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[P1-061] Identification Of Two New Genes Involved In Myocyte Fusion In Vertebrates

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In most animals, myocyte fusion is a cellular process highly regulated during skeletal muscle development, post embryonic muscle growth and regeneration. Myocyte fusion follows an ordered set of cellular events, including myocyte elongation, cell migration, recognition and adhesion, and membrane fusion. However, our knowledge regarding molecular mechanisms controlling this essential step in myogenesis is far from being complete. Our study aimed at identifying new genes involved in myocyte fusion step in vertebrates. First, we performed an in vitro functional screening in C2C12 cell line (murine model) based on siRNA knock-down. Using a selection of genes found to be expressed in proliferating and differentiating muscle C2C12 cells (Moran and al., 2002 ; Tomczak and al., 2004), our functional screening led to the identification of thirteen genes which in vitro knock-down induced a myocyte fusion default. To identify their roles in vivo, expressional and functional analysis of these genes was further conducted on zebrafish model. The expression of four genes out of thirteen was clearly seen in somite during embryonic myogenesis using whole mount in situ hybridization. To precise their functions, in vivo studies based on morpholino micro-injection were performed on zebrafish embryos. Knock-down of two candidate genes, one encoding a protein of the extracellular matrix and the other encoding a N-acetyltransferase enzyme, resulted in an inability of the injected embryo to swim after hatching. We hypothesize that a muscle structural disorganization was responsible of this functional default, a confocal observation is currently in progress to characterize the muscle structure.
