The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line

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Chinese hamster ovary (CHO)-derived cell lines are the preferred host cells for the production of therapeutic proteins. Here we present a draft genomic sequence of the CHO-K1 ancestral cell line. The assembly comprises 2.45 Gb of genomic sequence, with 24,383 predicted genes. We associate most of the assembled scaffolds with 21 chromosomes isolated by microfluidics to identify chromosomal locations of genes. Furthermore, we investigate genes involved in glycosylation, which affect therapeutic protein quality, and viral susceptibility genes, which are relevant to cell engineering and regulatory concerns. Homologs of most human glycosylation-associated genes are present in the CHO-K1 genome, although 141 of these homologs are not expressed under exponential growth conditions. Many important viral entry genes are also present in the genome but not expressed, which may explain the unusual viral resistance property of CHO cell lines. We discuss how the availability of this genome sequence may facilitate genome-scale science for the optimization of biopharmaceutical protein production.

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