An Online Compendium of CHO RNA-Seq Data Allows Identification of CHO Cell Line-specific Transcriptomic Signatures - DTU Orbit (22/12/2018)

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Chinese hamster ovary (CHO) cell lines can fold, assemble and modify proteins post-translationally to produce human-like proteins; as a consequence, it is the single most common expression systems for industrial production of recombinant therapeutic proteins. A thorough knowledge of cultivation conditions of different CHO cell lines has been developed over the last decade, but comprehending gene or pathway-specific distinctions between CHO cell lines at transcriptome level remains a challenge. To address these challenges, we compiled a compendium of 23 RNA-Seq studies from public and in-house data on CHO cell lines, i.e. CHO-S, CHO-K1 and DG44. Significantly differentially expressed (DE) genes particularly related to subcellular structure and macromolecular categories were used to identify differences between the cell lines. A R-based web application was developed specifically for CHO cell lines to further visualize expression values across different cell lines, and make available the normalized full CHO data set graphically as a CHO research community resource. This study quantitatively categorizes CHO cell lines based on patterns at transcriptomic level and detects gene and pathway specific key distinctions among sibling cell lines. Studies such as this can be used to select desired characteristics across various CHO cell lines. Furthermore, the availability of the data as an internet-based application can be applied to broad range of CHO engineering applications.

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