ABSTRACT

CRISPR/Cas9 technology is currently one of the most important tools of genome engineering. This technology allows a precise site-specific gene editing and such ability was applied to study the role of TALE (TALE - three amino acids loop extension) homeodomain transcription factors during neural crest cells development. The main genes of interest, belonging to sub-family of TALE proteins, are *Meis1* transcription factors that are present in the zebrafish genome as two paralogous genes, *meis1a* and *meis1b*. Their function was assessed by mutating their DNA-binding domain – homeodomain to abrogate the ability of transcription factor to bind DNA and by that disturb regulatory network, in which *Meis1* proteins operate in. Phenotype analysis of mutant fish would reveal a potential role of *Meis1* proteins in regulation of neural crest cells development and outline the functional significance of the homeodomain in regulatory operations. To determine the regulatory relationship between *meis1a* and *meis1b* genes morpholino-based knock-down of the genes was performed. Preliminary results suggest a dominant role of Meis1b in neural crest cells regulation and importance of its homeodomain. Furthermore, knock-down of *Meis1a* indicates its contribution to regulation of craniofacial development. However, a detailed description of factors will be completed after thorough analysis of genetic mutants generated by CRISPR/Cas9 system.

KEY WORDS

CRISPR/Cas9, transcription factor, neural crest, *Danio rerio,* Meis, mutagenesis, development