F2 crosses guided by trait patterns.

By combining high-throughput imaging, AI-driven analysis, and interactive access, the MIKK-P repository establishes a scalable framework for automated phenotyping. This resource accelerates genotype–phenotype studies in medaka and serves as a blueprint for large-scale morphological research in other model organisms.

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Session Classification: Parallel: Life (RT3)

Track Classification: RT3