

Identification and Validation of Promoter Candidates for Expression of Native Growth Factors in Cultivated Meat Cell Lines

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Abstract

In view of significant growth in global population coupled with rising food demand, cultivated meat has been explored as an alternative source of protein. One key challenge to the economical production of cultivated meat is the use of expensive growth factors and recombinant proteins in the maintenance of large-scale cell cultures. To reduce or eliminate the need for media supplementation with essential growth factors, we sought to identify promoter elements from the genomes of cattle and unagi that may be employed to drive high endogenous expression of species-specific growth factors in bovine and unagi cultivated meat cell lines which will eschew the introduction of undesirable xenogeneic sequences into the cells. These promoter candidates were identified from bioinformatics analyses of epigenome and transcriptome data, generated in-house through ATAC-seq, RAMPAGE and/or RNA-seq of bovine satellite cells and unagi adipose-derived stem cells, as well as publicly available data of adult bovine [1] and early developmental unagi tissues [2]. By transient transfection of bovine and unagi cells in reporter gene assays, the candidates were assessed for and ranked based on the intensity of their promoter activity. This subsequently informed the prioritization of selected promoters for incorporation into expression plasmids that drive expression of native growth factors in bovine and/or unagi cell lines to promote autonomous expansion in the absence of exogenous growth factors.

References

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