



Proteome expression profiling of differentiated versus undifferentiated mouse embryonic stem cells

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Embryonic stem cells (ESCs) are of immense interest as they are capable of dividing and renewing themselves for long periods of time and give rise to any adult cell type, serving as a potentially unlimited source for tissue replacement in regenerative medicine. Proteomics analysis showed to be an effective approach to comprehensively unravel the regulatory network of differentiation. We applied 2-DE based proteomic approach to gain more sight about the molecular mechanism of pluripotency of two ESC lines, Royan B1 and D3. The proteome profiling of differentiating cells of these stem cell lines at days 0, 6 and 18 of differentiation revealed 51 down-regulated and 17 up-regulated proteins in differentiated cells compared to ESCc in both lines. Thirty-five protein spots of ESCs could not be detected in at least one of differentiation stags. Mass spectrometry analysis of these regulated proteins led to identification of 90 proteins including participants in transcription; protein biosynthesis, folding, and degradation; signal transduction; cytoskeletal rearrangement; and regulation of cell cycle. To complement the proteomic approach, differential expression of a selection of these proteins was analyzed by quantitative real-time reverse transcription polymerase chain reaction. However, with the exception of SEP1, no concordance was detected between the changes in levels of gene and protein expression during mouse ESCs differentiation. In conclusion, proteomics can reveal novel markers that can be used for ESCs isolation and monitoring differentiation.