# Determination of Efficacies of Somatic Muscle Cell Transcription Factors for Direct Reprogramming into Induced Muscle Stem Cells

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The biochemical versatility of direct reprogramming—based upon induced pluripotency—is one that continuously intrigues the scientific community with its applications in regenerative medicine and simulation of human tissue in experimentation. The purpose of the experiment detailed in this paper is thus one that investigates the reprogramming efficacies of specific transcription-factor coding genes (hereon referred to as TFs) for myoblastic cell development, chosen for its role as the most basic and prevalent tissue unit of work in the human body. Various articles of scientific literature (notably those written by Yu, X., et. al and Weirauch, M. T., et al.) and data regarding TF signal expression and biochemical function obtained from various transcriptome databases, i.e. Amazonia (which entailed the use of one to three probes, each analyzing signal expression from five different muscle tissue samples), NCBI, OMIM, and KEGG, were collected and averaged for the extrapolation of the most efficacious TFs. From these calculations, comparisons were drawn between data analyzing the highest rates of signal expression, the biochemical significance in myoblastic differentiation, and the least potential for carcinoma, HIV-1, and other disease development. From this analysis, 5 out of 21 genes were evaluated as crucial for myoblastic direct reprogramming: MAMSTR, MYOD1, MEF2A, TBP, and EGR1. These five genes, controlling cellular functions ranging respectively from centralized administration of myoblastic differentiation to the promotion of cell growth and division, thus suggest that, in their absence, myoblastic cell differentiation cannot occur.