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FINAL PROGRAMME

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[O-I-6] Identification Of Novel Ovarian Predominant MiRNAs In Medaka (*Oryzias Latipes*)

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MicroRNAs (miRNAs) are small and highly conserved non coding RNAs involved in the regulation of thousands of genes. miRNAs play important roles in both normal physiological and pathological pathways in many organisms. The involvement of miRNAs in vertebrate oogenesis remains however poorly documented. The present study aimed at getting new insight on the role of miRNAs fish oogenesis and maternal contribution to early embryonic development. Based on the assumption that ovarian-specific or ovarian-predominant genes usually play important roles in oogenesis and/or early development in vertebrates, we searched for ovarian-predominant miRNAs in the medaka (*Oryzias latipes*) ovary. We designed a genome-wide microarray displaying 3800 distinct miRNAs from different teleost and vertebrate species. The microarray analysis was performed using 10 different tissues of adult medaka, including the ovary. We identified twenty miRNAs predominantly expressed in the ovary that had never been described in medaka. Among them, miR-202 was previously shown to be predominantly expressed in the rainbow trout gonads. Among these novel ovarian medaka miRNAs, three had previously been identified in the mouse ovary or germline (miR-743a, miR-878 and miR487b), and sixteen (including miR-6352, miR-478, miR-1305, and miR-5581) had never been reported as ovarian-predominant miRNAs in any vertebrate species.

To characterize the cognate miRNA sequences in medaka, heterologous miRNA sequences were aligned to the medaka genome and to medaka miRNA sequences predicted from existing RNA-seq data. Real time PCR was used to confirm ovarian-predominant expression of novel miRNAs and to analyze their expression profiles during oogenesis and early embryogenesis. Here we show that miR-202 is differentially expressed throughout oogenesis and is maternally-inherited in the medaka egg. This suggests a role of miR-202 during oocyte formation process and/or early embryonic development in medaka. Finally, our study led to the identification of previously uncharacterized medaka miRNAs predominantly expressed in the ovary, and should contribute to a further understanding of the roles of specific miRNAs in female gamete formation in this model species.