



ZNANSTVENI SASTANAK
GENOMSKE TEHNOLOGIJE



Genomika CHO stanica
- dosezi i izazovi u farmaceutskoj biotehnologiji -

CHO cells genomics
- trends and challenges in pharma biotechnology -

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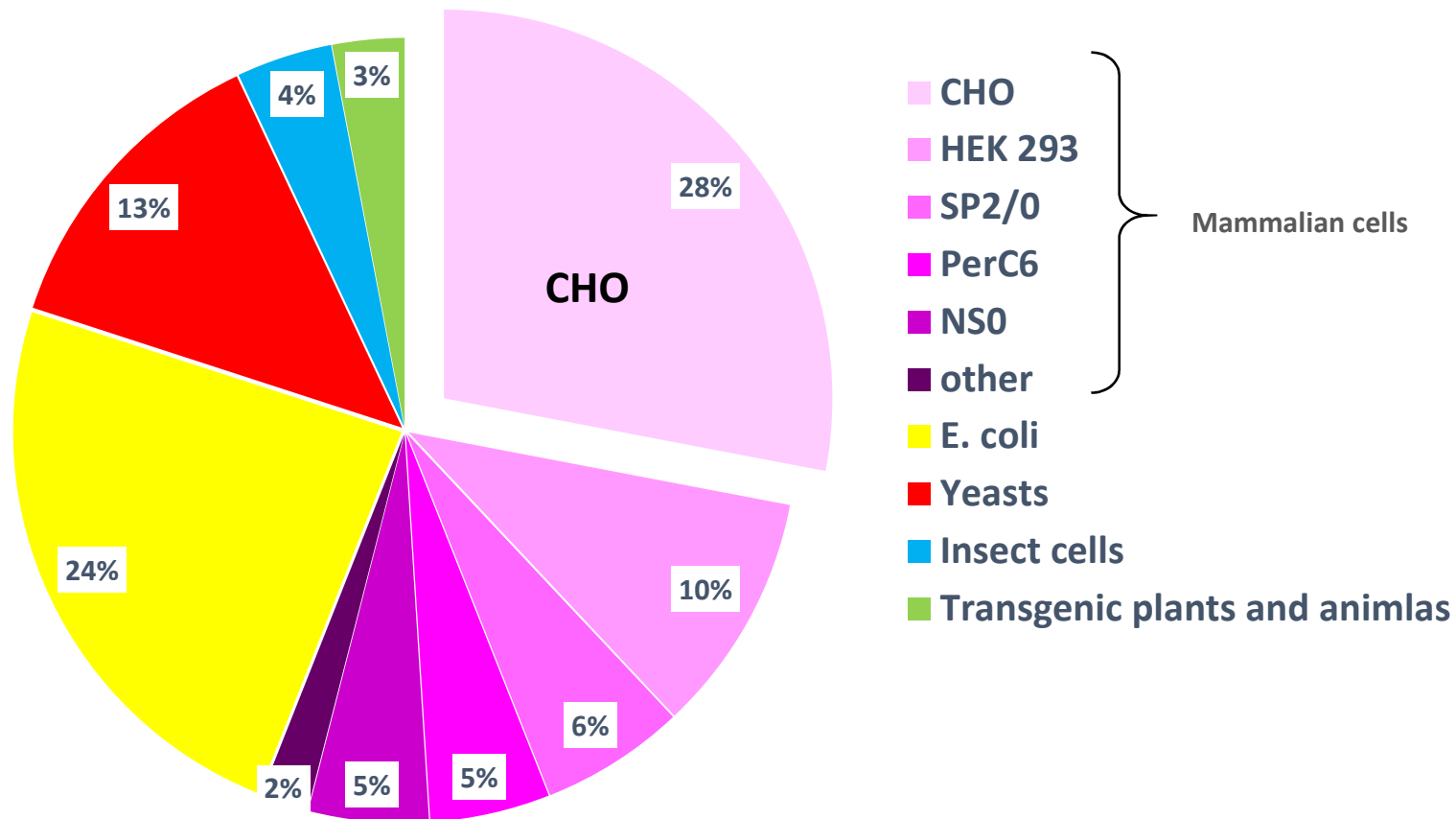
Chinese hamster ovary (CHO) cells

T. Puck (1957) from *Boston Cancer Research Foundation*

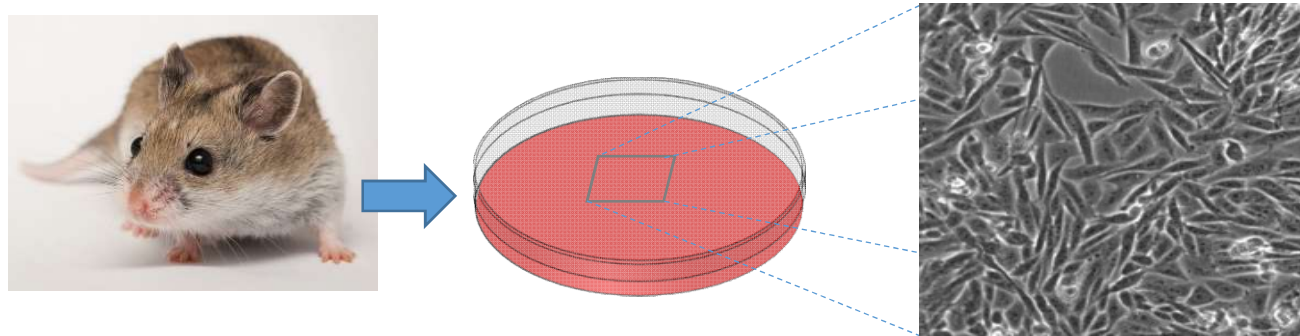


Chines hamster (*Cricetulus griseus*)

Expression systems for therapeutic protein production



Reasons for CHO cell success in biotechnology



Small number of chromosome

- Human 46; Mouse 48 (Lab strains 40); Chinese hamster 22

Frequent, easily quantified chromosomal aberration

- At the time (cold war, nuclear weapon testing) CHO cells were used as standard for irradiation research

Large number of genetic variants available

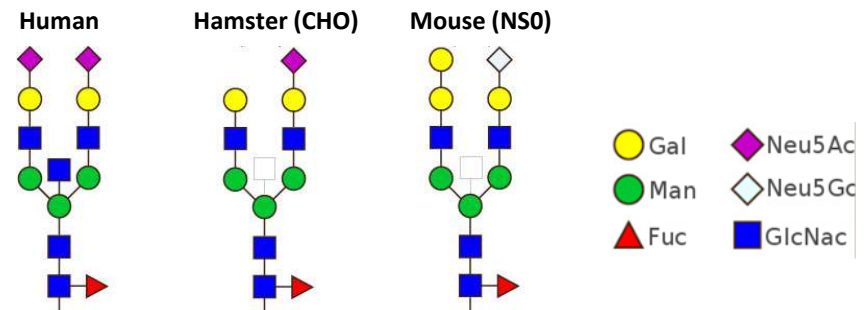
- Modified by irradiation or viral transduction
- Mutants for amino-acid (gs-) or nucleotide synthesis (dhfr-)

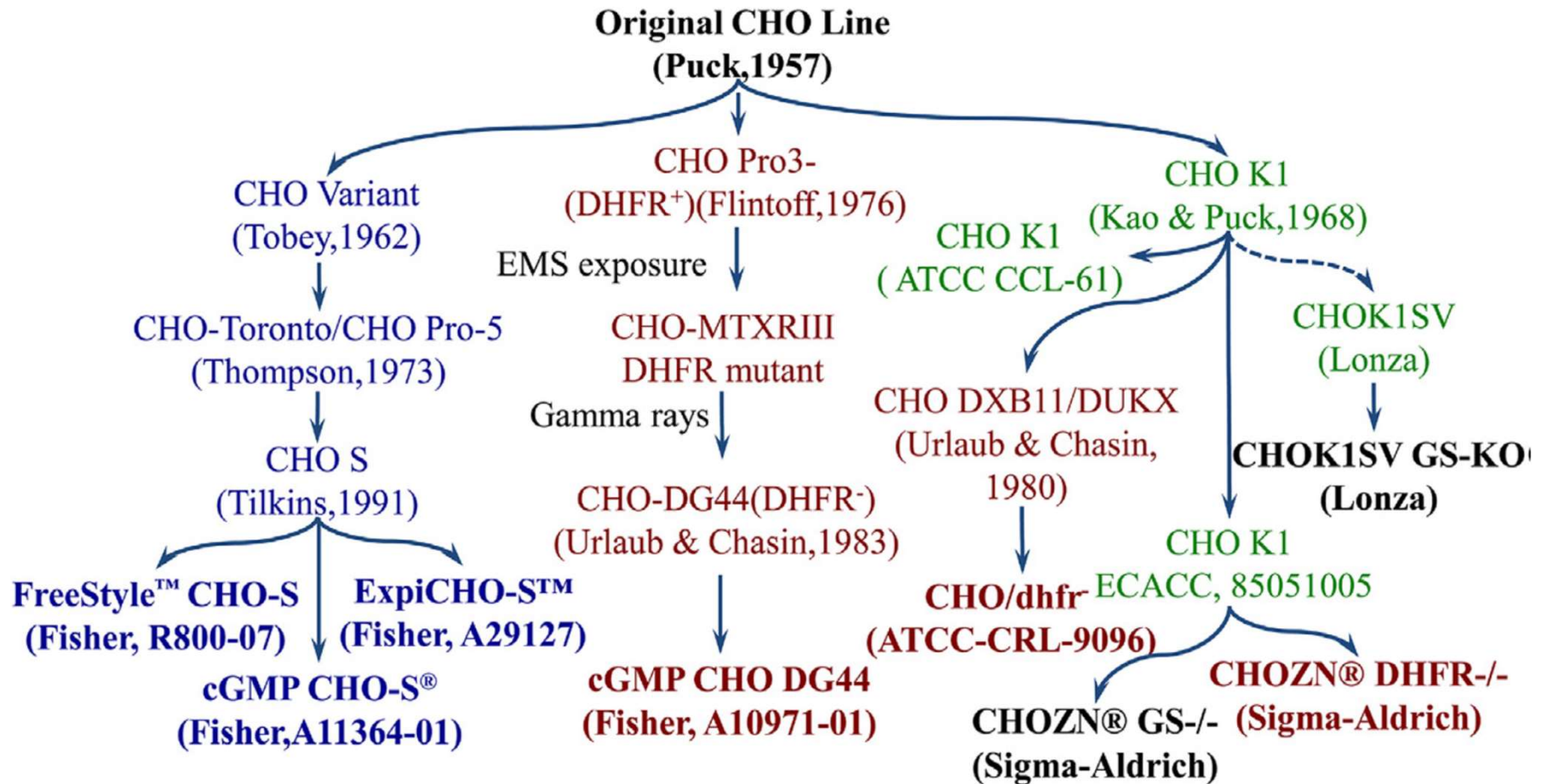
Lacks significant number of viral receptors

- Resistant to viral infection/contamination

Posttranslational protein modifications → human-like

- Standard disulfide bonds
- Glycosylation pattern similar to human

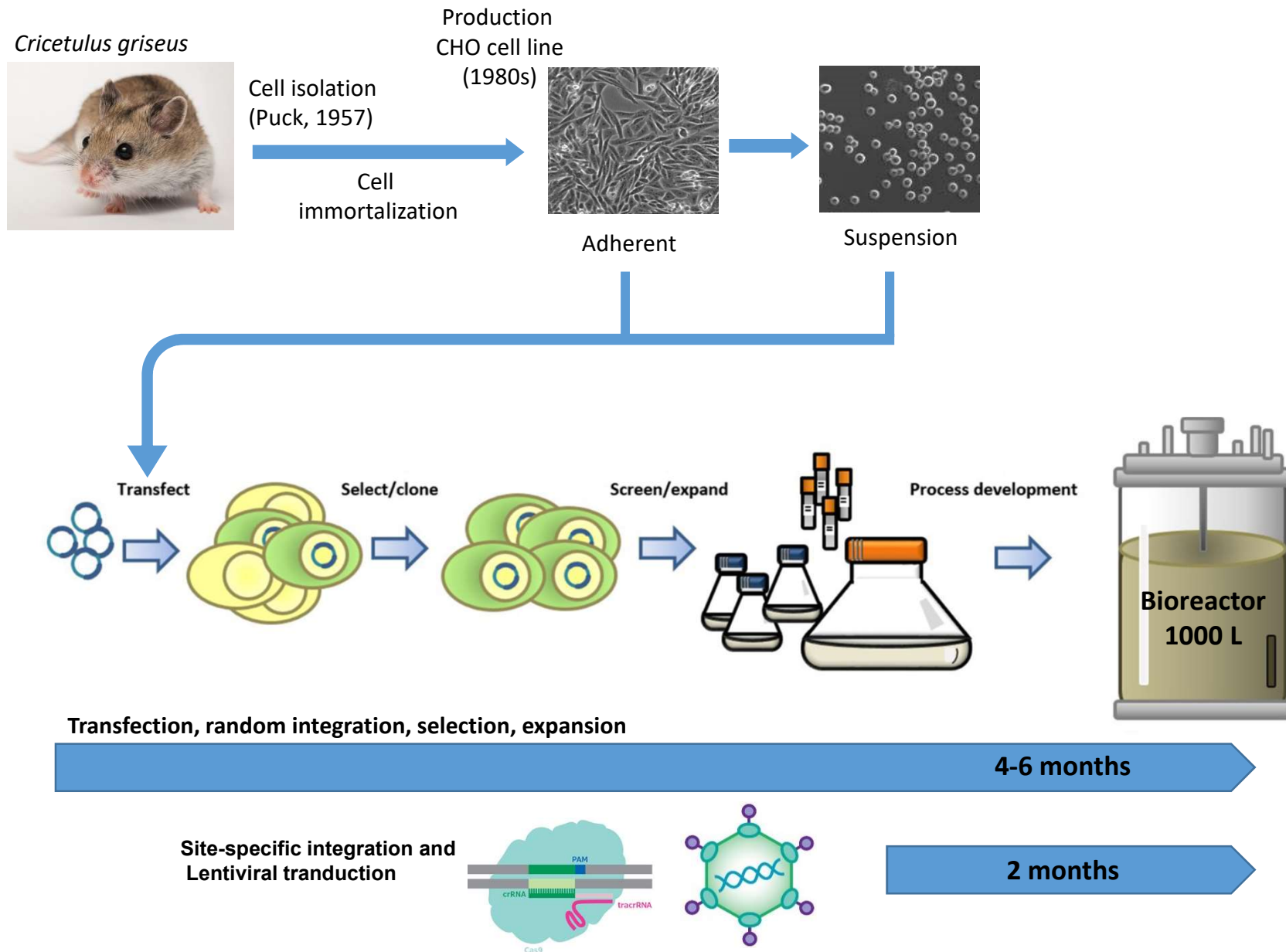




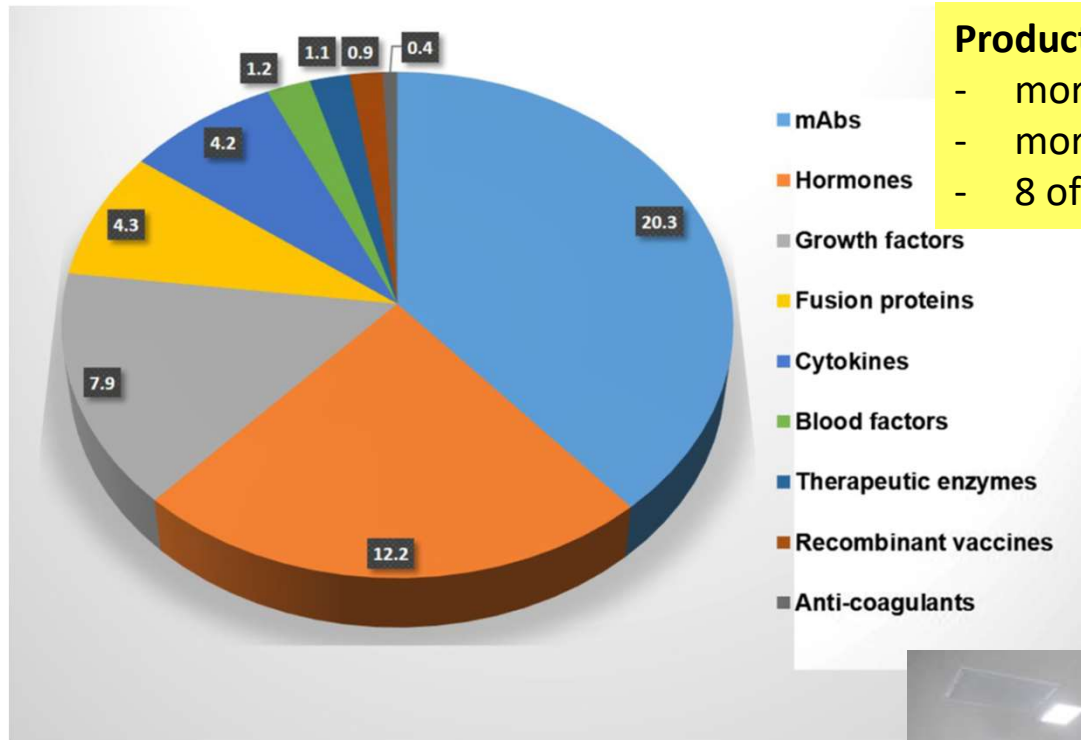
CHO cell lineage

The generation of nutritional auxotrophs led to the development of a powerful gene amplification systems used to produce therapeutic proteins in CHO cells.

CHO cell line development for stable r-protein production



Mammalian cell culture technology (2016)



Products

- more than 100 biotherapeutics (mAbs 20%)
- more than 400 in the pipeline
- 8 of 10 best-selling drugs



Platform technology

- Cells grow in suspension
- Cell doubling time 18-24h
- Protein free growth media
- r-protein production:
IgG → standard 3 g/L
titers up to 20 g/L reported



Lewis N.E. et al. (2013) Genomic landscapes of Chinese hamster ovary cell lines as revealed by the *Cricetulus griseus* draft genom. *Nat. Biotech.* 8 (31) 759–765.

Brinkrolf, K. et al. (2013) Chinese hamster genome sequenced from sorted chromosomes. *Nat. Biotechnol.* 31, 694–695

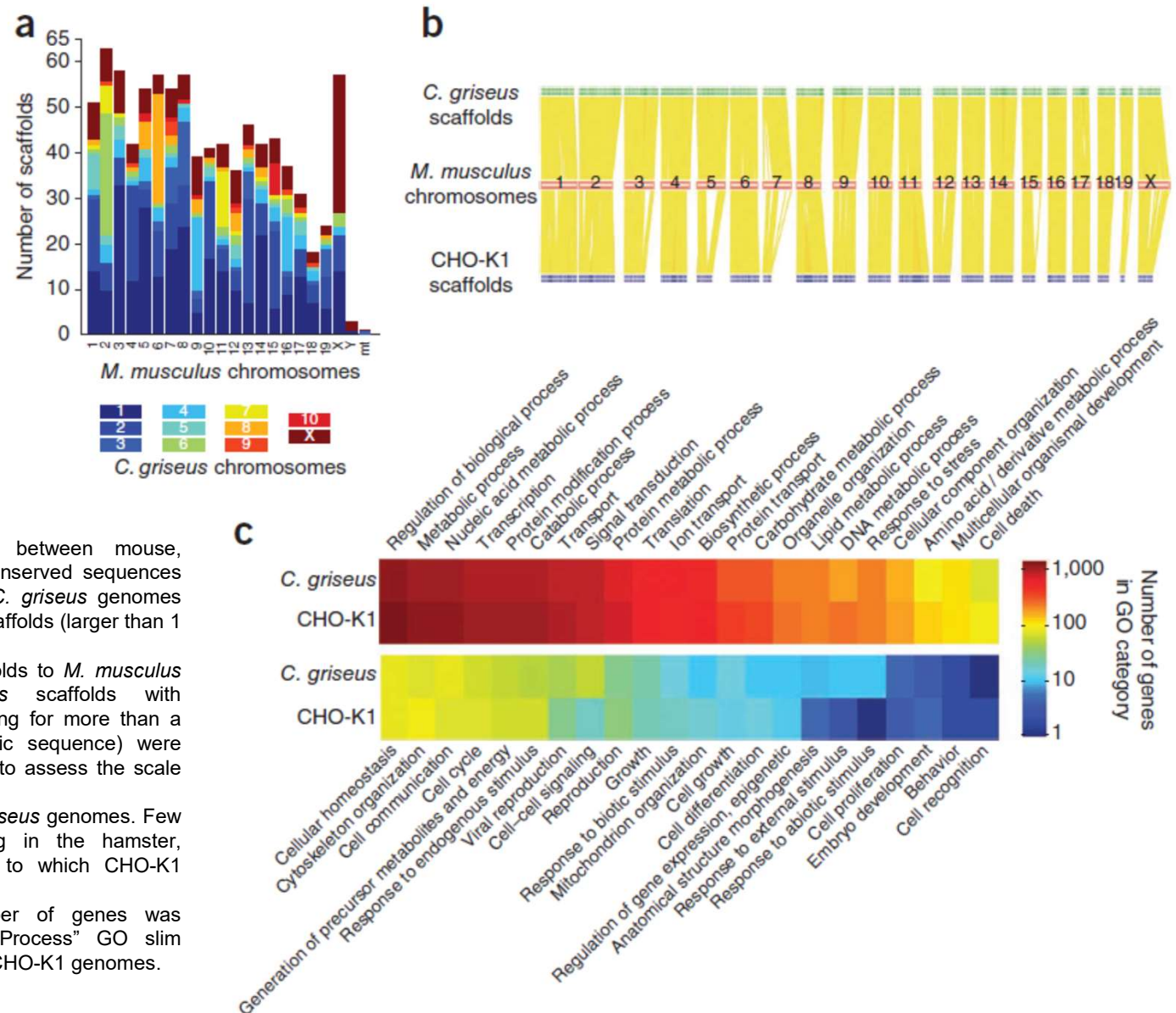


Figure 2. Genome comparison between mouse, Chinese hamster and CHO-K1. Conserved sequences among the mouse, CHO-K1 and *C. griseus* genomes were determined by aligning their scaffolds (larger than 1 Mb) to the mouse genome.

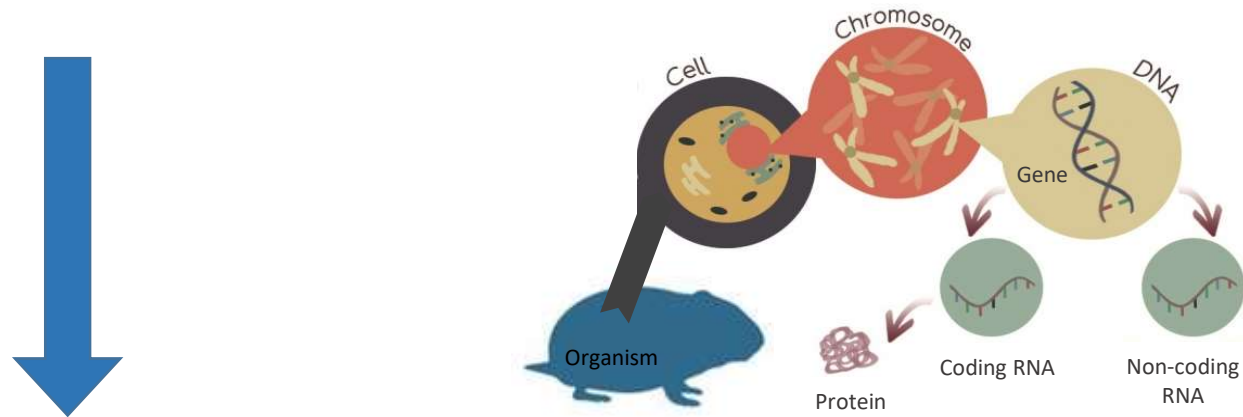
(a) Assignment of *C. griseus* scaffolds to *M. musculus* chromosomes. The *C. griseus* scaffolds with chromosomal assignment (accounting for more than a quarter of the 2.4 Gb of genomic sequence) were compared to mouse chromosomes to assess the scale of chromosomal rearrangement.

(b) Alignment of CHO-K1 and *C. griseus* genomes. Few large DNA stretches are missing in the hamster, whereas there are more regions to which CHO-K1 scaffolds could not align.

(c) Gene annotation. The number of genes was determined for each “Biological Process” GO slim category in both the *C. griseus* and CHO-K1 genomes.

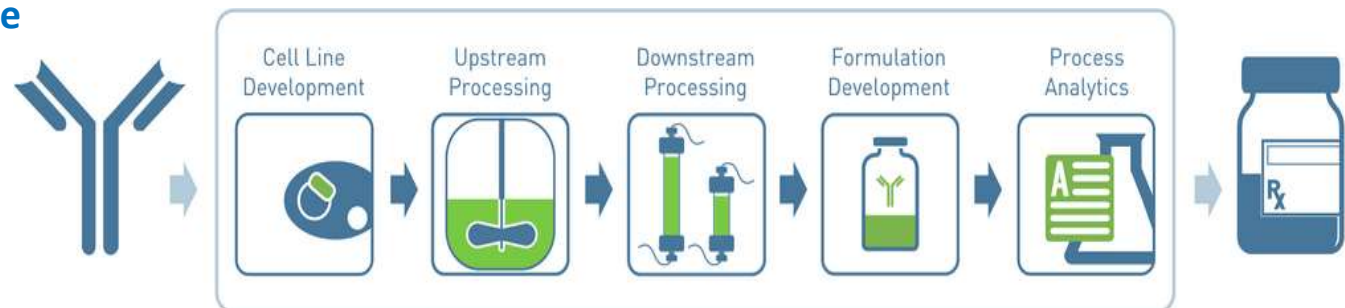
CHO genome:

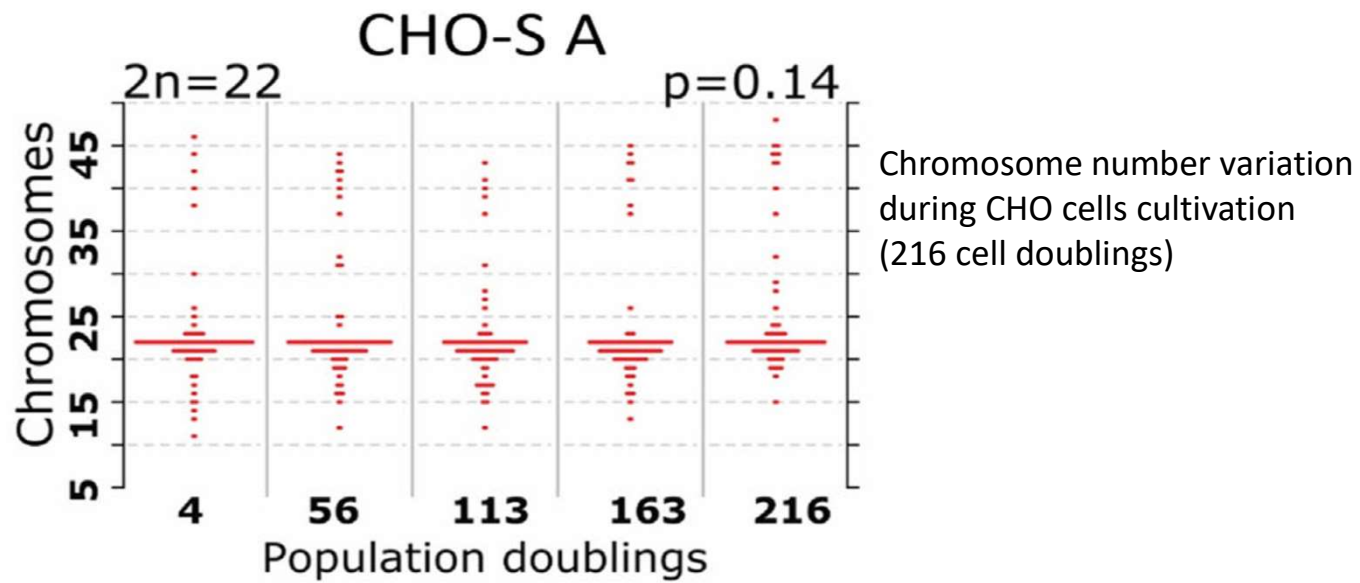
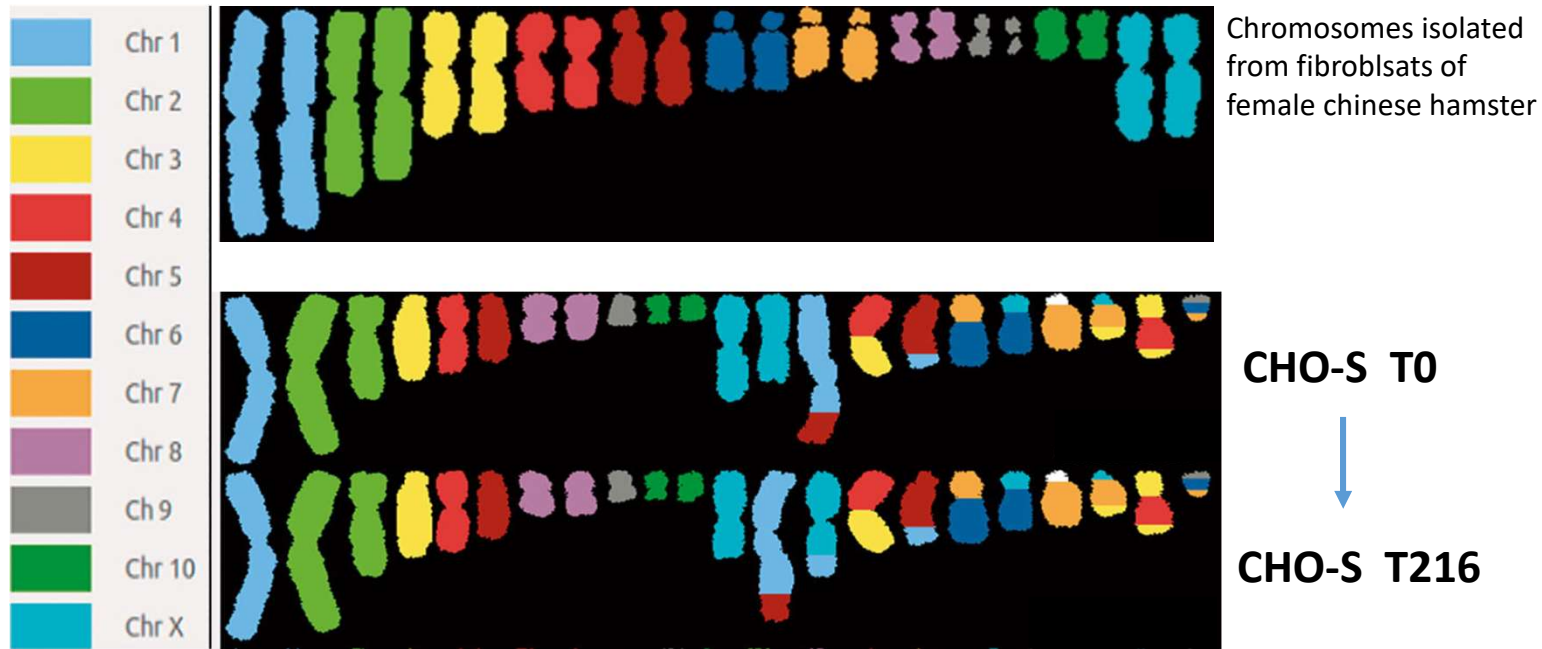
- ca. **2.35 Gb**, ca. **28k genes** and 10-13k expressed in every cell
- Contains genes for more than **100 cell types**
- Multiple levels of regulation: chromatin state, transcription, post-transcription, translation, post-translation, protein activity



Reflection in biotech therapeutic production:

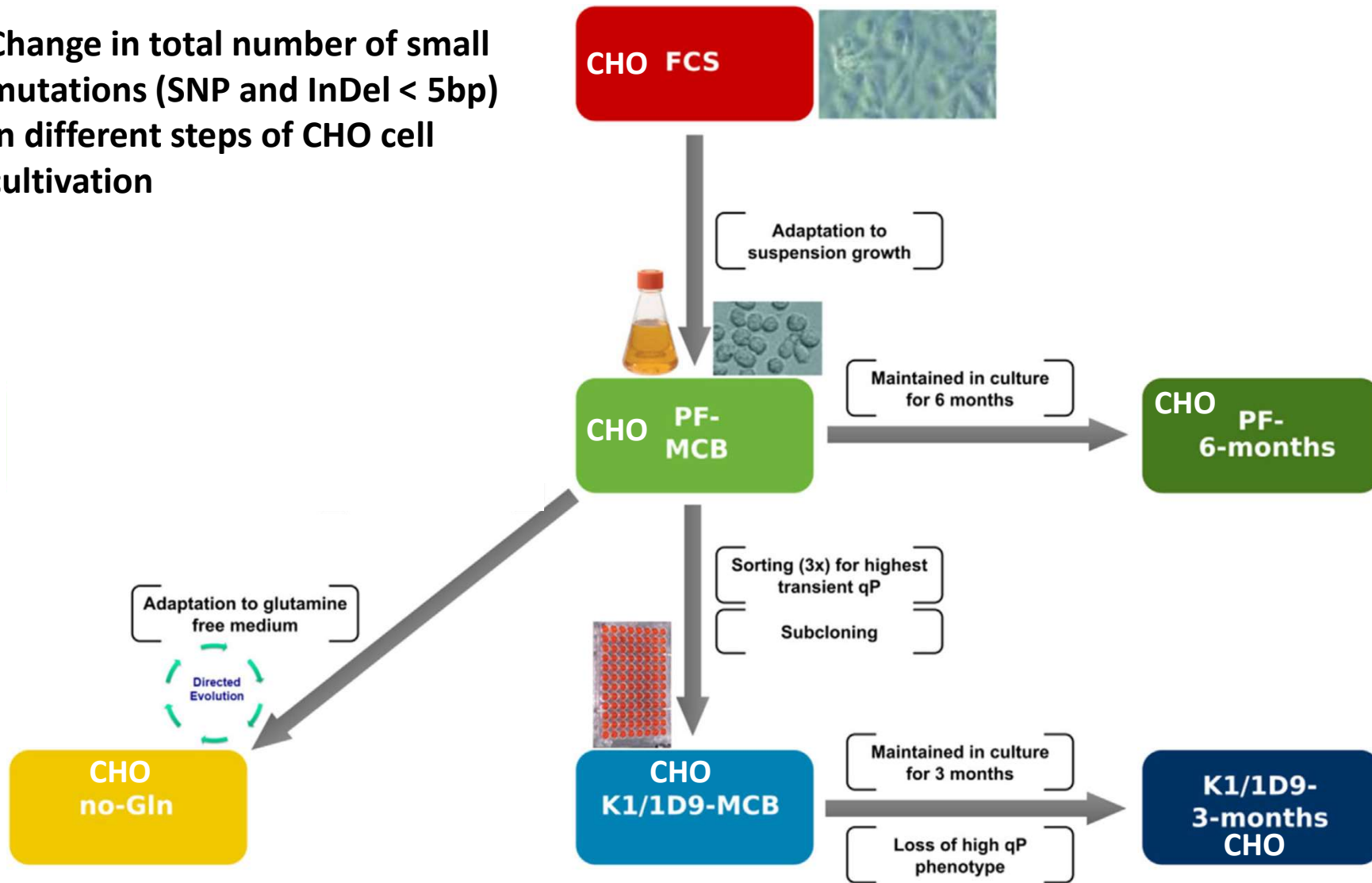
- High genomic **variation** even within clonal population → subclones
- Gene expression **instability**
- **Lack** of production process predictability
- **Big effort** in GMP and QC documentation
- **Delay** in product commercialization
- Product **price increase**





Veclar S. et al (2018) Karyotype variation of CHO host cell lines over time in culture characterized by chromosome counting and chromosome painting. *Biotech. Bioeng.* 115:165–173

Change in total number of small mutations (SNP and InDel < 5bp) in different steps of CHO cell cultivation



Data mining tools

<https://chogenome.org>

The screenshot shows the homepage of CHOgenome.org. At the top, there is a navigation menu with 'General Info', 'Genomes', 'Resources', and 'Partners'. The main content area is divided into three columns. The left column features a 'Featured Article' titled 'A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism' published on November 3, 2016. The middle column has a 'Search RefSeq' section with a search box and a 'Search' button. Below this is a 'Welcome to the CHO Genome website!' message and links for 'CHOSTart' and 'CHOMine'. The right column contains an 'Events' section with 'Previous Events' including a 'Mammalian Systems Biotechnology Workshop' in Singapore (August 11-12, 2016) and a 'Cell Culture Engineering XV' conference in La Quinta, California (May 8-13, 2016). At the bottom, there is a 'News' section and several small circular icons.

- The access point for all publicly available genome-wide data of chinese hamster and CHO cell lines
- CHOgenome-specific literature
- CHO-specific BLAST service

<https://chomine.boku.ac.at>

The screenshot displays the CHOMine v1.0.0 interface, described as 'An integrated database for Cricetus griseus and CHO cells'. The top navigation bar includes 'Home', 'Templates', 'Lists', 'QueryBuilder', 'Regions', 'Data Sources', 'API', 'License', 'CHOModel', and 'MyMine'. A search bar at the top right contains the text 'e.g Th, G3IGV3' and a 'GO' button. The main interface is divided into three primary sections: 'Search', 'Analyse', and 'Welcome Back!'. The 'Search' section prompts users to search for names, identifiers, or keywords for genes, proteins, pathways, ontology terms, authors, etc., with an example 'e.g. X, Y, Z' and a 'SEARCH' button. The 'Analyse' section asks for a list of identifiers, with a dropdown menu for 'Gene' and an example 'e.g. P97891_Q8NH3, Q5DKN8', and an 'ANALYSE' button. The 'Welcome Back!' section includes a 'TAKE A TOUR (VIA FLYMINE)' button. Below these sections, there are tabs for 'GENES' and 'PROTEINS'. The 'GENES' tab is active, showing 'Genes of CHOMine Read more' and a 'Query for genes:' section with a radio button for 'Gene' and a link for 'Proteins'. A 'More queries' link is also present. A green diagonal banner in the bottom right corner reads 'popular queries'.

- A warehouse for CHO genome data with analysis tools
- Provides links to external websites and integrates recently published genome scale models
- Translates gene IDs and names
- Support cell line engineering approaches and CHO cell bioprocesses

CHO cells in Croatian biotech



Biosimilar production (rhEPO) in CHO cells

Parnham M.J. *et al.* (2007) Non-clinical safety studies on biosimilar recombinant human erythropoietin 100(2):73-83.



Biosimilar production → filgrastim

Non-glycosylated form in *E. coli*
CHO?



BIotech Student graduation theses



prehrambeno
biotehnološki
fakultet

Sveučilište
u Zagrebu

Laboratory for cell culture technology and biotransformation

Current HRZZ research project *Hydro-pep-cell* (2017) (prof. V. Gaurina Srček)
- growth media optimisation for improved (CHO) cell cultivation

Thank you for your attention!

