

Jiří Kaňka

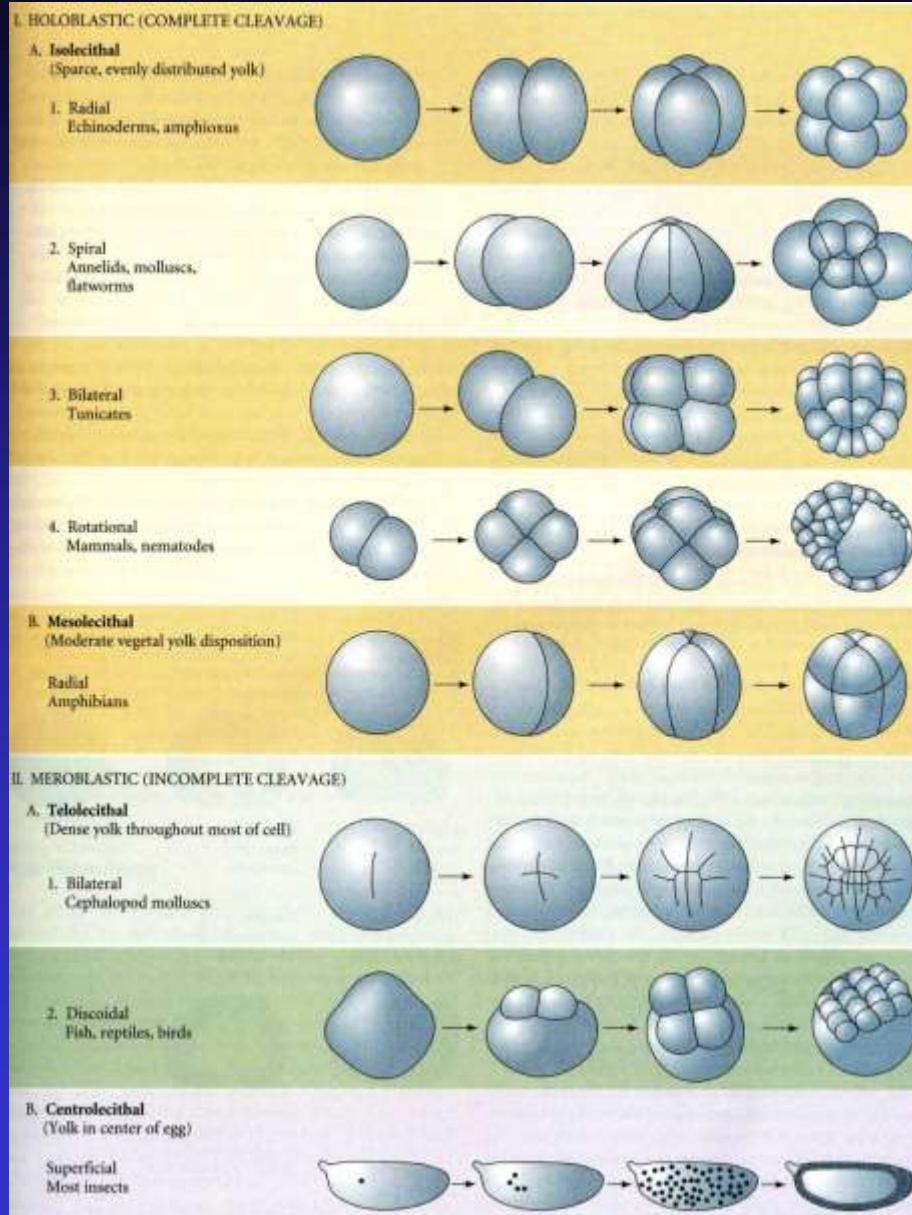
Embryonální vývoj savců

Ústav živočišné fyziologie a genetiky
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Summary of the main patterns of cleavage

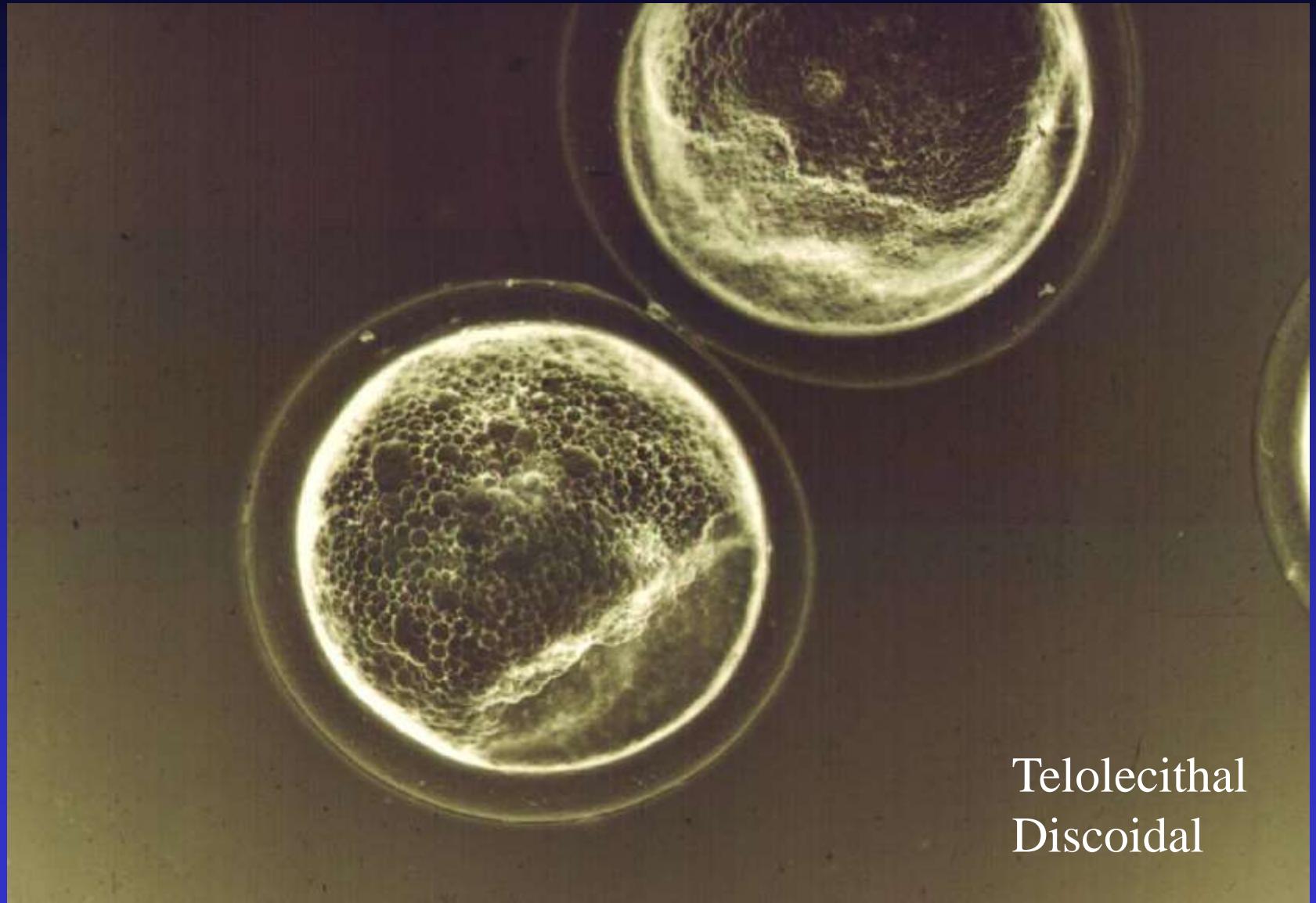
Isolecithal



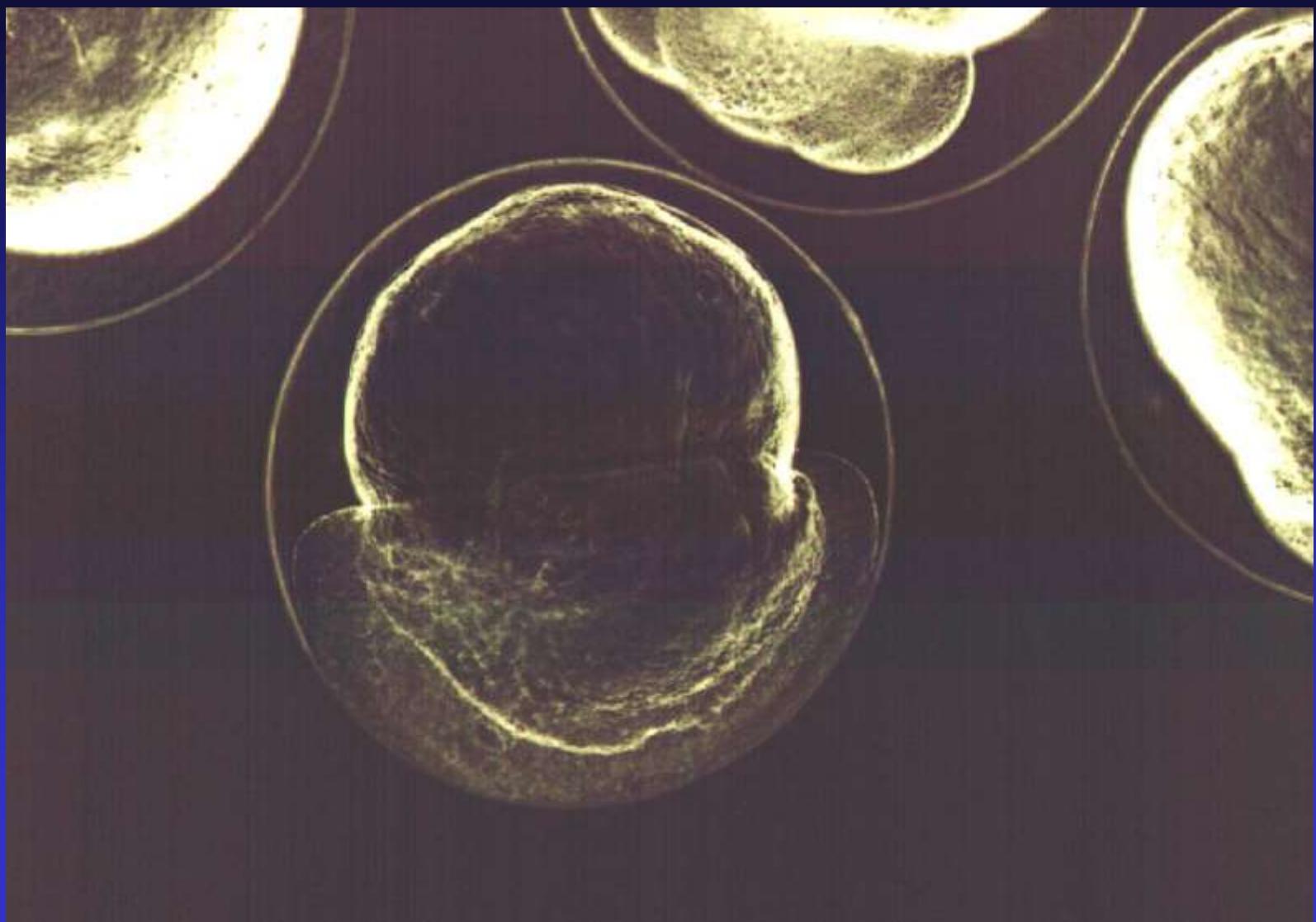
Mesolecithal

Telolecithal

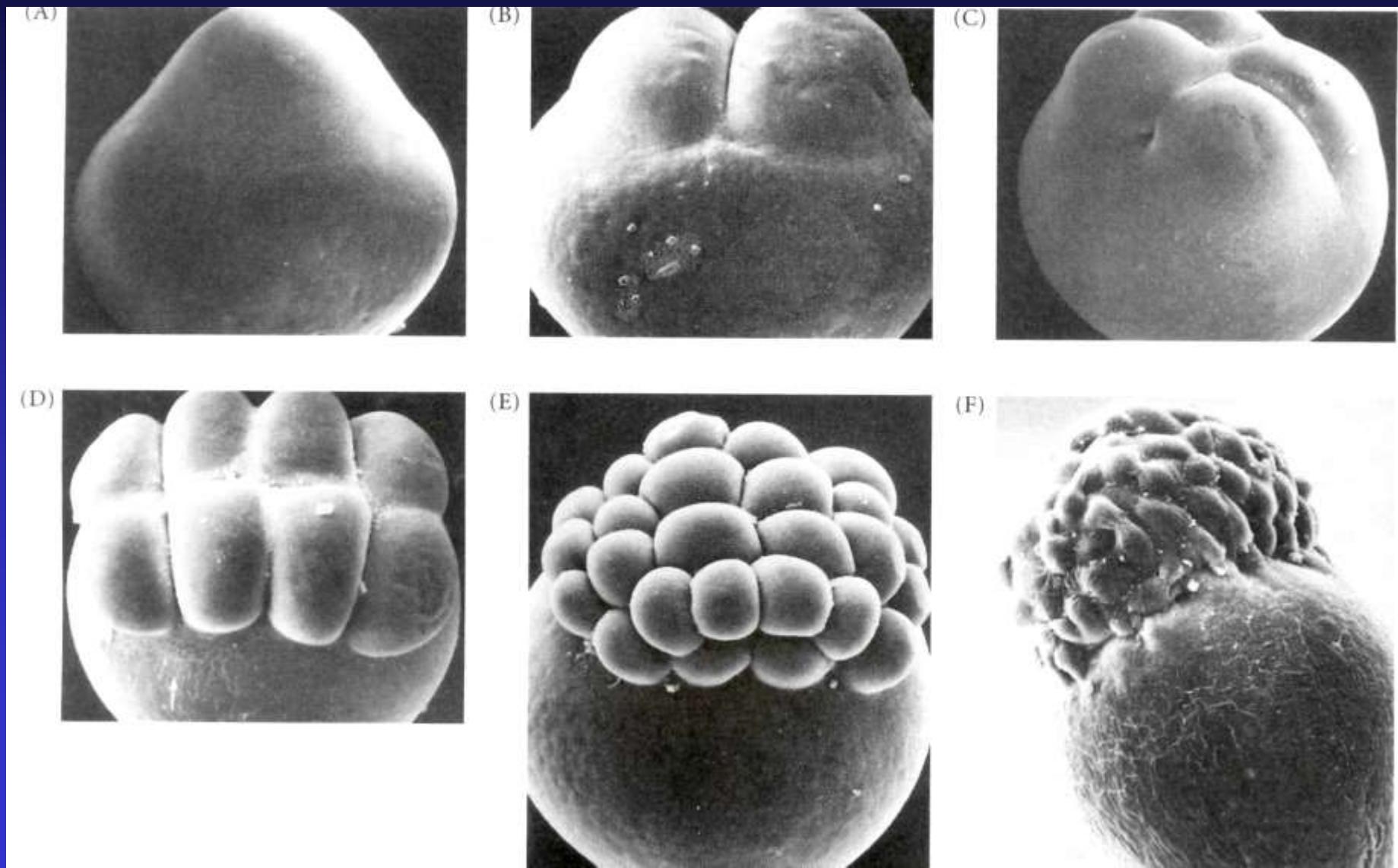
Centrolecithal

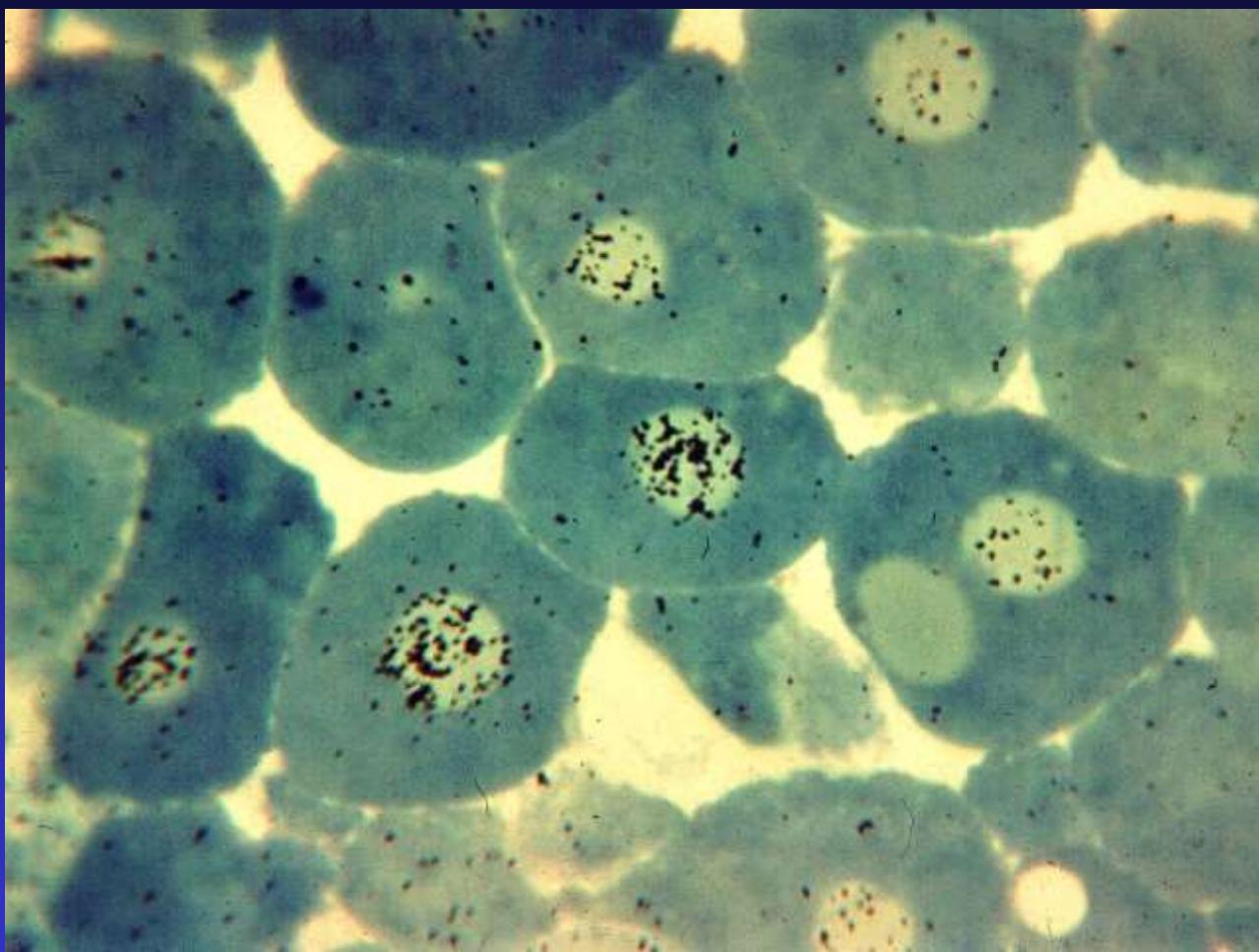


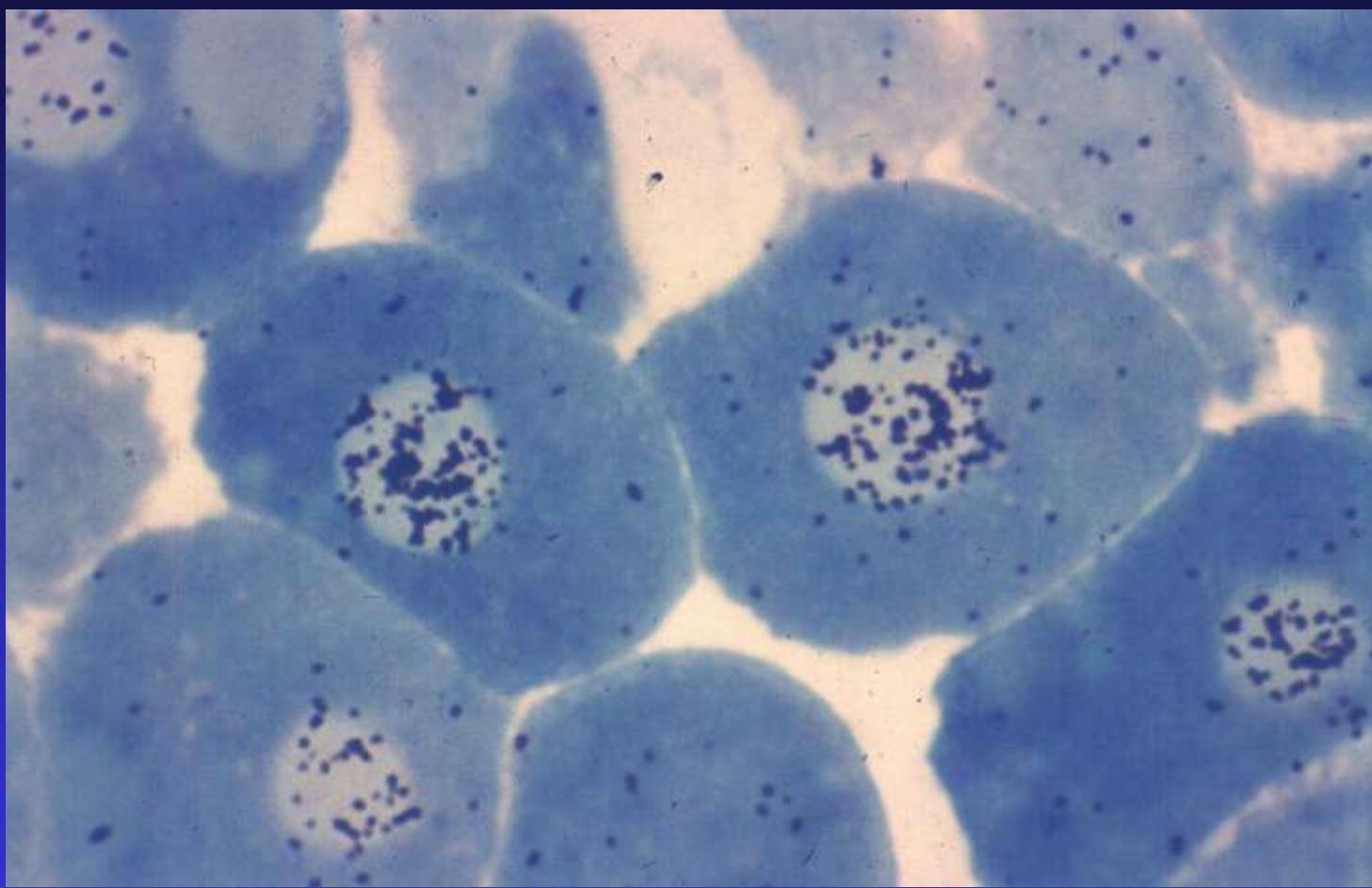
Telolecithal
Discoidal



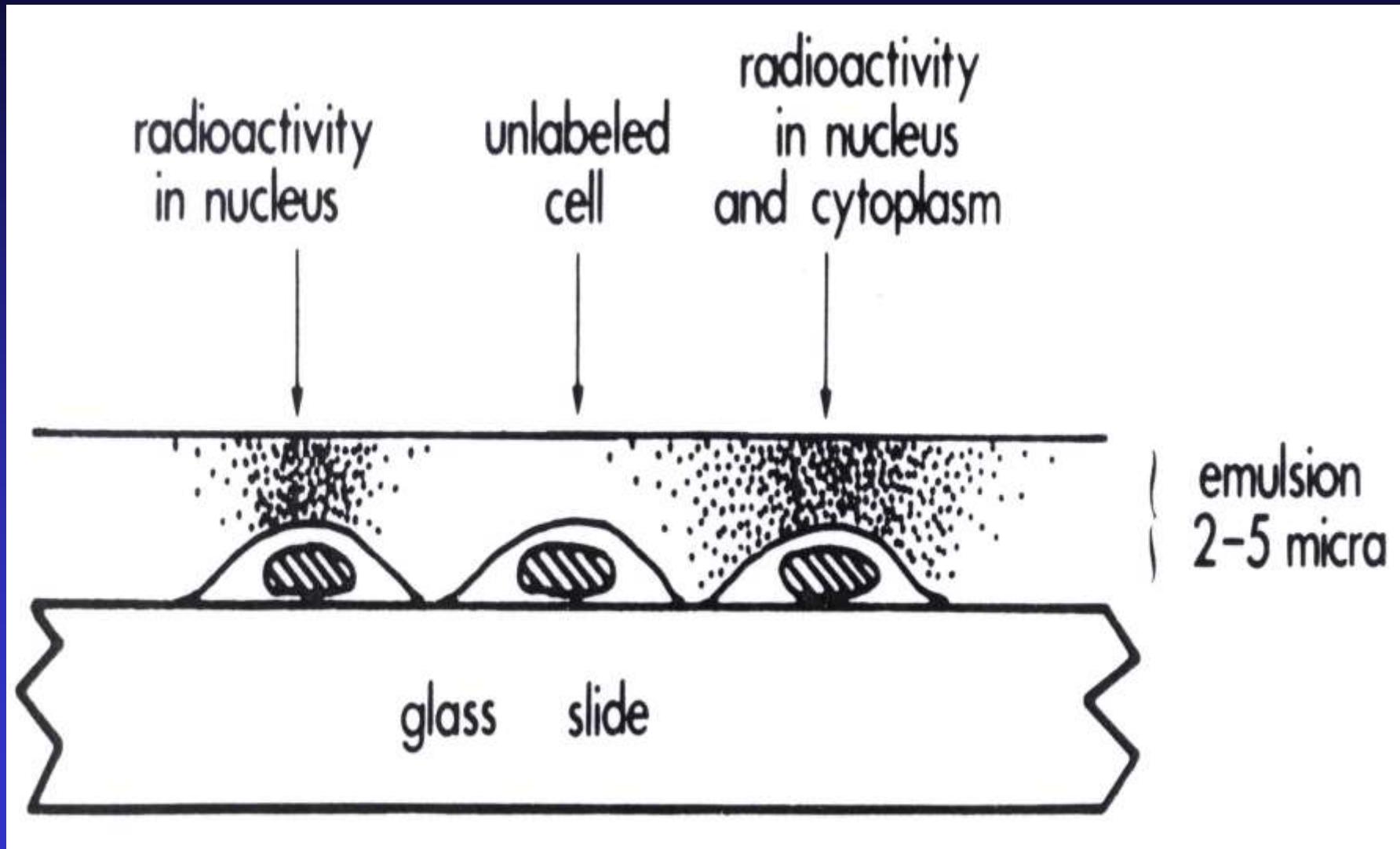
Discoidal cleavage in zebrafish egg



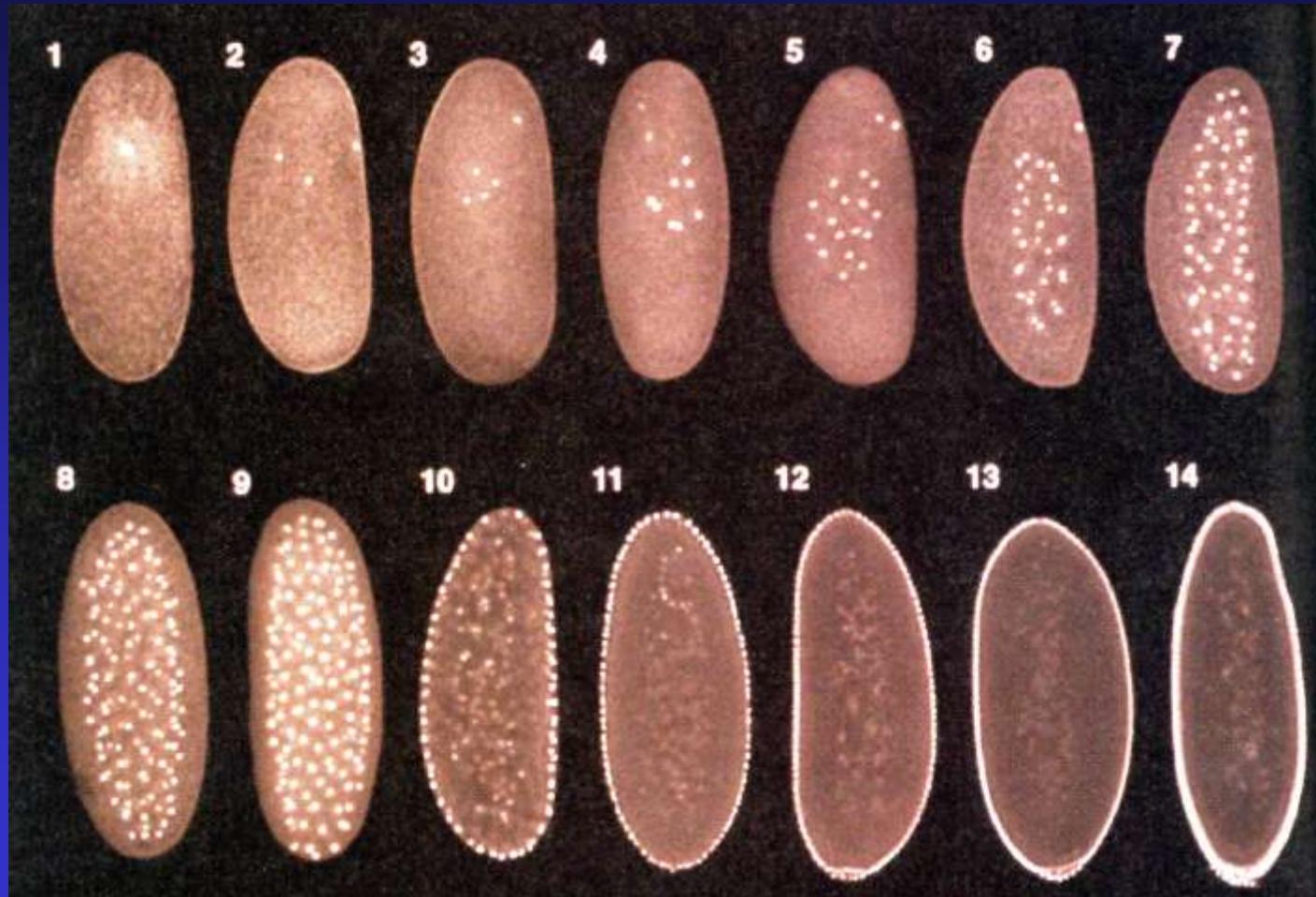




Autoradiografie

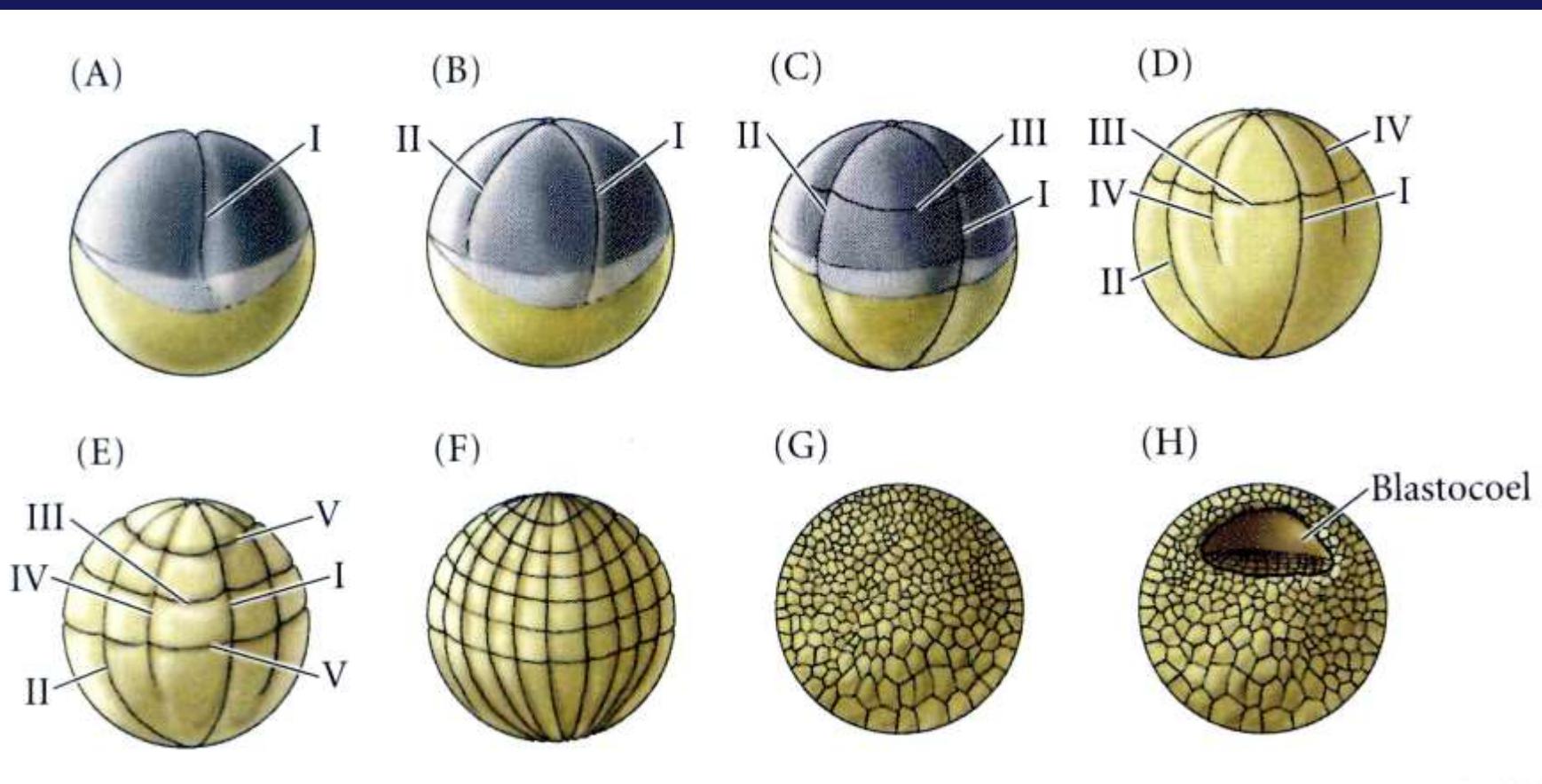


Superficial cleavage in a *Drosophila* embryo

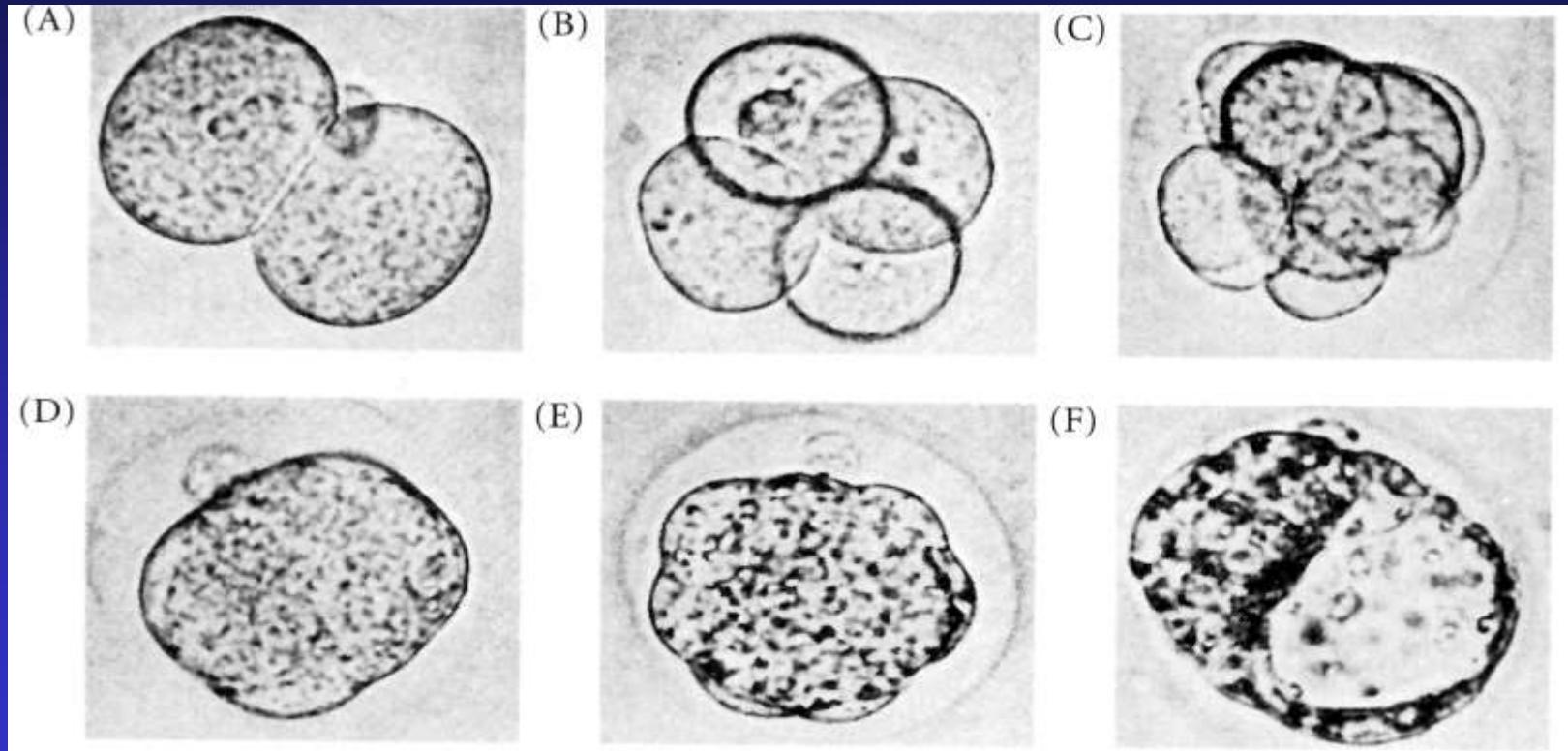


Centrolecithal

Cleavage of a frog egg (Mesolecithal, radial)



Cleavage of a single mouse *in vitro*



Isolecithal

Mus musculus

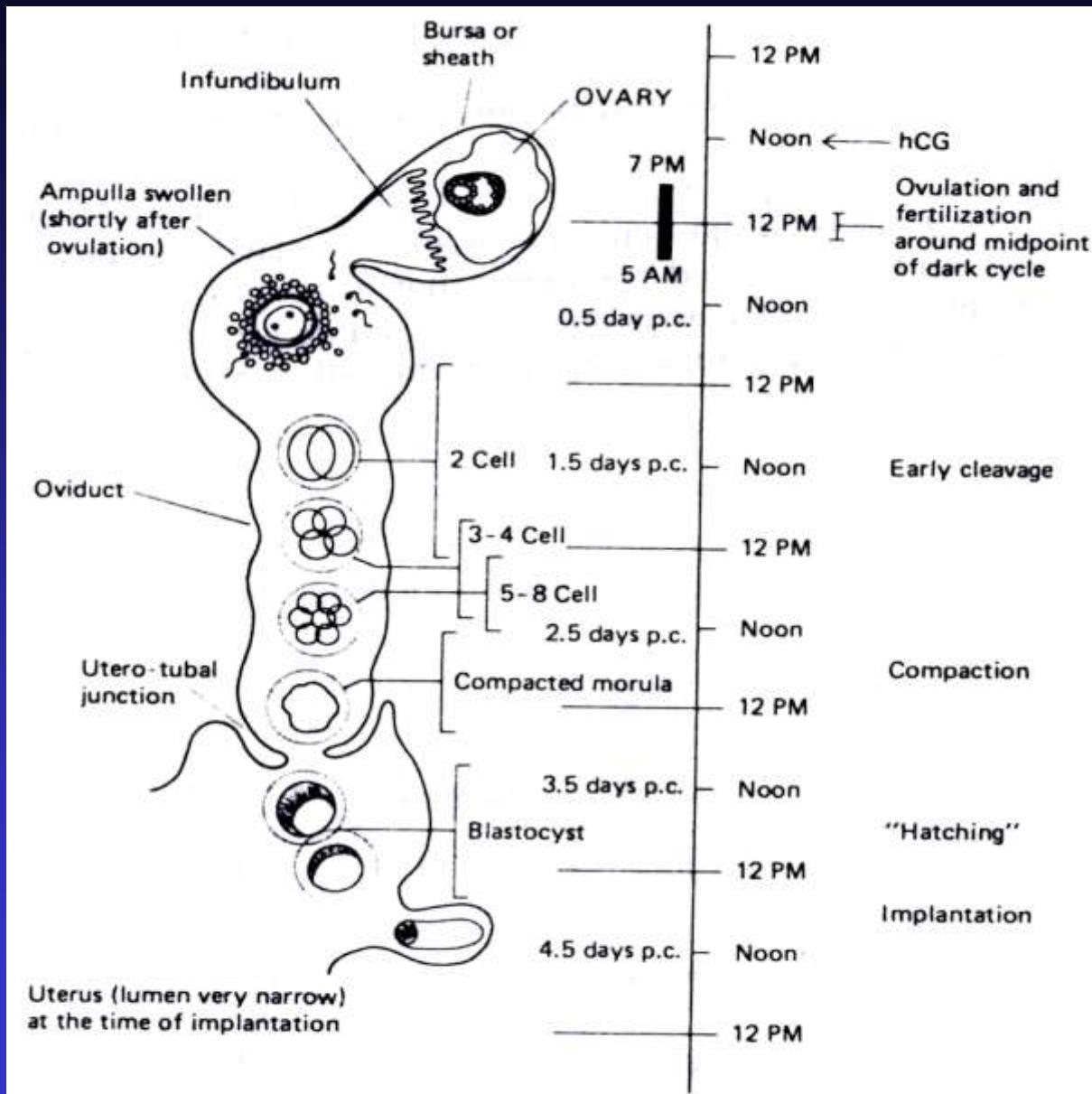
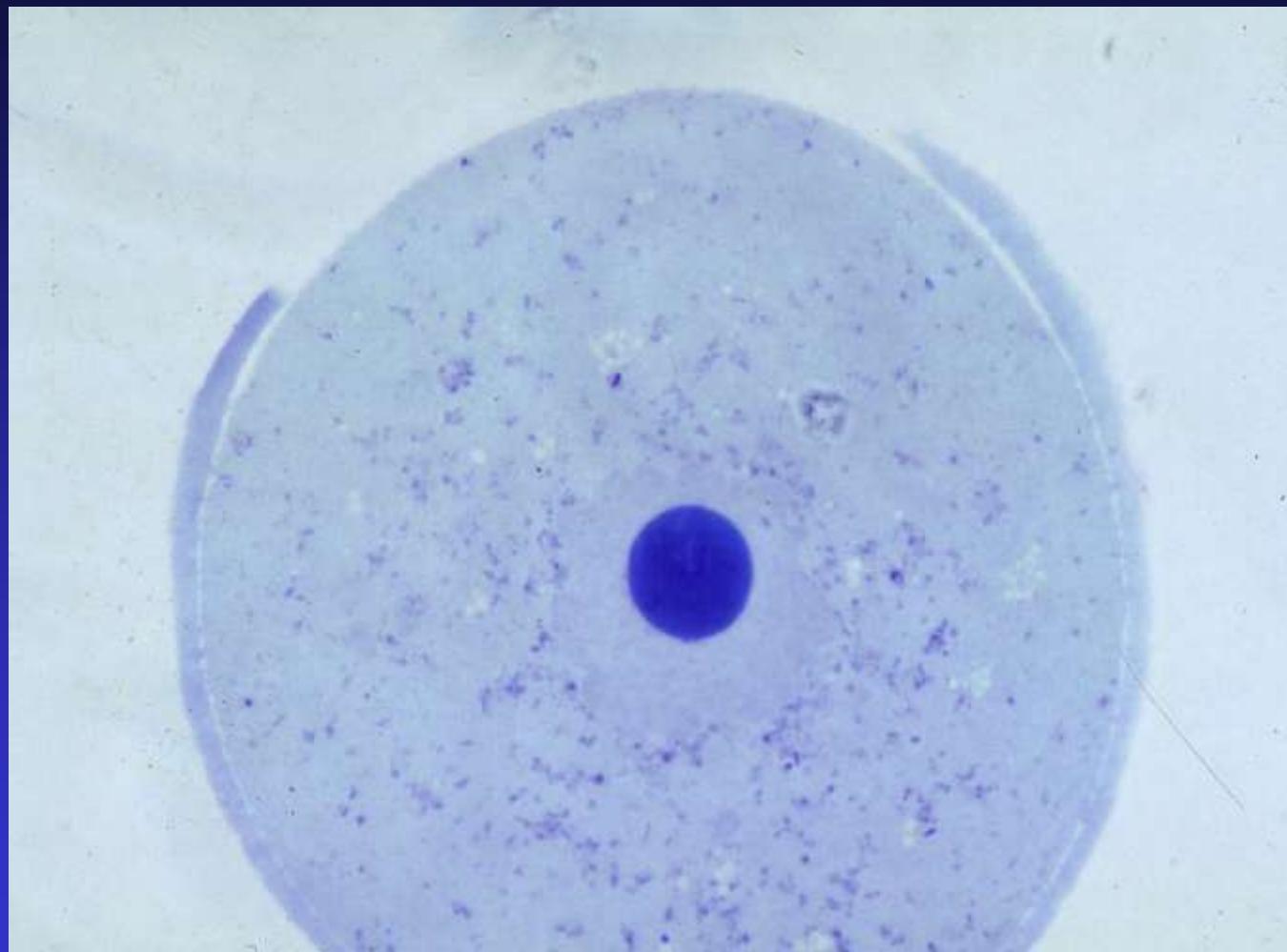
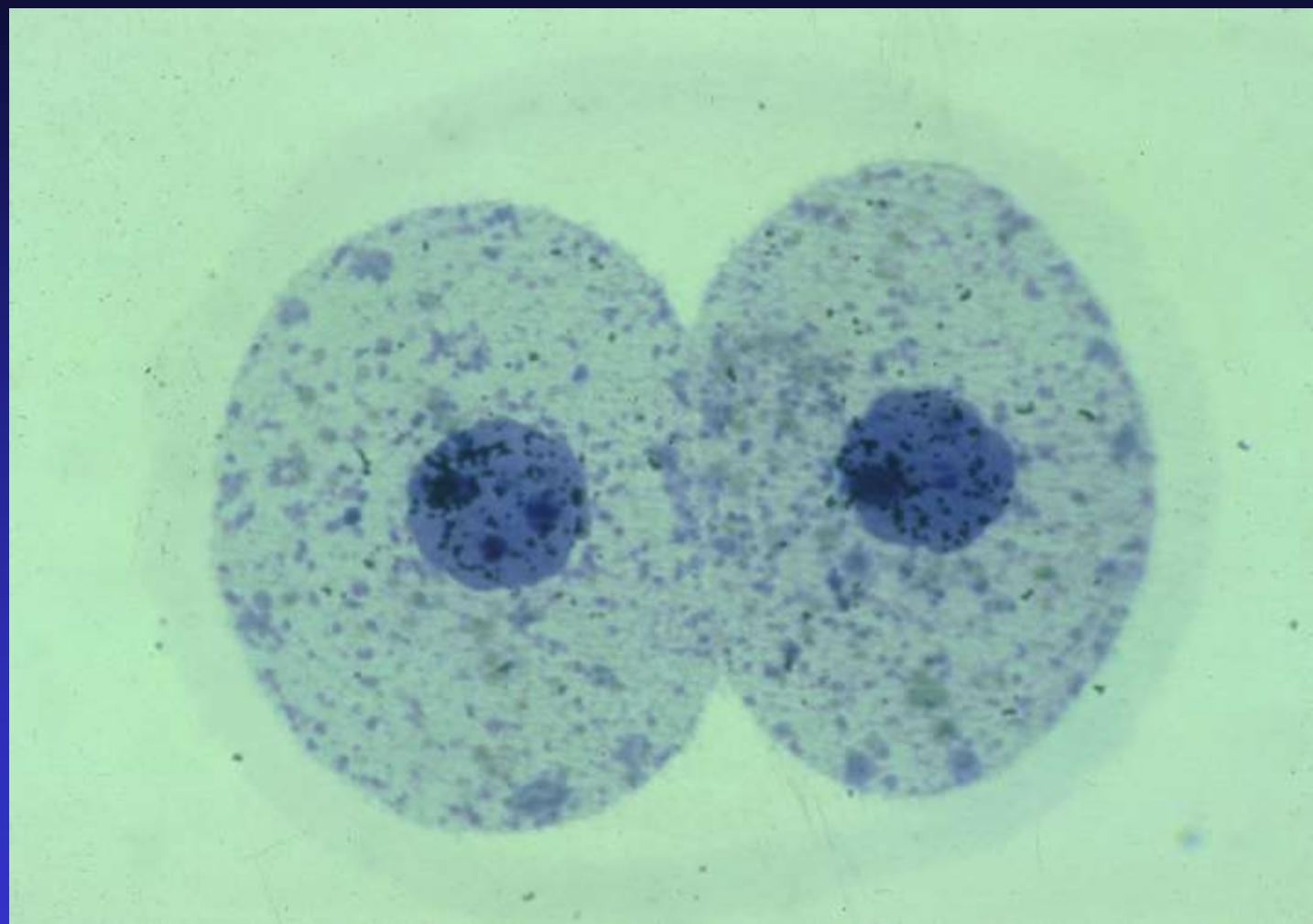
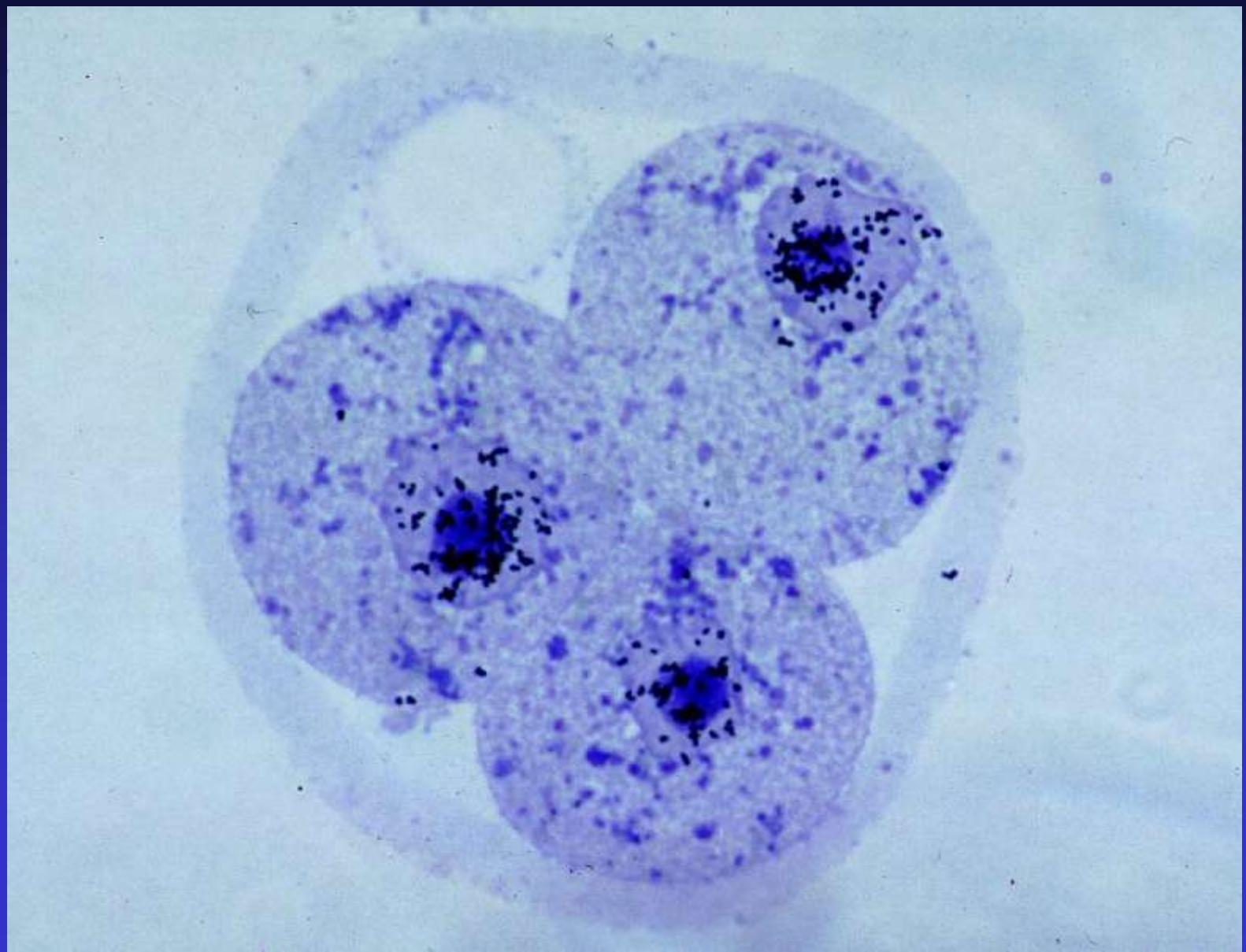


Figure 9 Summary of preimplantation development.

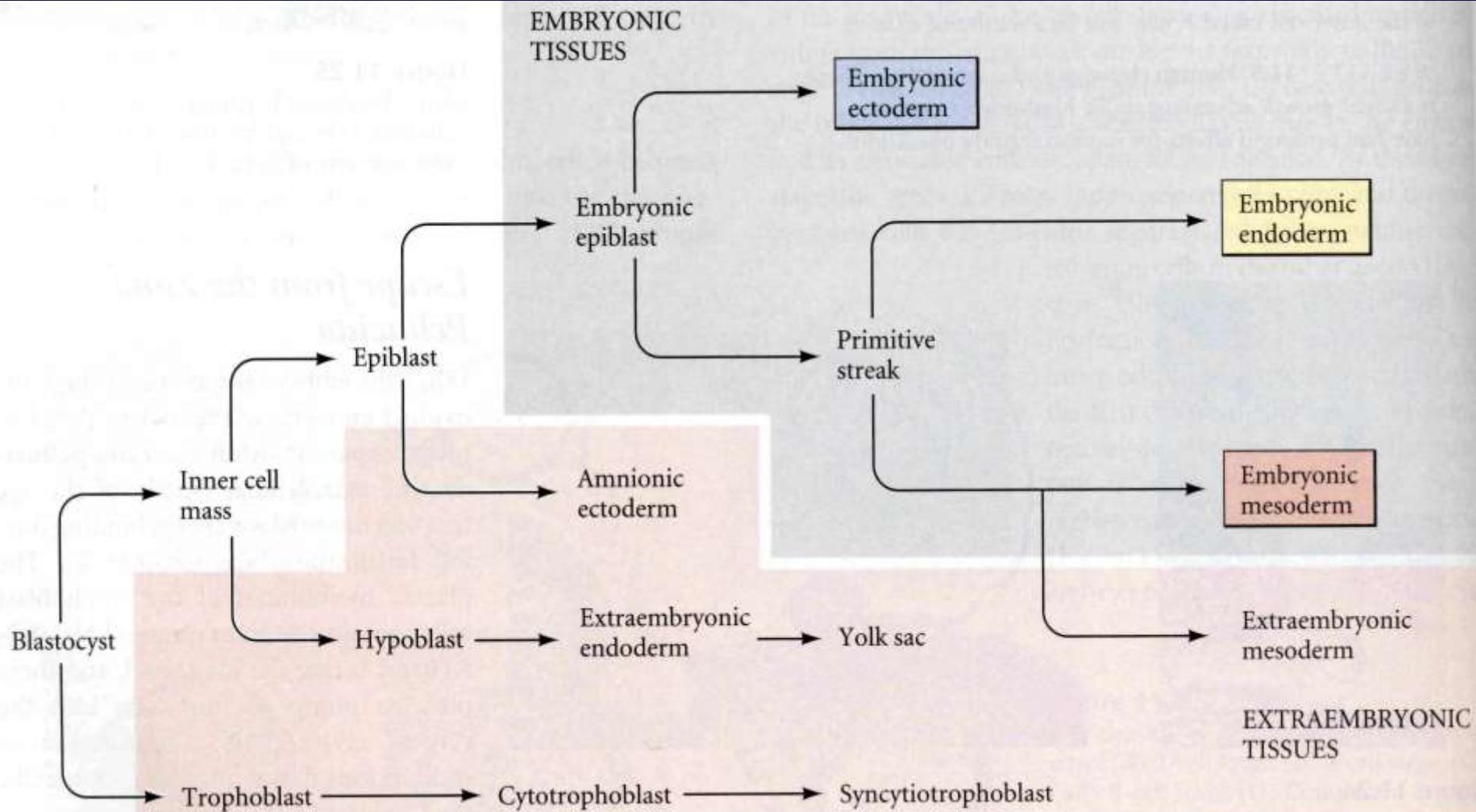






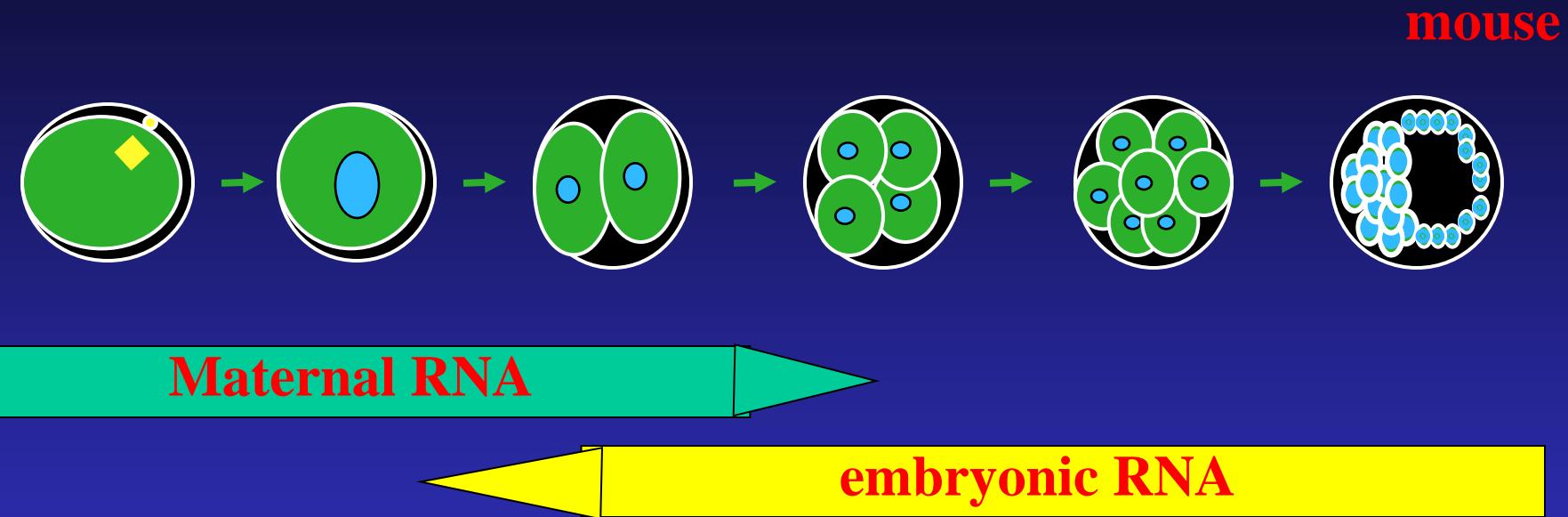


Derivation of tissues in human and rhesus monkey embryos



Gene expression

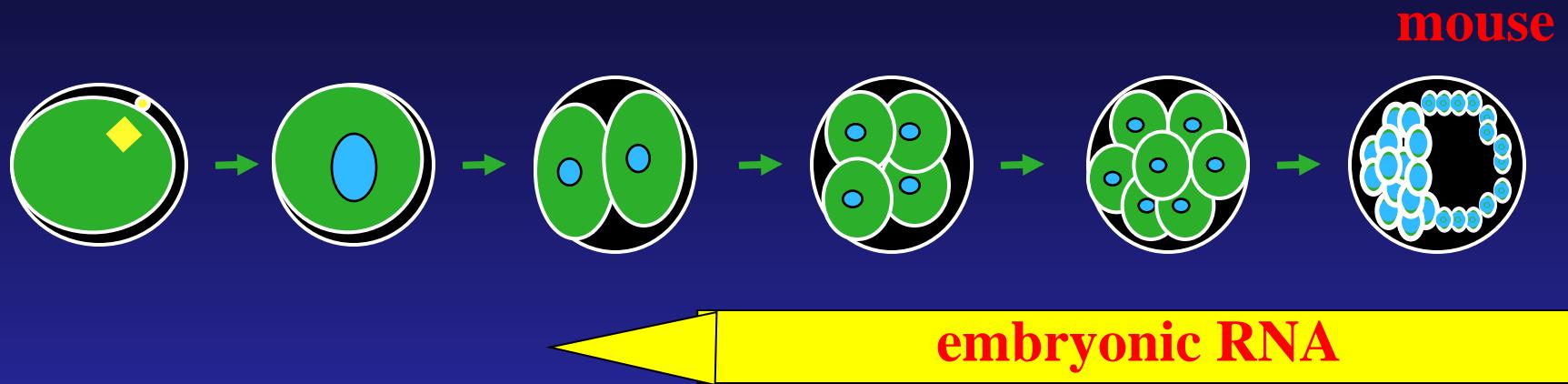
Embryonic genome activation (EGA)



Pre-implantation period of mammalian development is characterized by important developmental transitions that occur following fertilisation

In vitro culture system
cryopreservation techniques
nuclear transfer techniques

Development of ideas about embryonic genome activation (EGA)

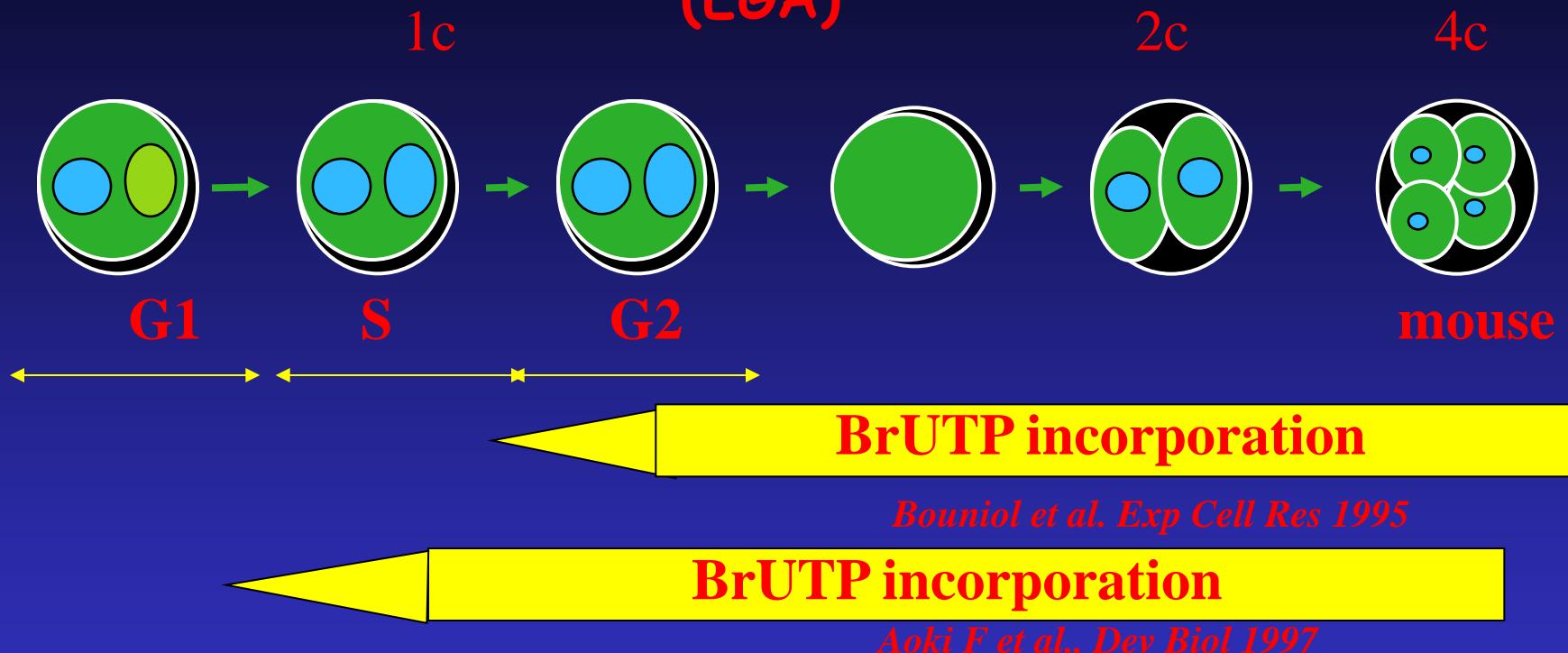


-poly (A)+ and poly (A)- RNA synthesis revealed transcription at the 2-cell stage (*Clegg, Piko, Nature 1982; J Embryol Exp Morph 1983*).

-HSP 68 and HSP 70 (*Bensaude et al., Nature 1983*), 67kDa polypeptides (*Flach et al., EMBO J 1982*), which synthesis it was possible to inhibit by α -amanitin

- EGA starts at the 2-cell stage, with a minor activation event at the early 2-cell stage and major activation event at the late 2-cell stage.

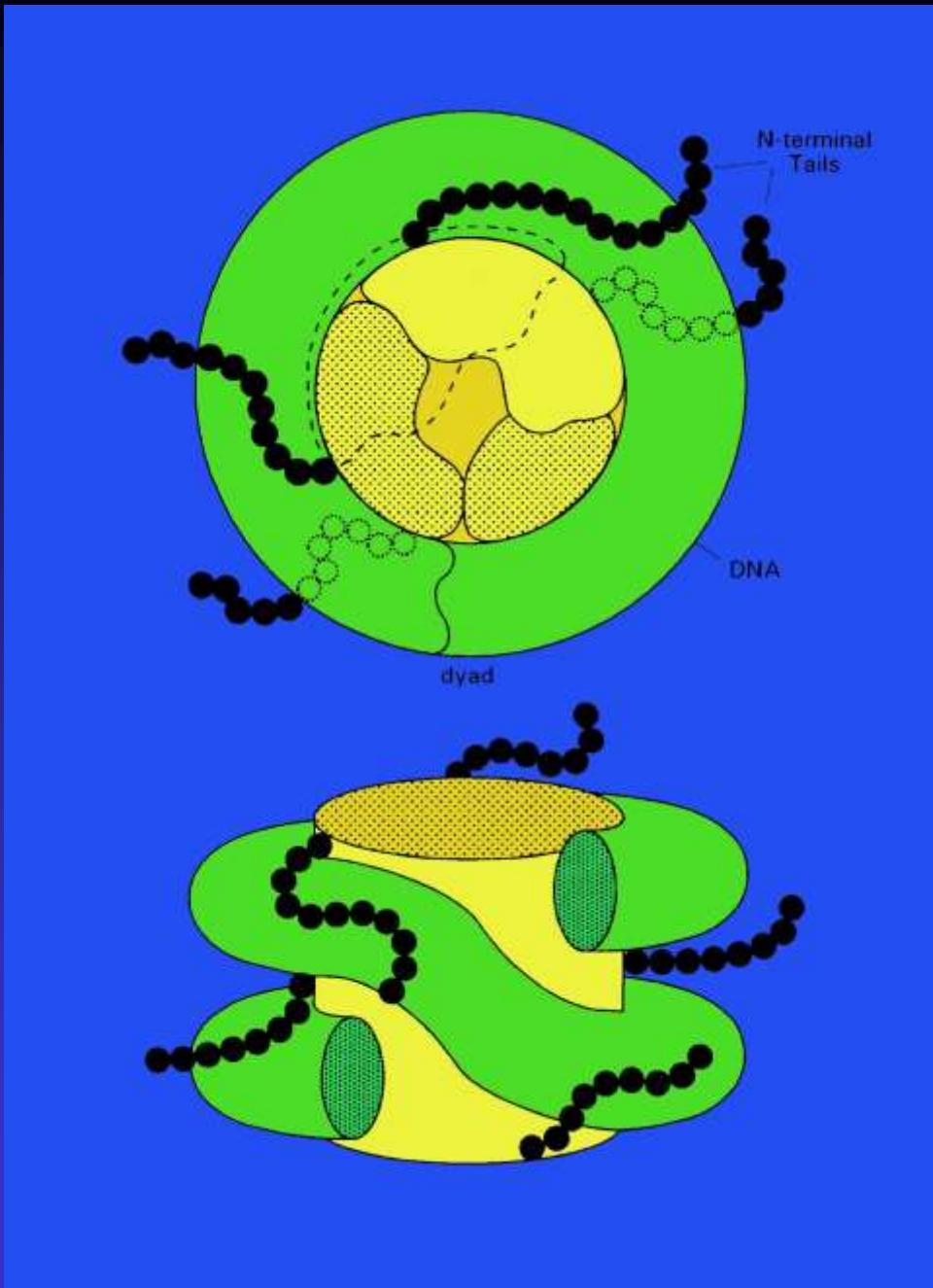
Development of ideas about embryonic genome activation (EGA)



Late 1-cell stage supports the transcription of some 2-cell stage specific genes within transplanted 2-cell stage nuclei (U2afbp-rs, ERV-L, 70 kDa TRC complex) (*Latham, Schultz Frontiers in Bioscience, 2001*)

These studies support the hypothesis that genome activation occurs in a stepwise manner in the mouse embryo

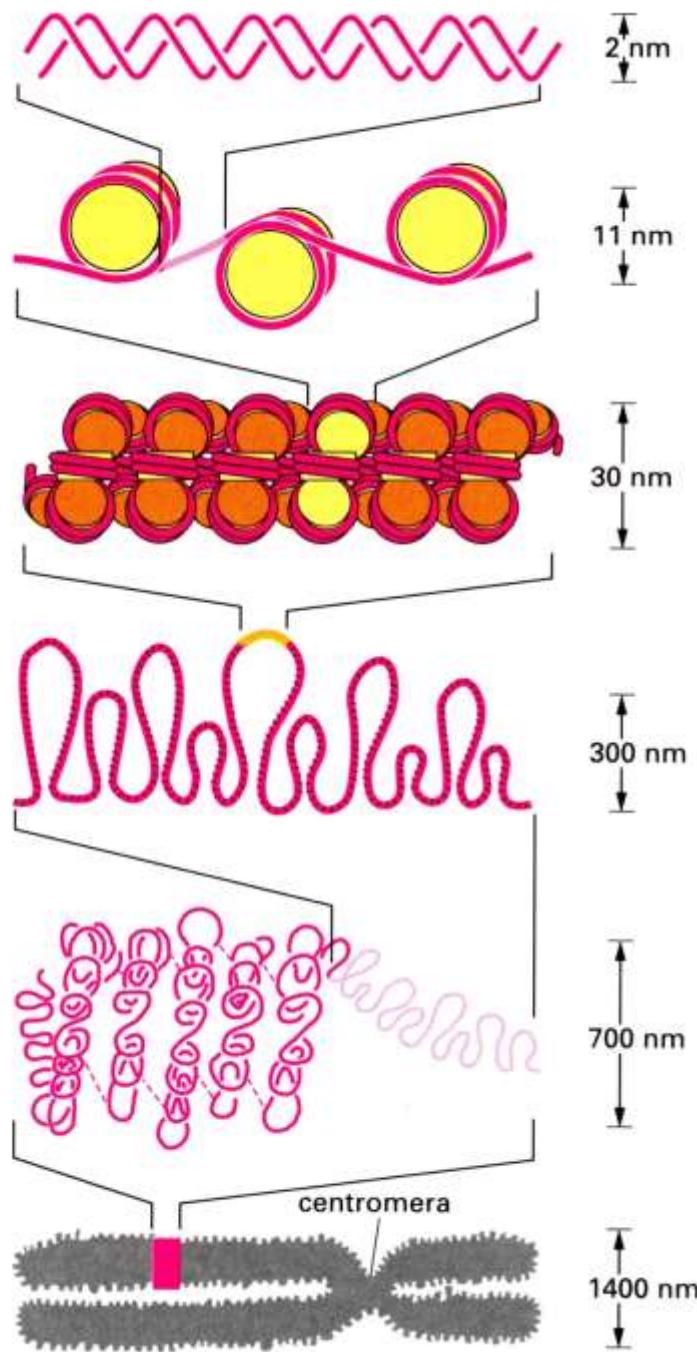
Chromatin structure



Two molecules of each of the four core histones (H2A, H2B, H3 and H4) wrap 160 bp of DNA. N-termini (19 and 26 amino acids) of the core histones H3 and H4 are among the most highly conserved sequences in eukaryotes.

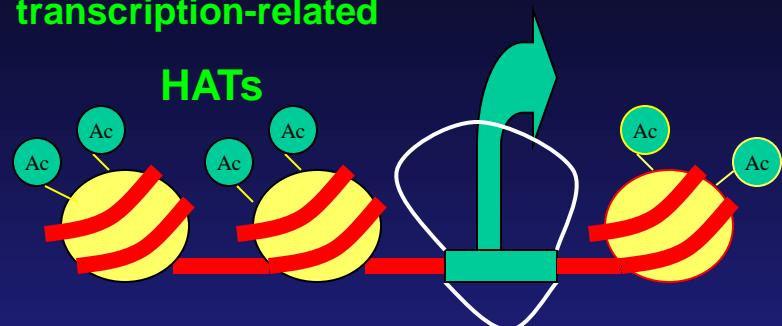
Chromatin structure

single molecule of linker histone (H1) organize 180–190 bp of DNA



Histone acetylation

transcription-related



ATPase
Remodelers

HDACs

HAT – histone acetylase

HDAC - histone deacetylase

HMT – histone methyltransferase

Ac – acetylation

HP1 – heterochromatin protein 1

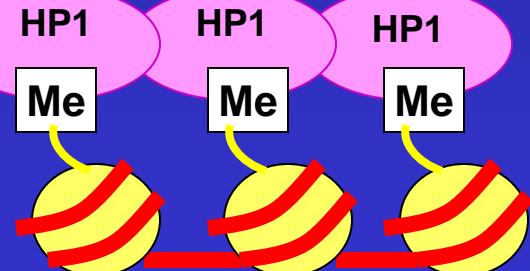
Acetylation of nucleosomal histones influences all aspects of chromosomal organization

Acetylation is central to the switch between permissive and repressive chromatin structure

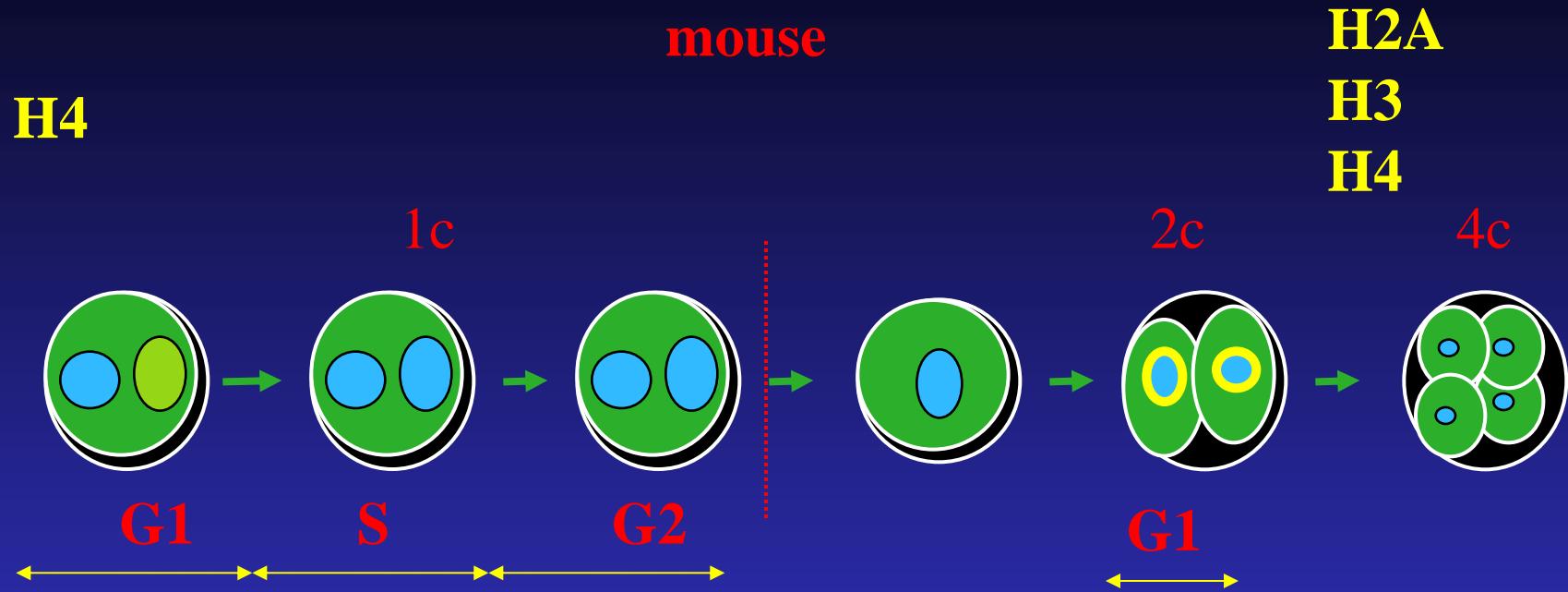
Acetylation permits ATP-dependent chromatin remodeling factors to open promoters

HMTs

HATs



Histone acetylation

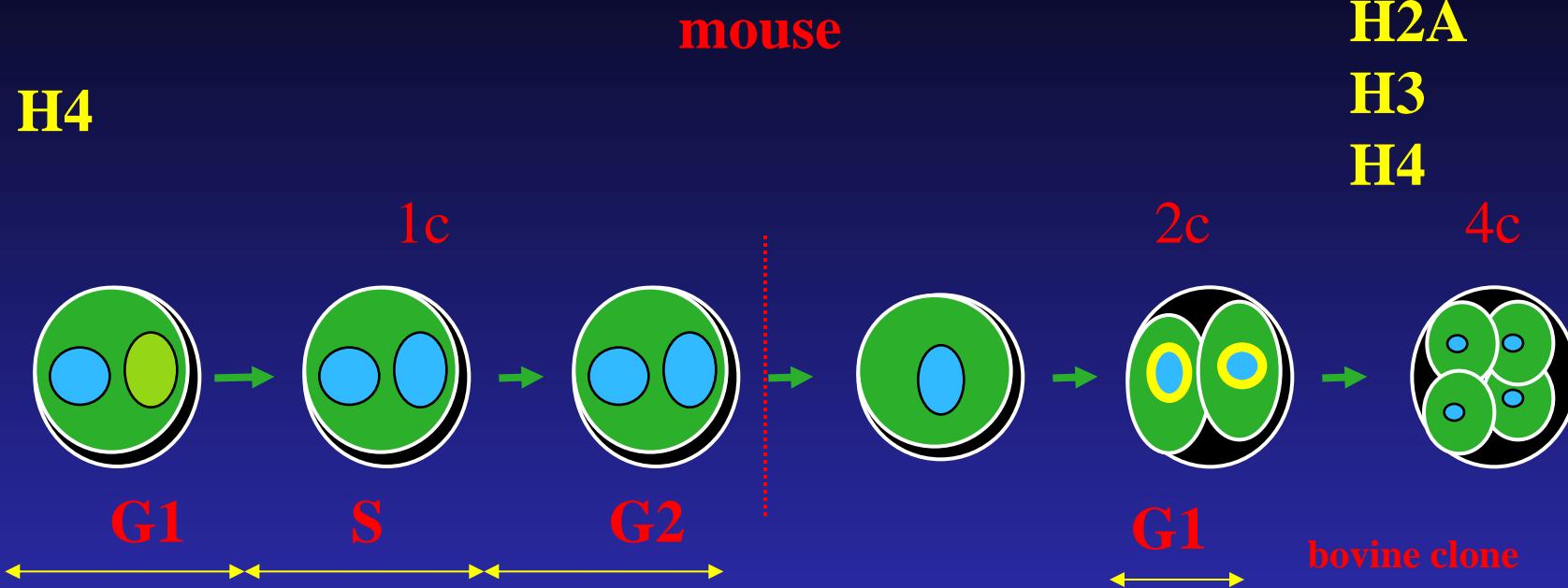


hyperacetylated H4 - G₁ phase,
the male pronuclei exhibited
higher levels

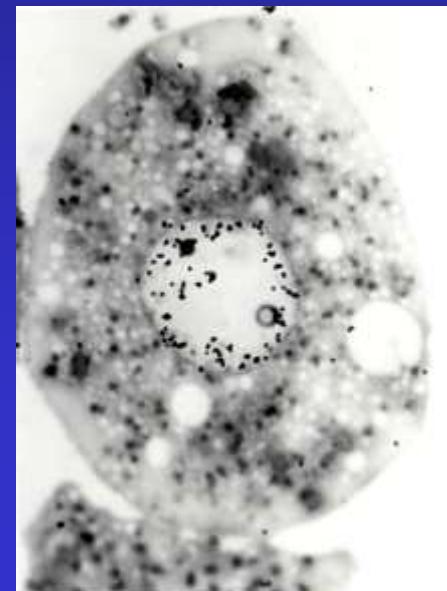
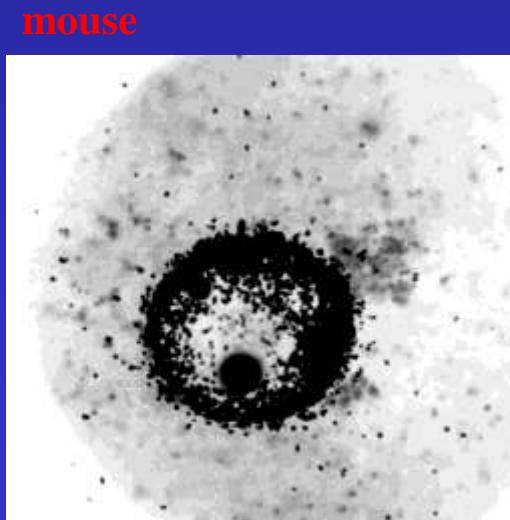
Worrall et al., Development 1995
Stein et al., Mol Reprod Dev 1997

H4 acetylated on lysine 16 is uniformly distributed in the nucleoplasm of 1- and 2-cell stage
H4, acetylated on lysines 5, 8 and 12, is enriched at the nuclear periphery in 2-cell stage
H3 acetylated at lysine 9 and/or 18 and the single acetylated forms of H2A become transiently enriched at the nuclear periphery in the 2-cell

Histone acetylation



histones acetylation is involved in chromatin remodelling during development



DNA methylation

-addition of methyl groups to the 5-position of cytosine within cytosine-guanine dinucleotides (CG)

High level of methylation – gene silencing

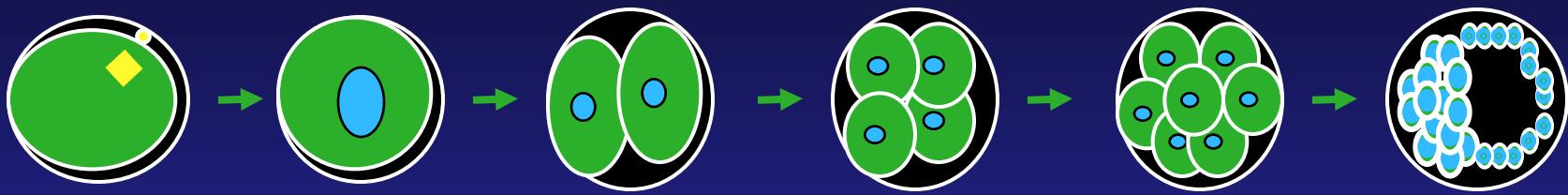
Imprinted genes – difference of methylation status of the regulatory region determines whether the maternal or paternal derived allele is expressed

Methyltransferases – DNMT1

DNMT3A

DNMT3B

Transcription factors

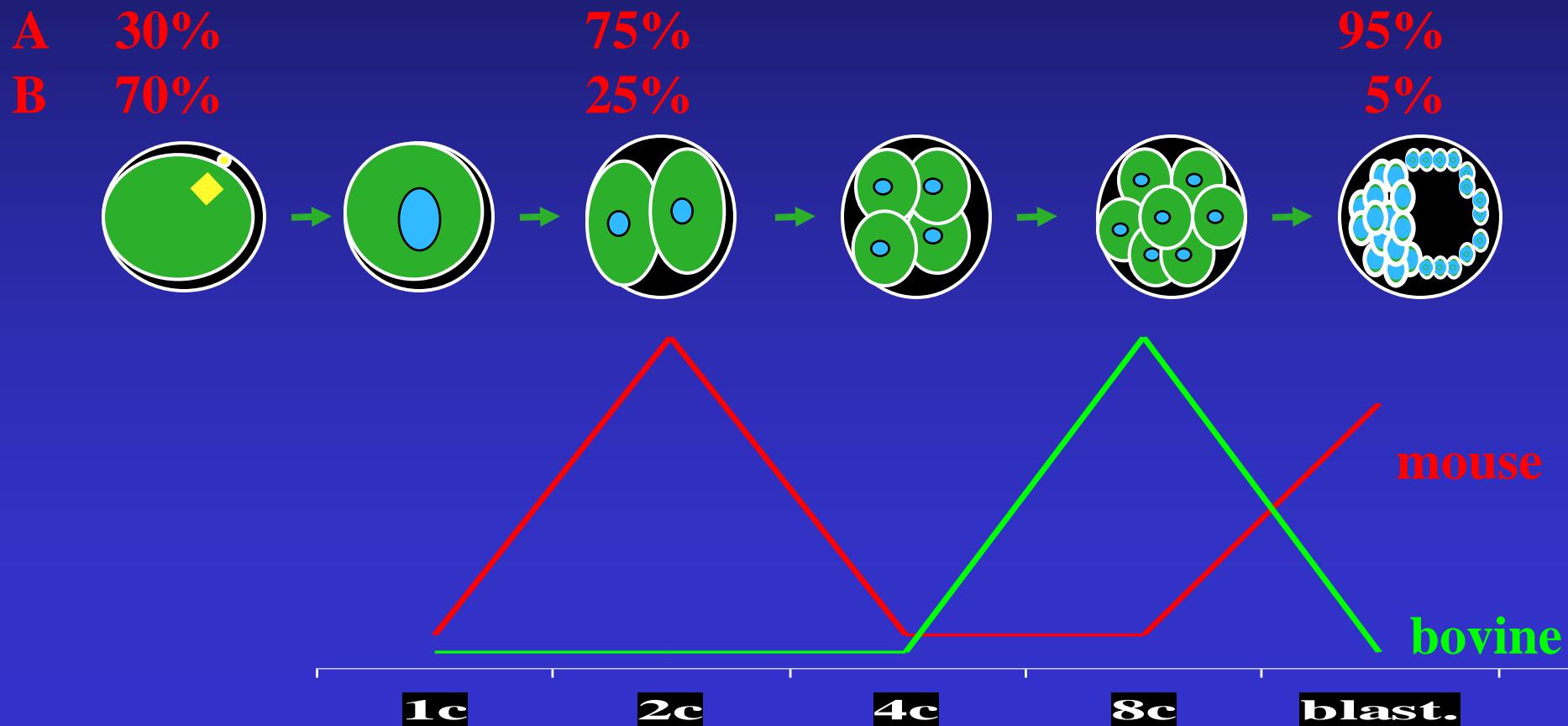


Transcriptional factors are proteins that binds to enhancer or promoter region and interact to activate or repress the transcription.

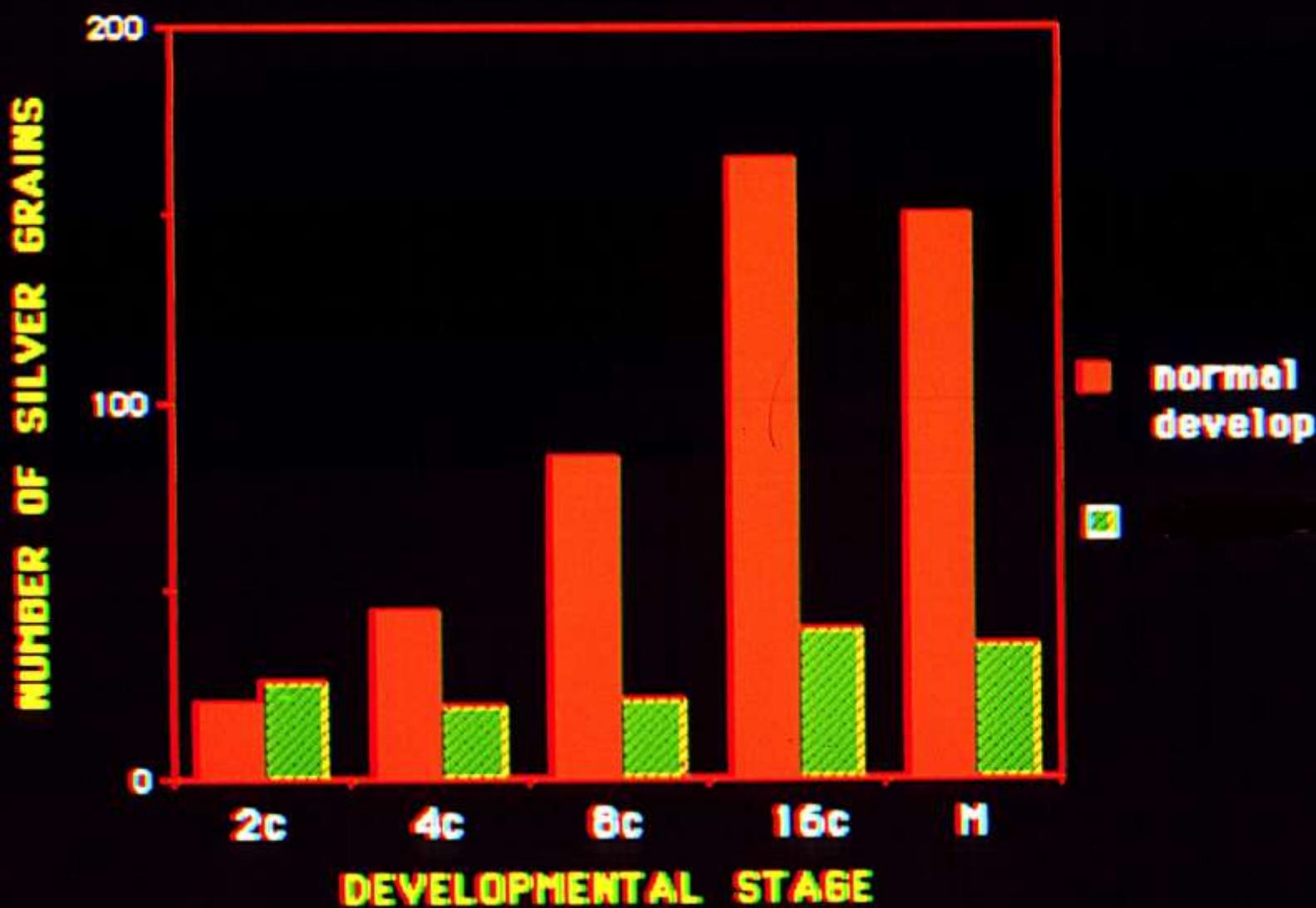
Transcriptional factors are expressed as maternally derived proteins in the early embryo. Transcript abundance of factors Sp1, TBP, CBP and mTEAD-2 starts to decrease during oocyte maturation and then increases at the 2-cell stage

Translational initiation factor eIF-1A

TATA-less promoter

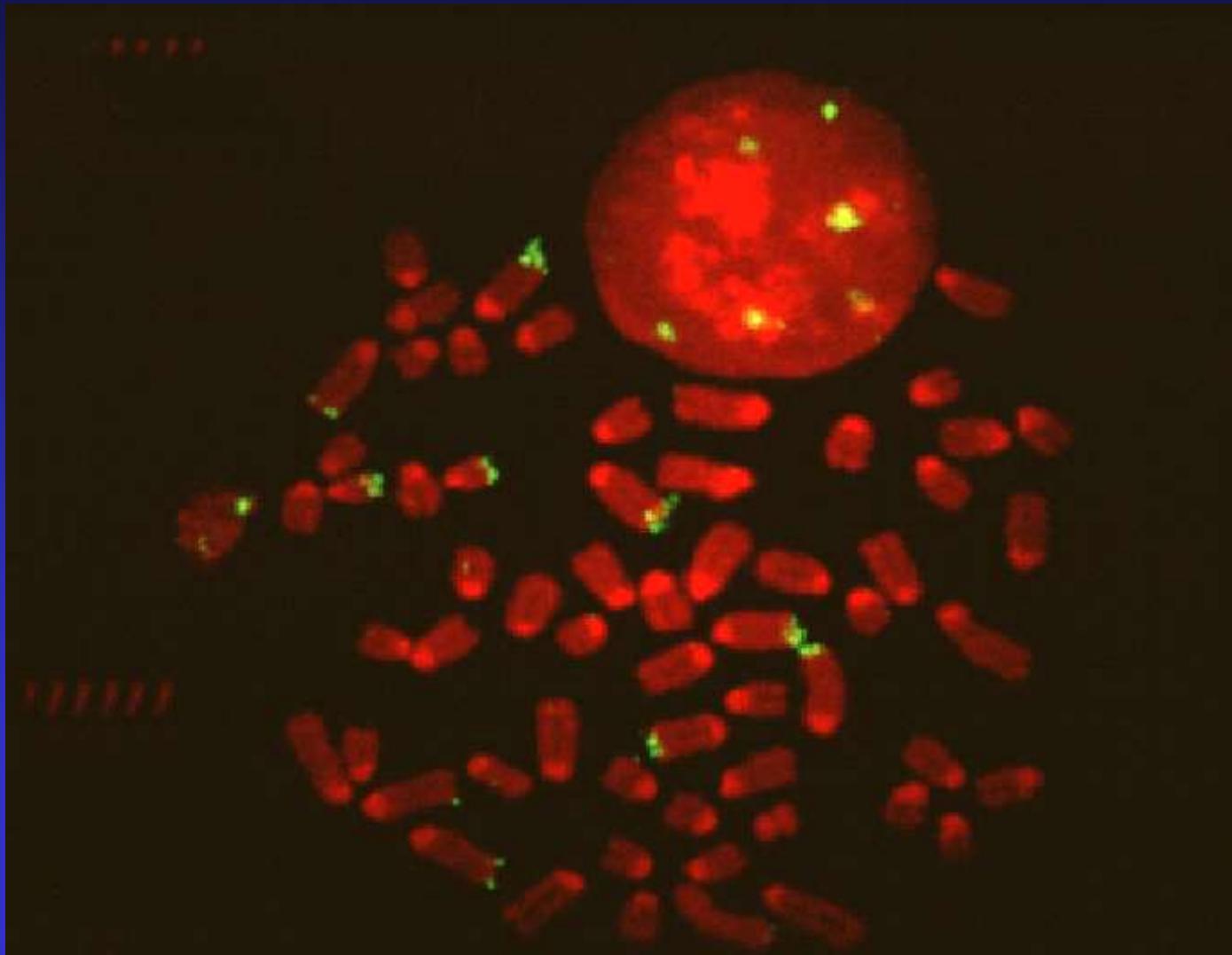


INCORPORATION OF ^3H URIDINE

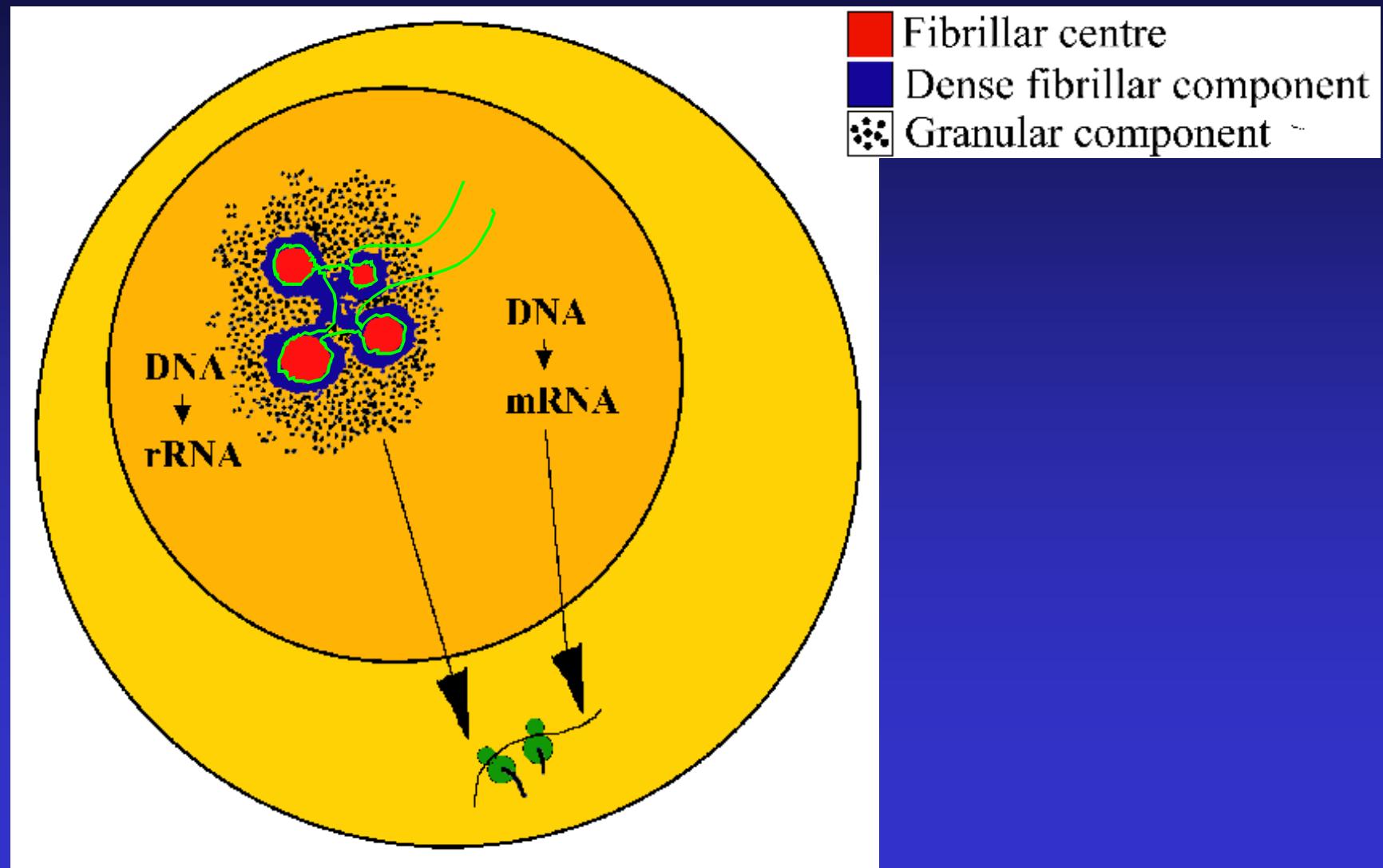


Bovine rRNA genes

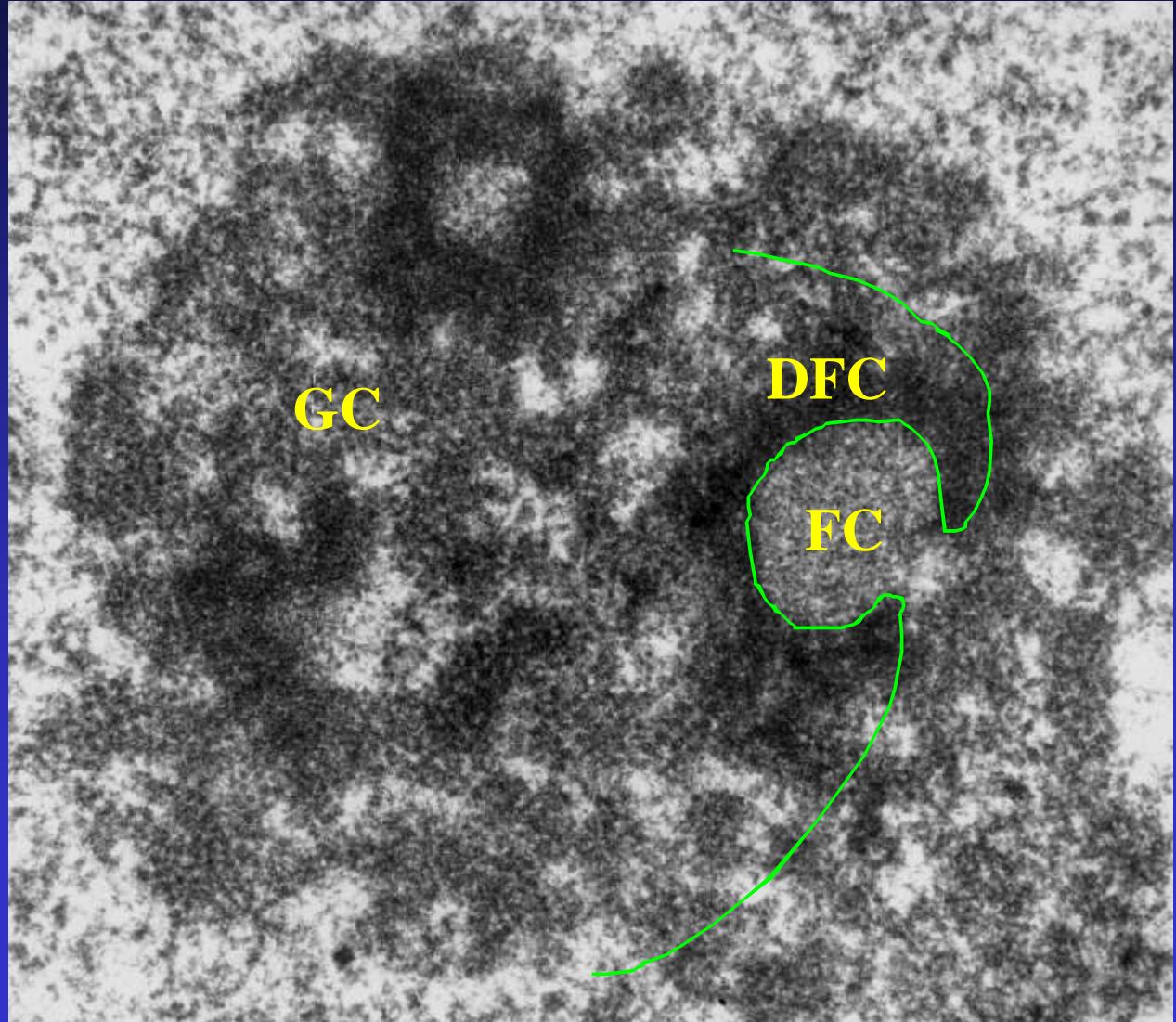
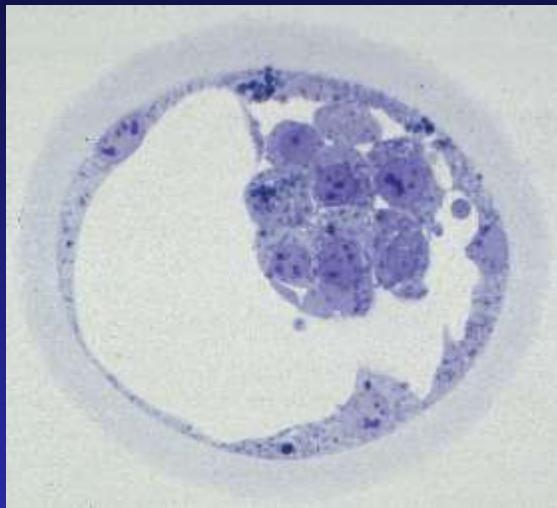
10 nucleolus organizer regions on chromosomes 2, 3, 4, 11, 28.



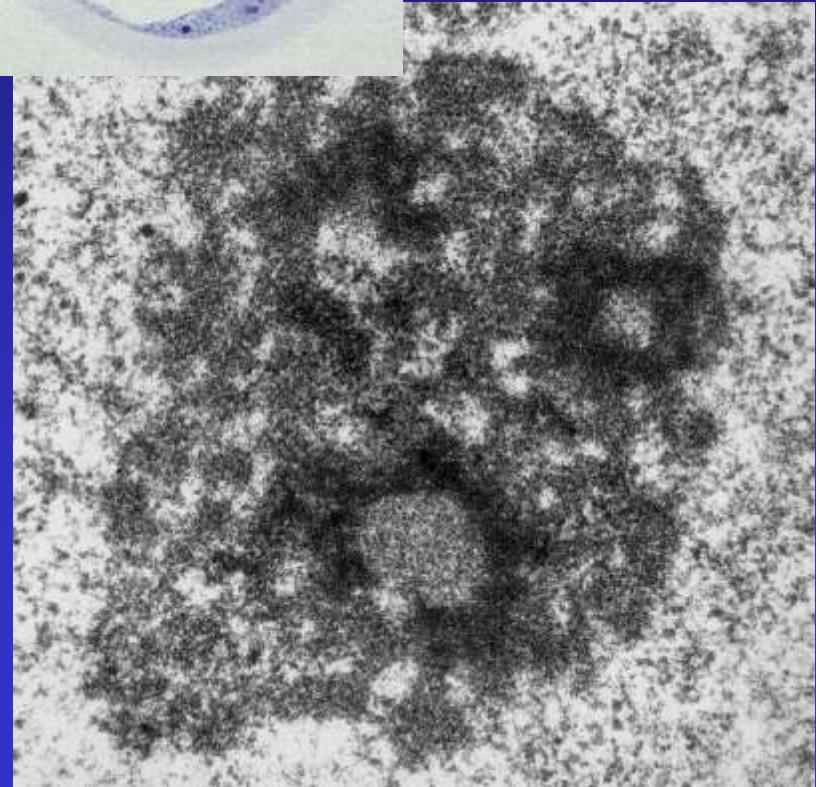
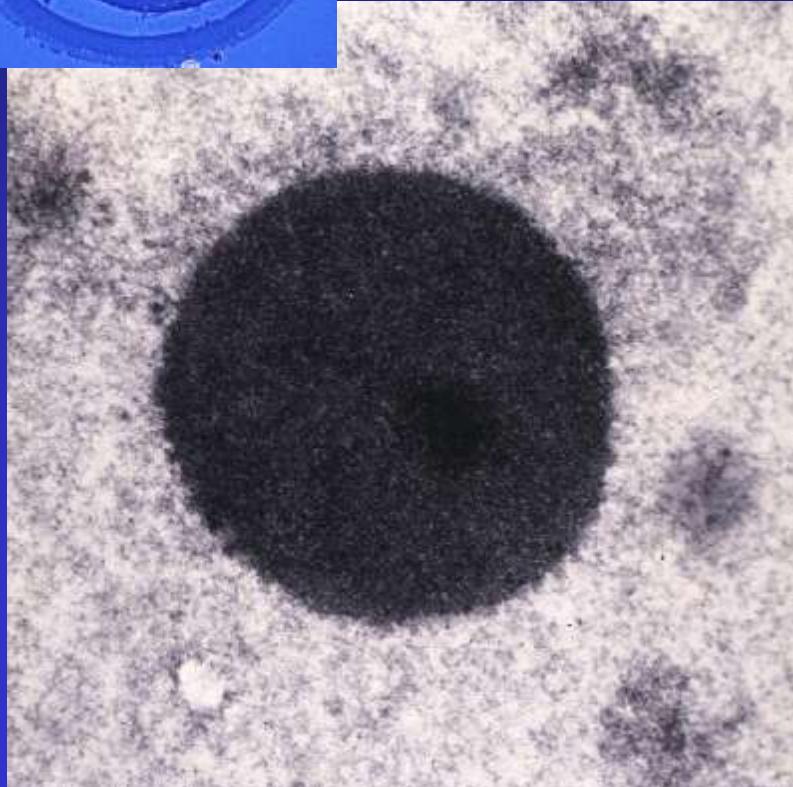
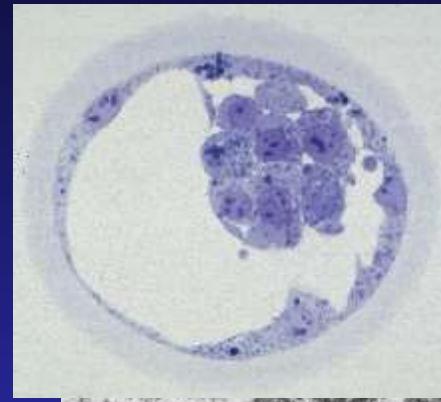
Ribosomal RNA (rRNA) genes and nucleolus



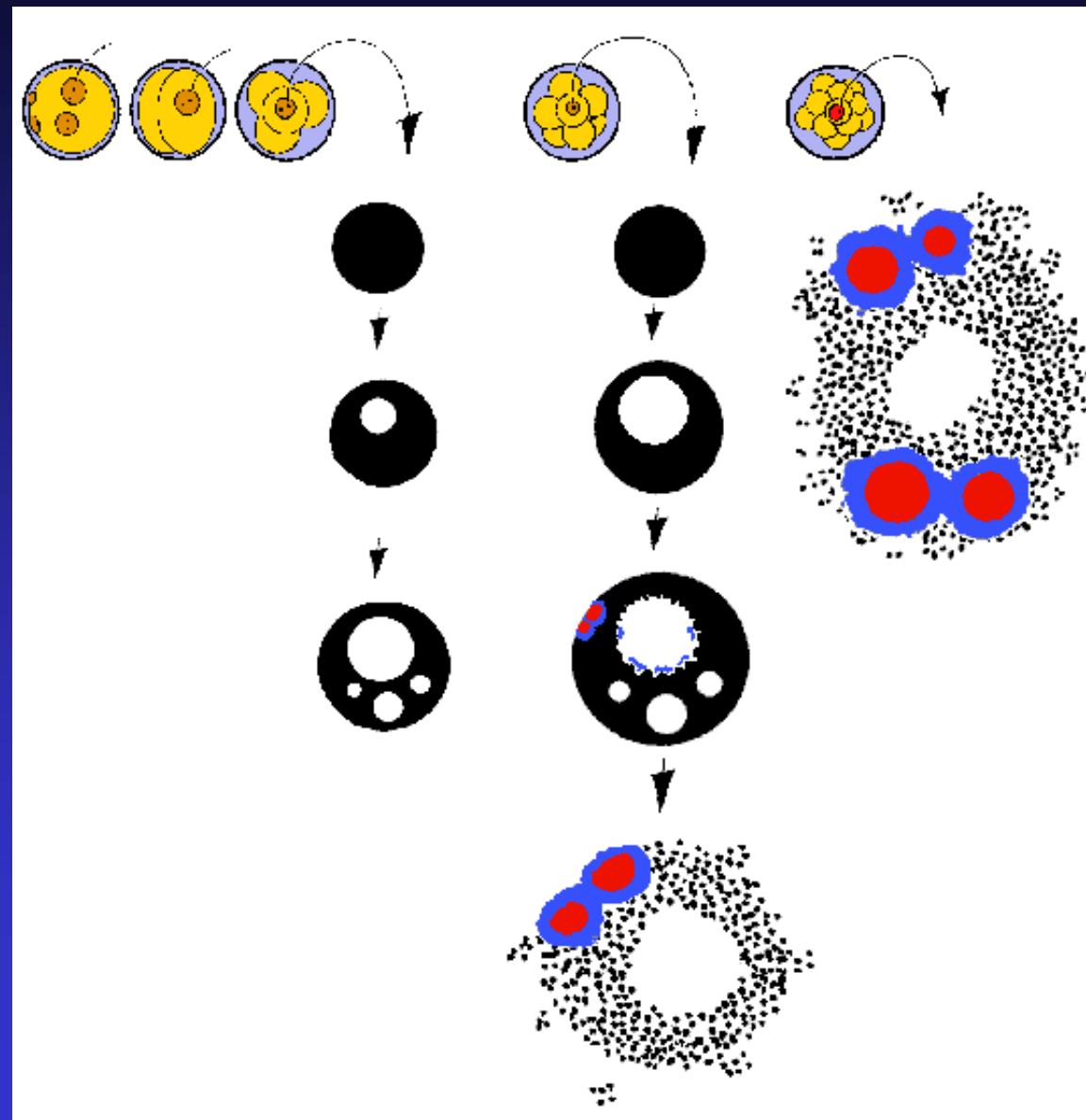
Ultrastructure of the bovine blastocyst nucleolus



rRNA genes as a marker for embryonic gene activation

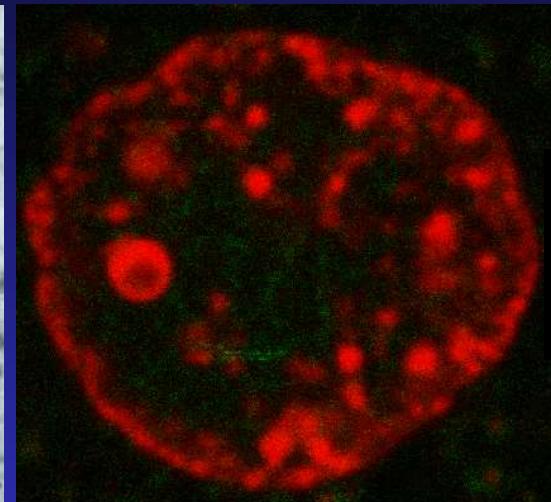
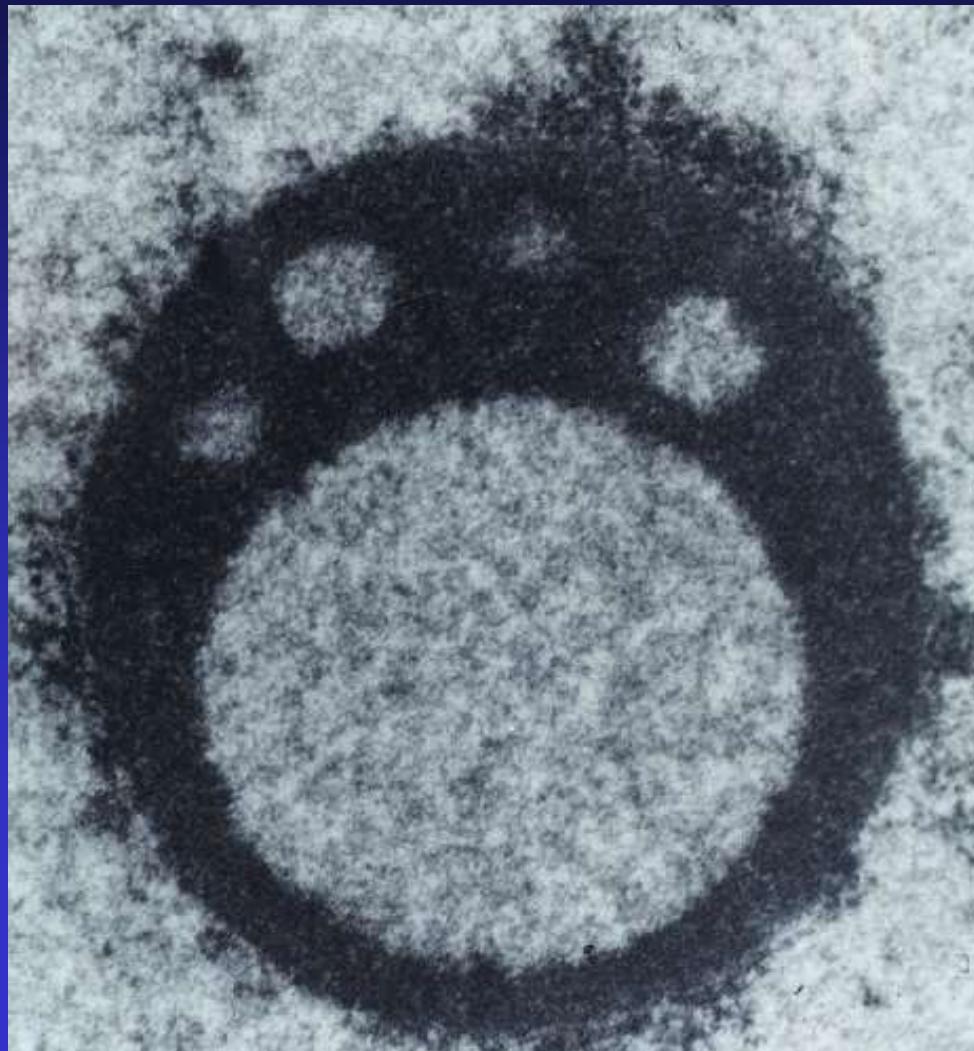


Nucleolar ultrastructure in bovine embryos

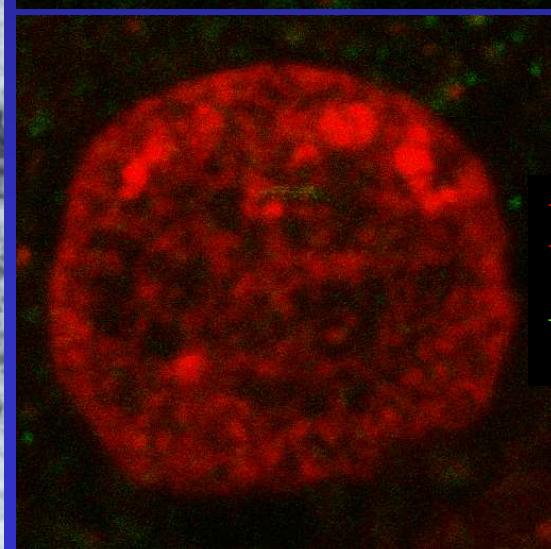


Nucleolar proteins in bovine embryos

4th cell cycle, 8-cell stage - Early

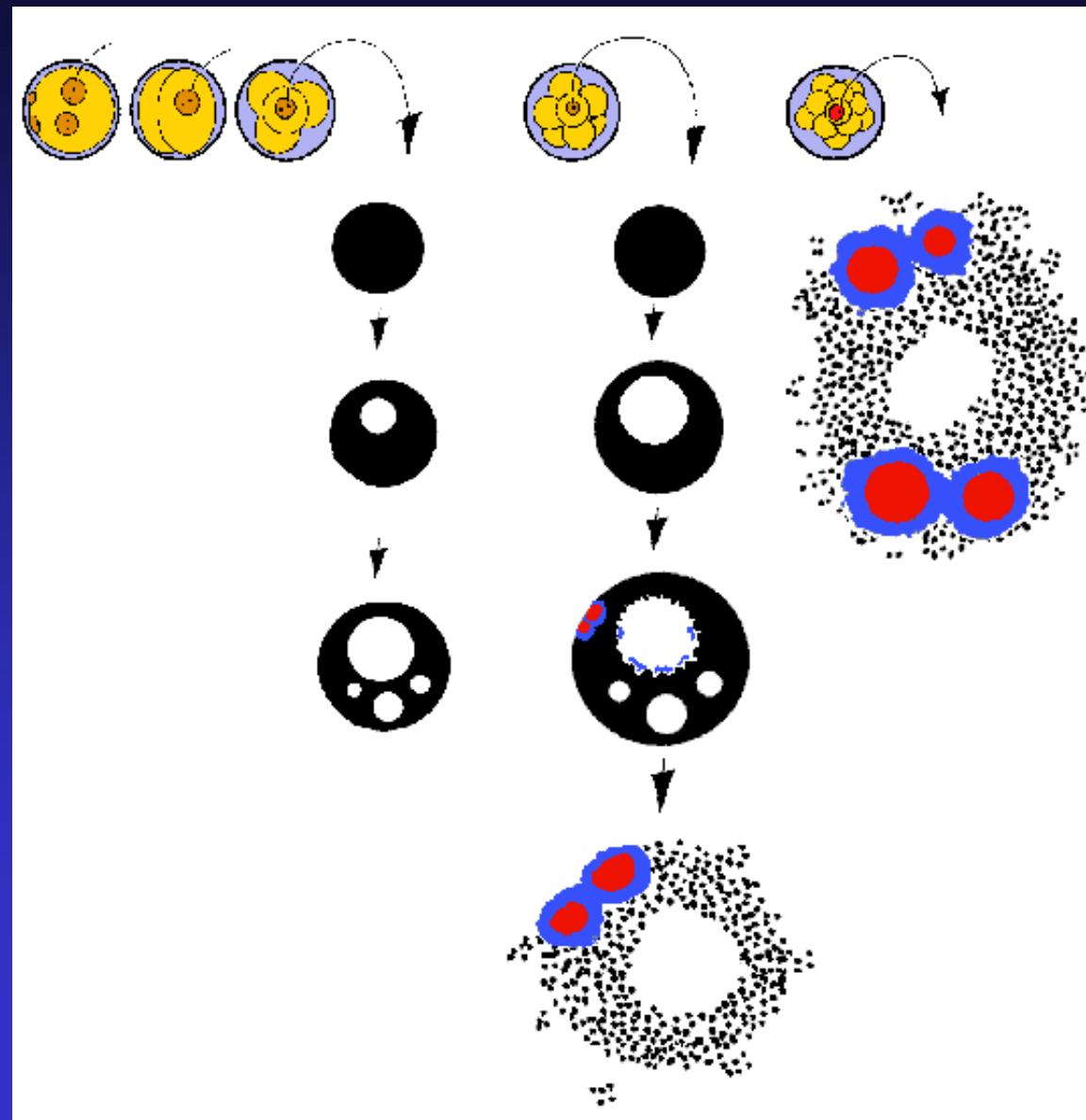


DNA
RNA pol I



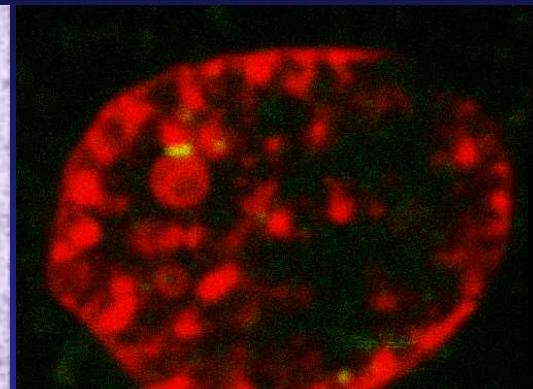
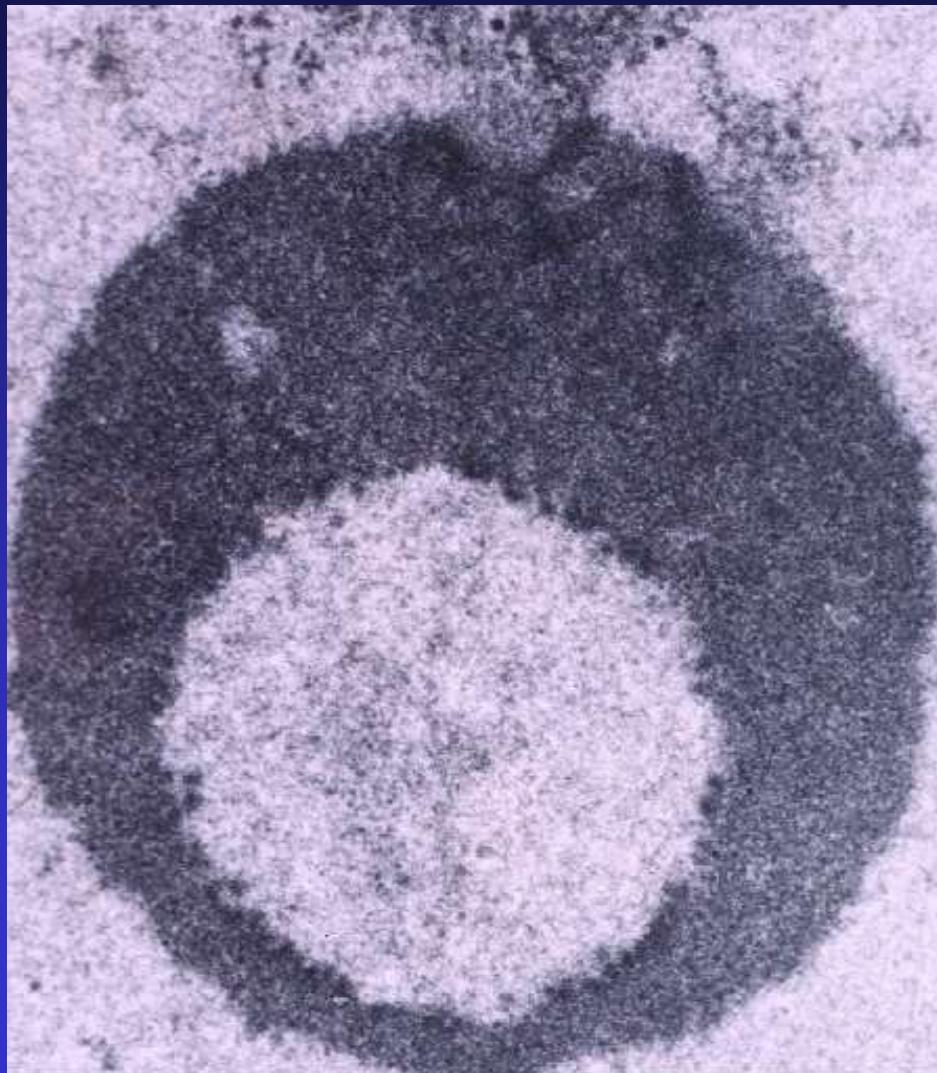
DNA
UBF
Upstream
binding
factor

Nucleolar ultrastructure in bovine embryos

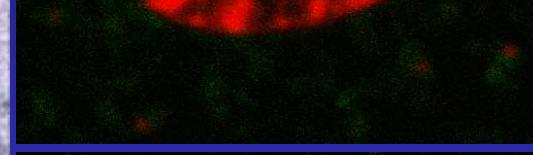


Nucleolar proteins in bovine embryos

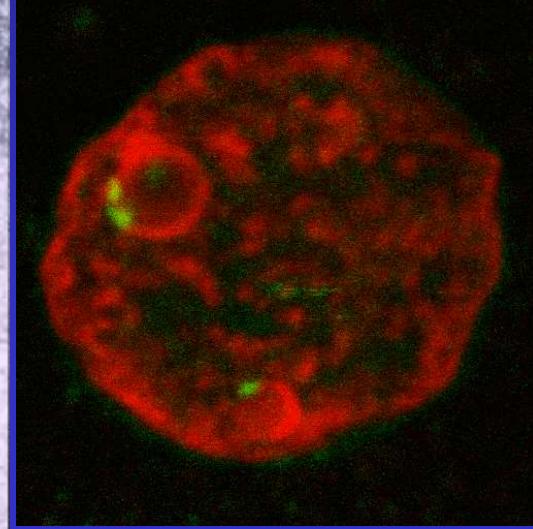
4th cell cycle, 8-cell stage - Late



DNA



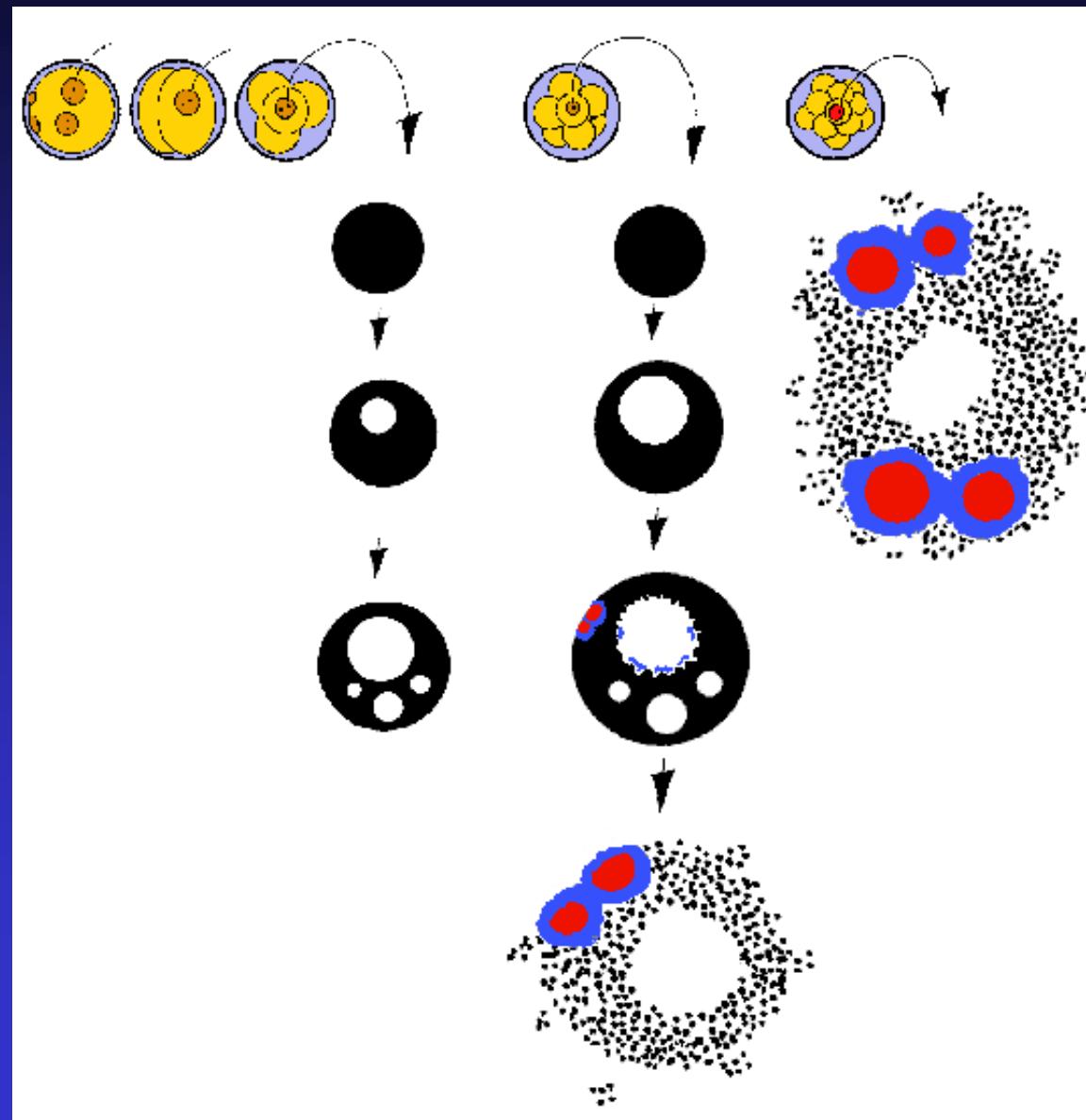
RNA pol I



DNA

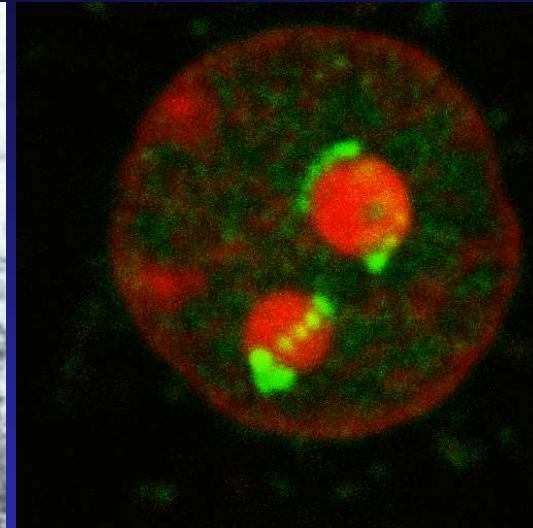
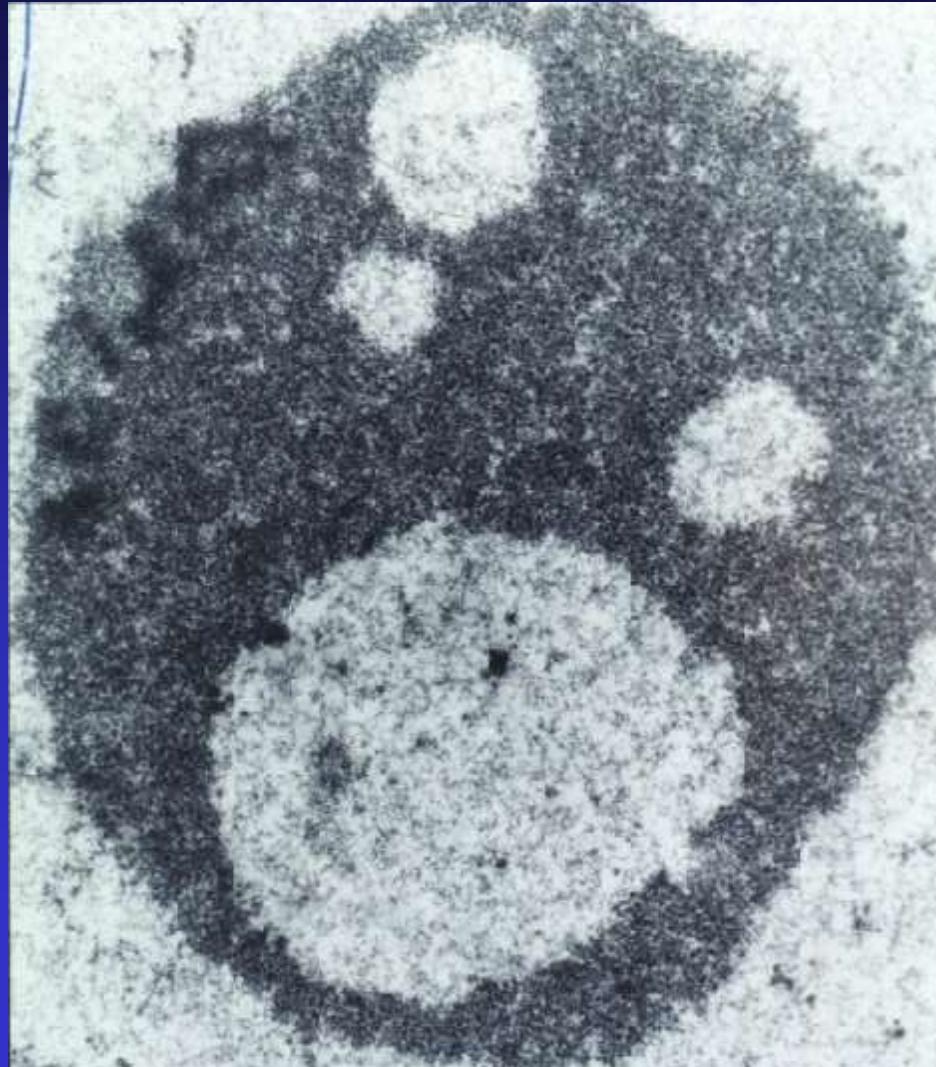
UBF

Nucleolar ultrastructure in bovine embryos



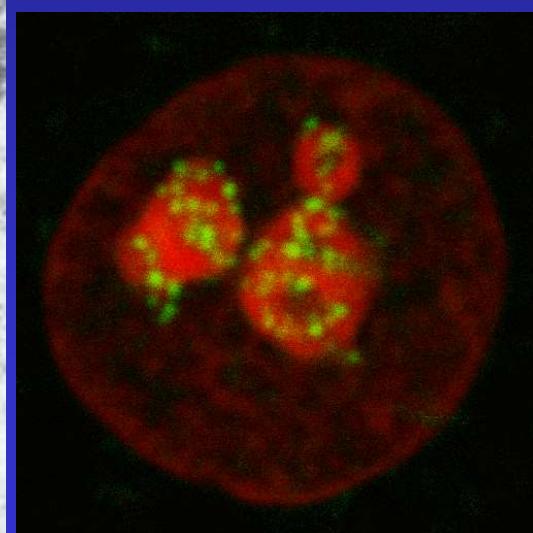
Nucleolar proteins in bovine embryos

5th cell cycle, 16-cell stage



DNA

RNA pol I



DNA

UBF

Nucleolar proteins in bovine embryos

Single nuclei from bovine embryos

1-cell

2-cell

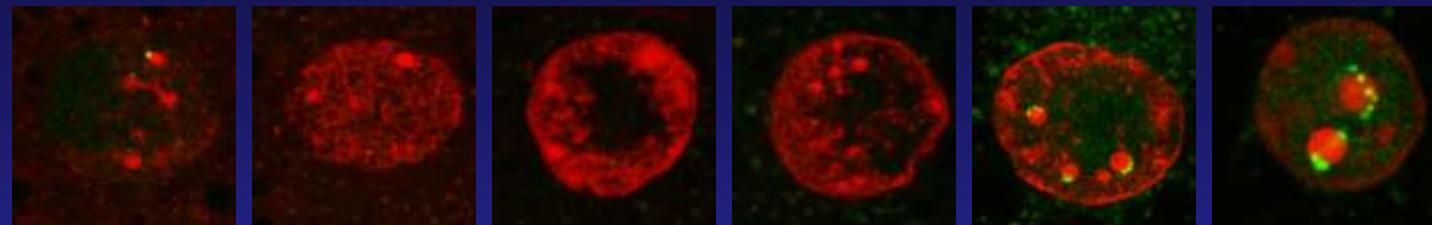
4-cell

8-cell-e

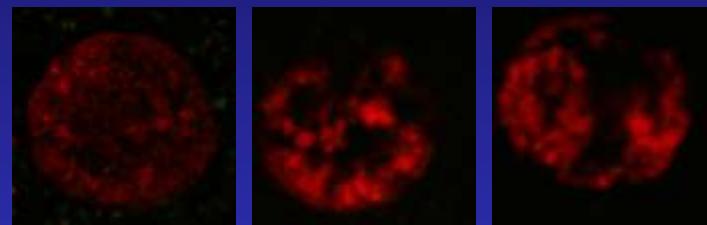
8-cell-l

16-cell

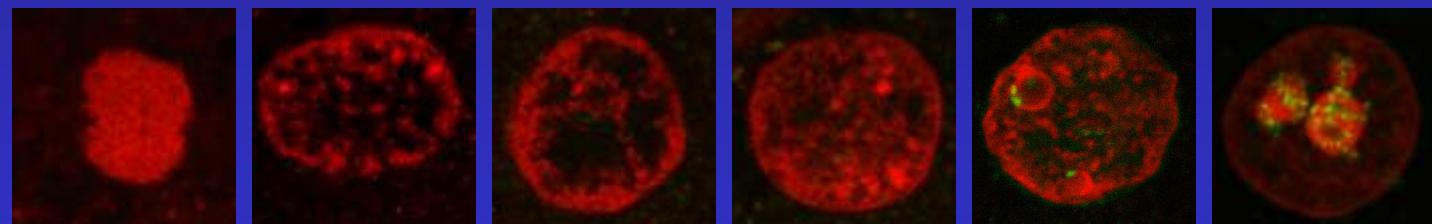
RNA pol I



RNA pol I (amanitine)



UBF



UBF (amanitine)



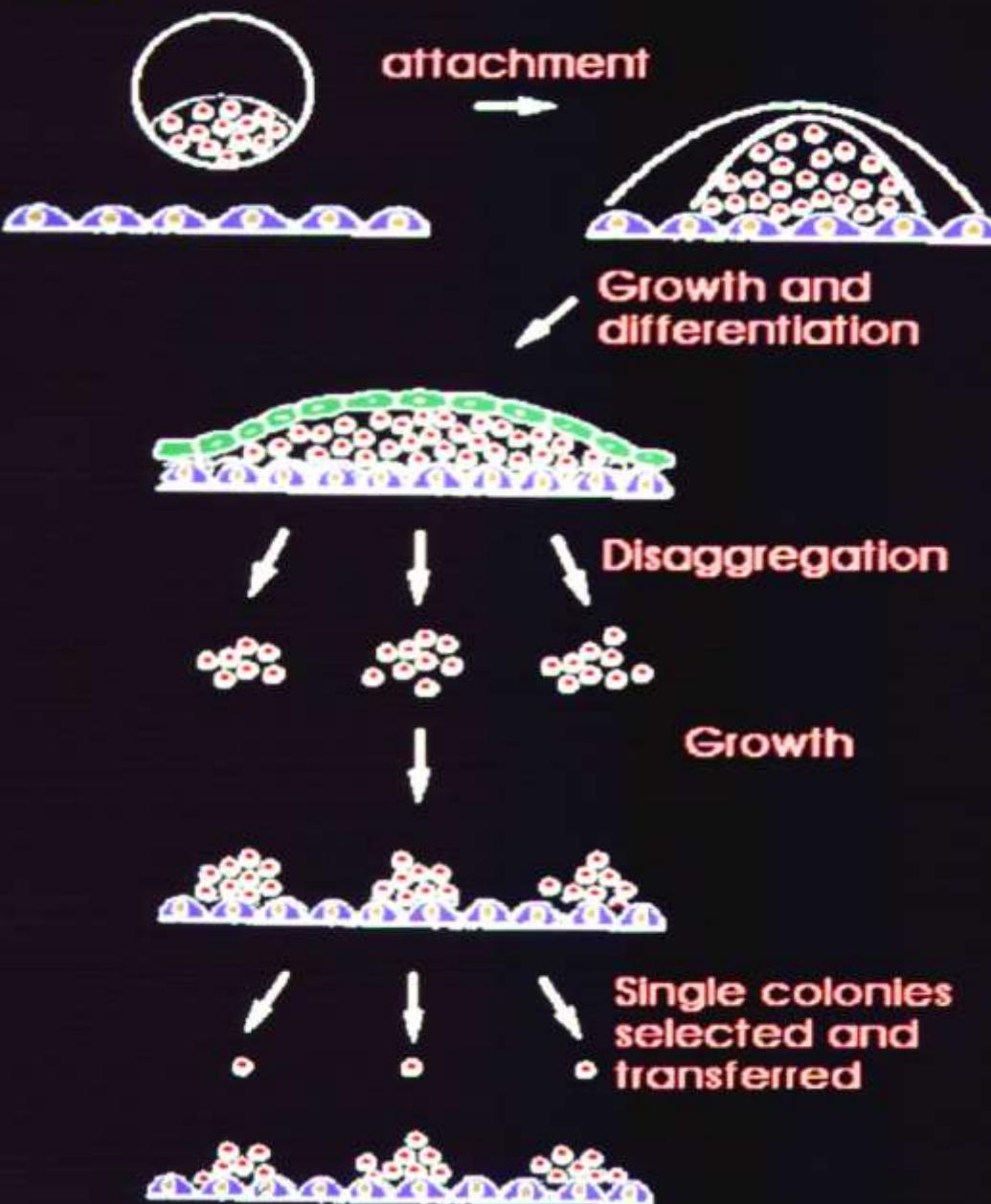
Jiří Kaňka

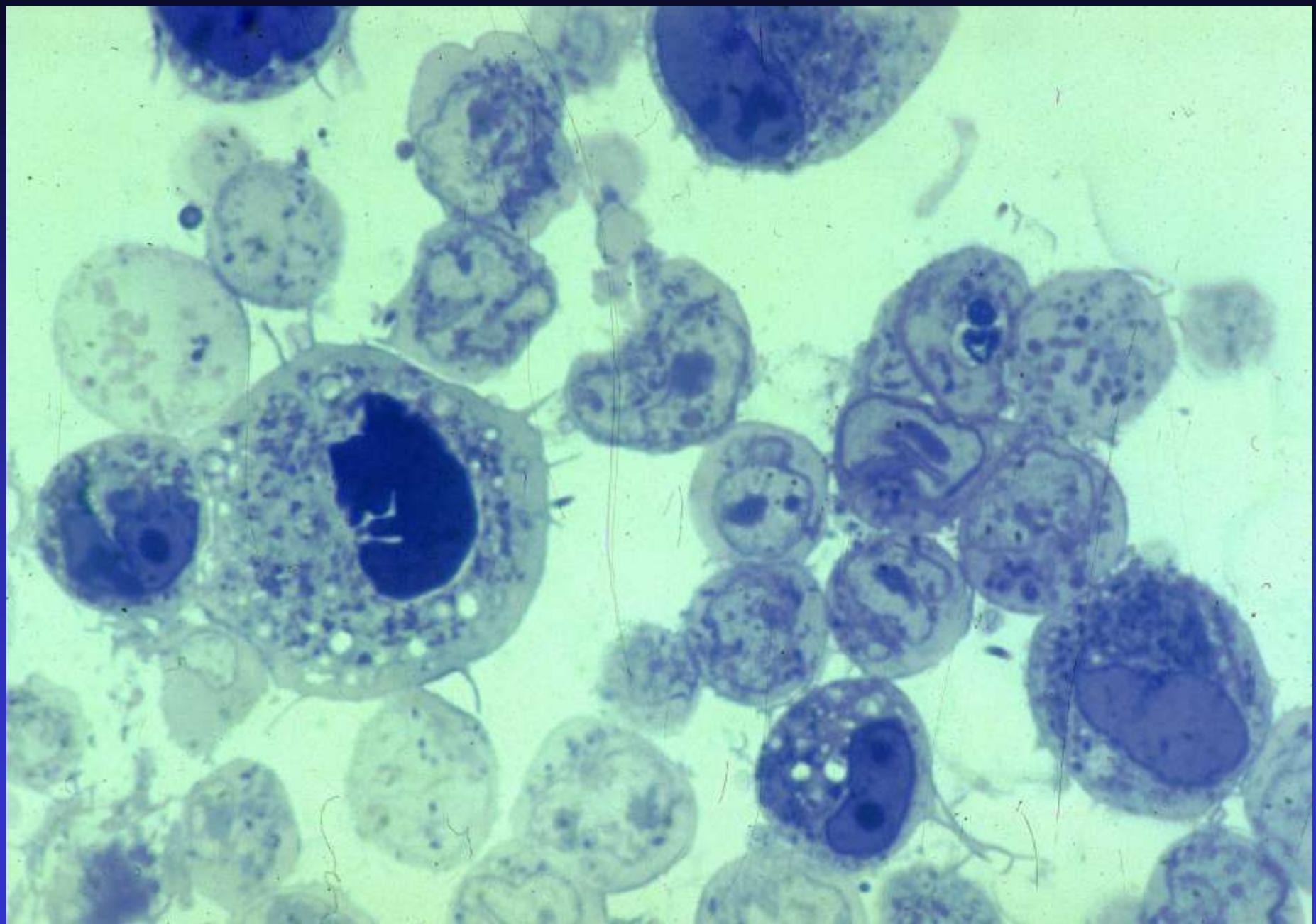
Embryonální kmenové buňky savců

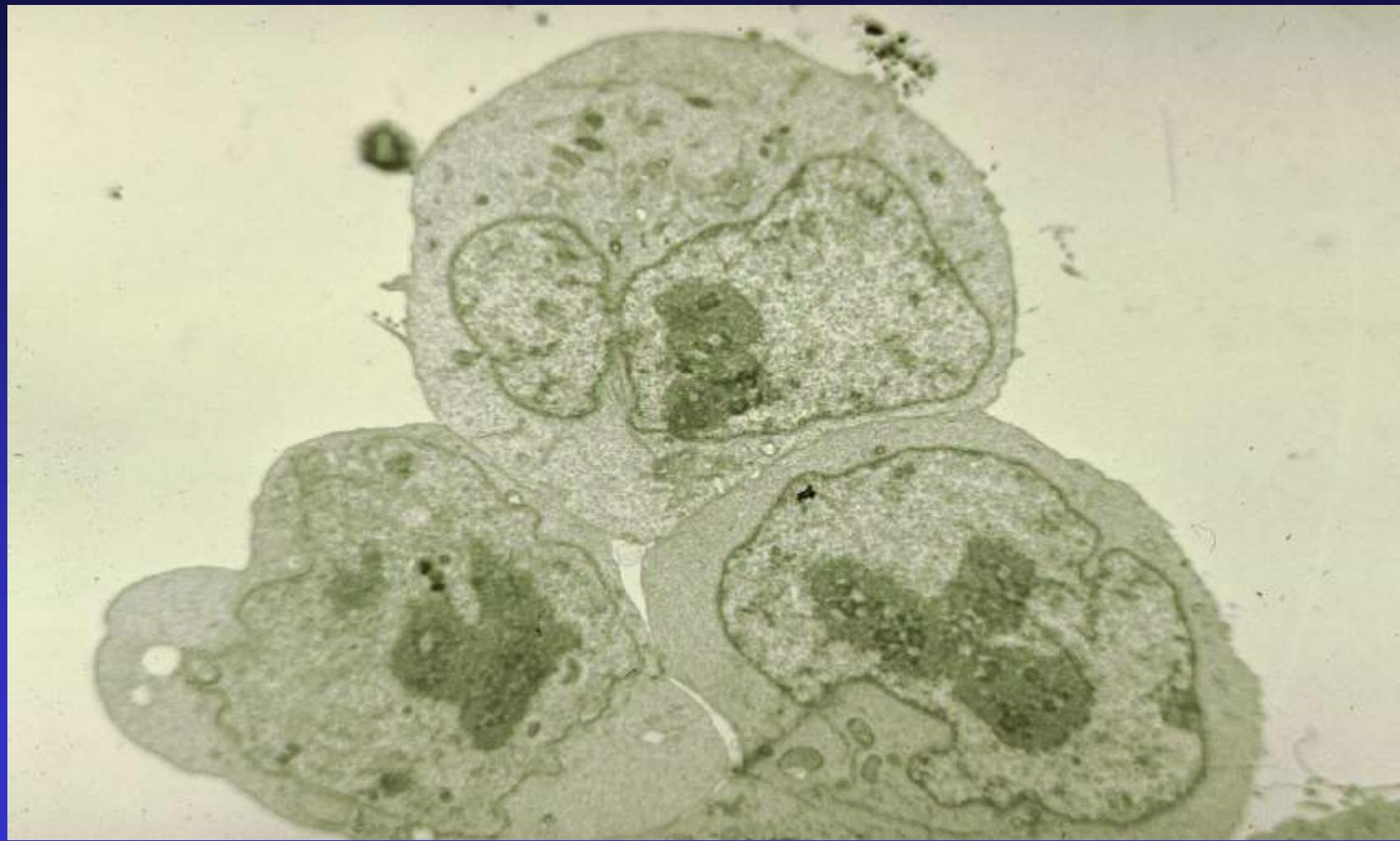
Ústav živočišné fyziologie a genetiky
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277 21 Liběchov

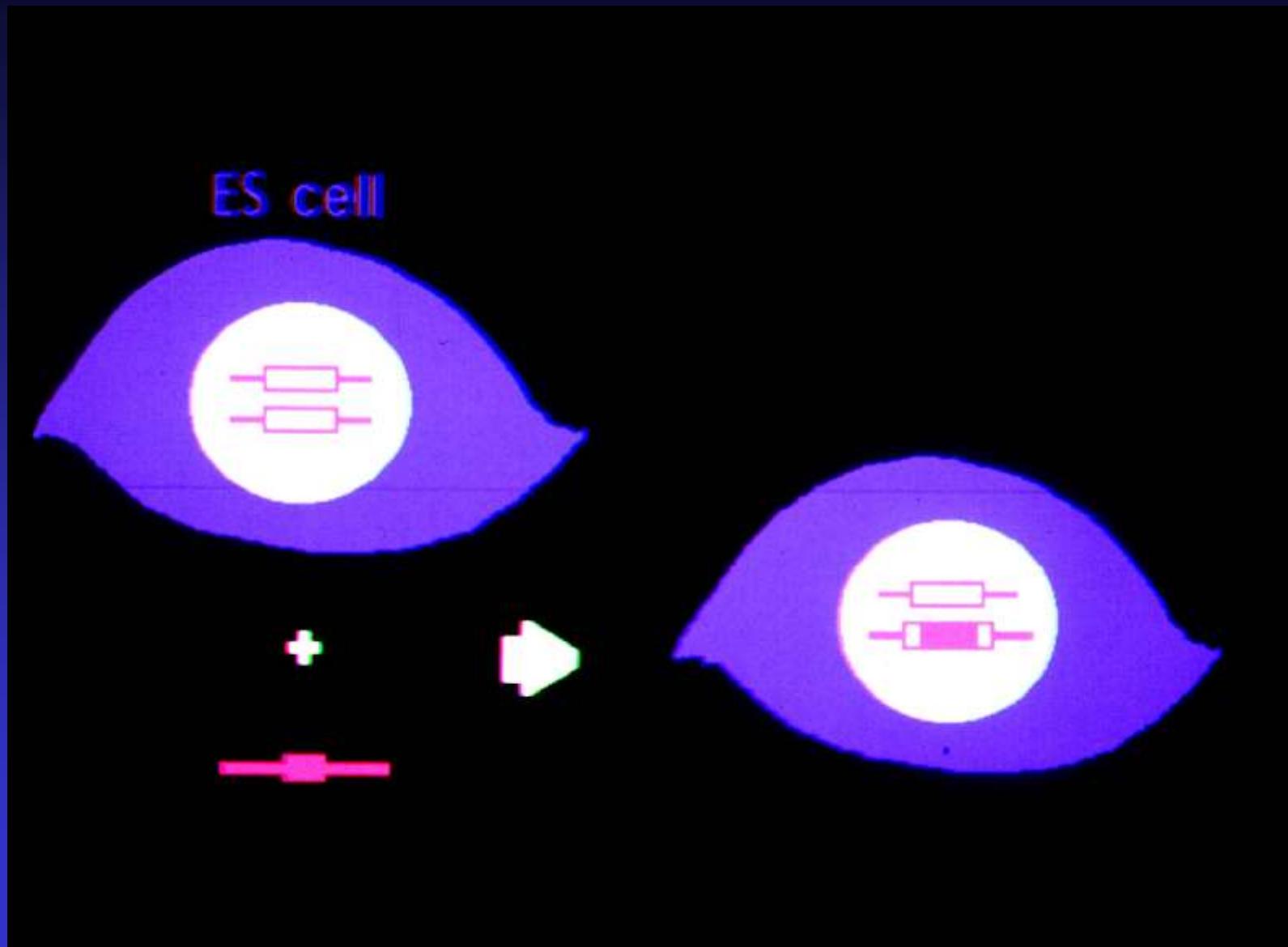
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e-mail :kanka@iapg.cas.cz

Isolation of embryo-derived stem cells









EMBRYONIC STEM CELLS

STEVENS (1959, 1964) TERATOCARCINOMA

PIERCE (1960) EC

KLEINSMITH, PIERCE (1964) EC

STEWART, MINTZ (1981)

EVANS, KAUFMAN (1981) ES

MARTIN (1981)

SMITH, HOOPER (1987) - FEEDER CELLS, LIF

FOLGER, THOMAS, CAPECCHI (1982) - HOMOLOGOUS RECOMBINATION

THOMSON (1989) - GENE TARGETING, GERM LINE

SIMS, FIRST (1993) - CLONING, FARM ANIMAL

STEWART et al. (1994), MATSUI (1992) – GERM CELLS

J. GEARHART'S GROUP (SHAMBLOTT et al., 1998) – HUMAN EG UNIV. OF WISCONSIN (THOMSON et al., 1998) – HUMAN ES

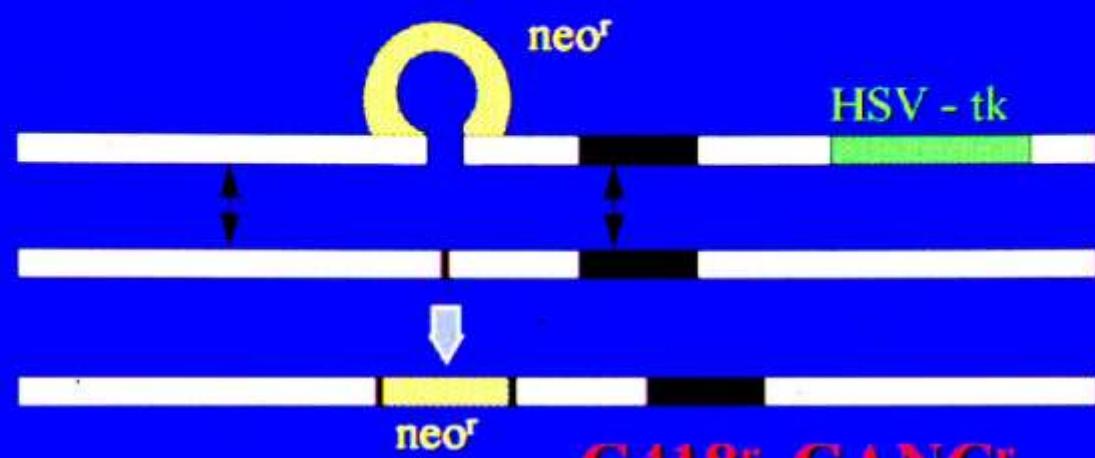
POUŽITÍ EMBRYONÁLNÍCH KMENOVÝCH BUNĚK

**GENE TARGETING EXP.
SUBTLE MUTATION (HIT AND RUN)
CRE RECOMBINASE**

**GENE TRAP
ENHANCER TRAP
CLONING**

POSITIVE - NEGATIVE SELECTION

A/ Gene Targeting



B/ Random Integration

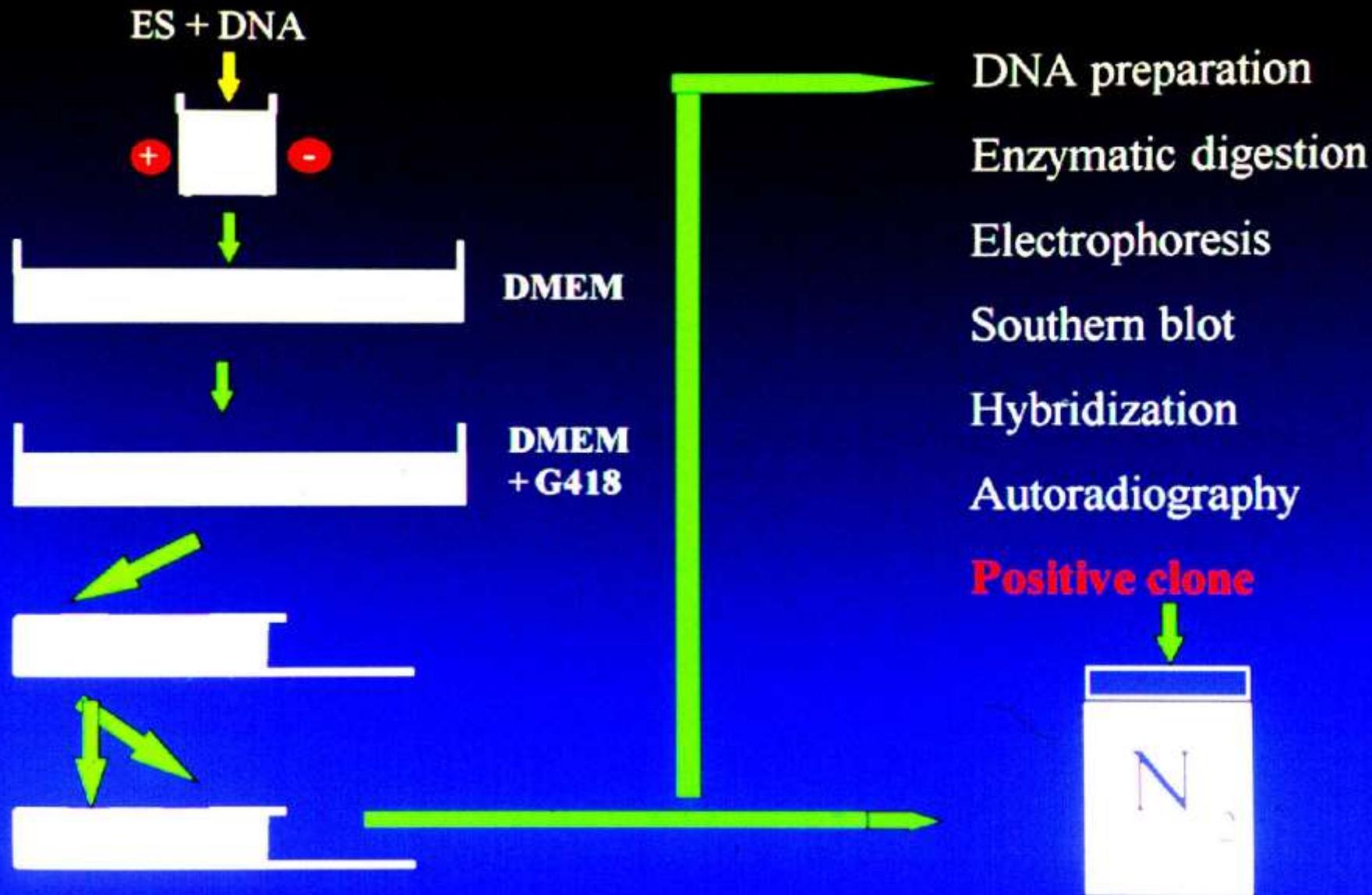


M. Capecchi,
K. Thomas

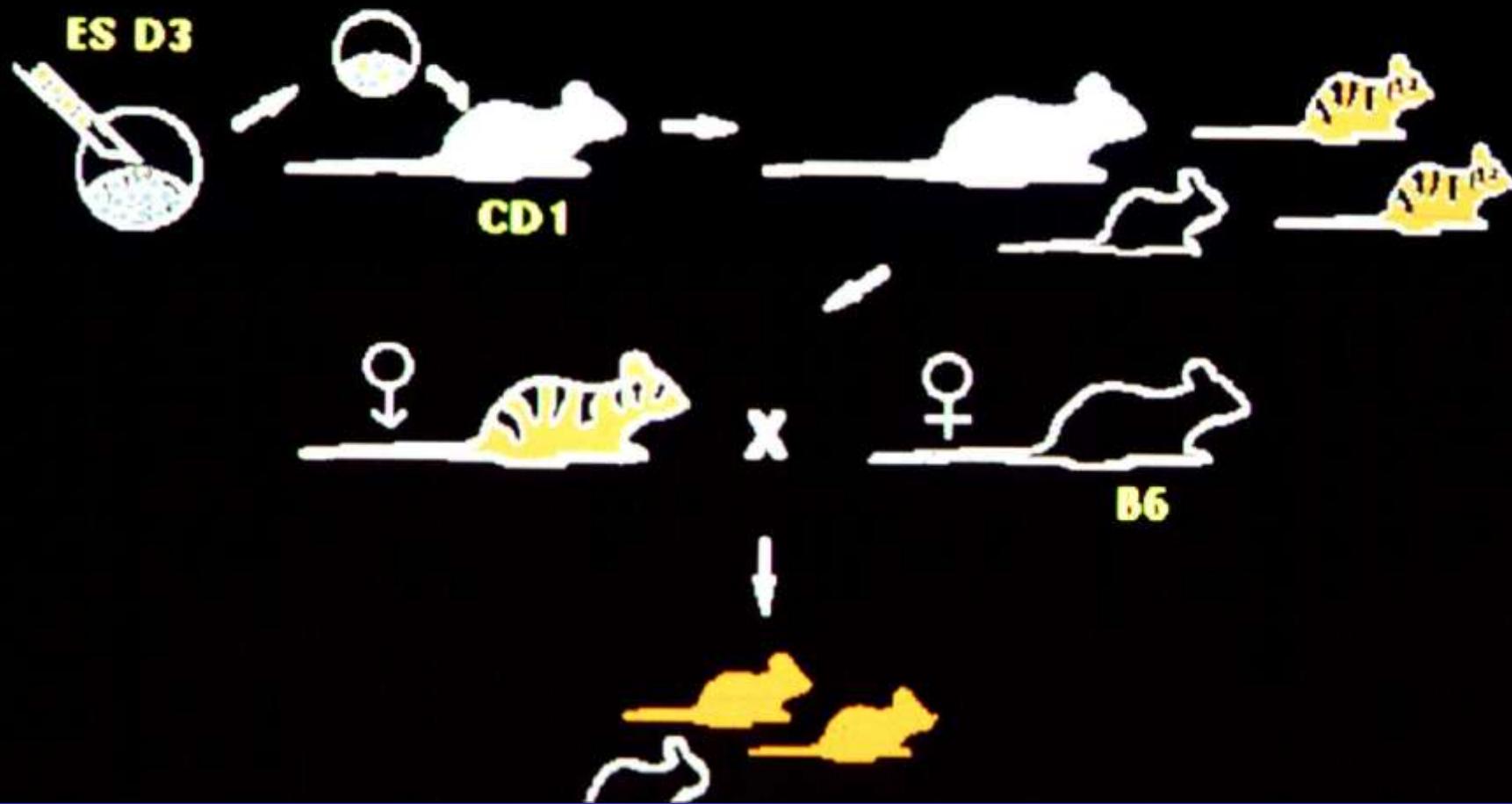
neo - neomycin-
phosphotransferase

HSV-tk - Herpes
simplex virus
thymidine kinase

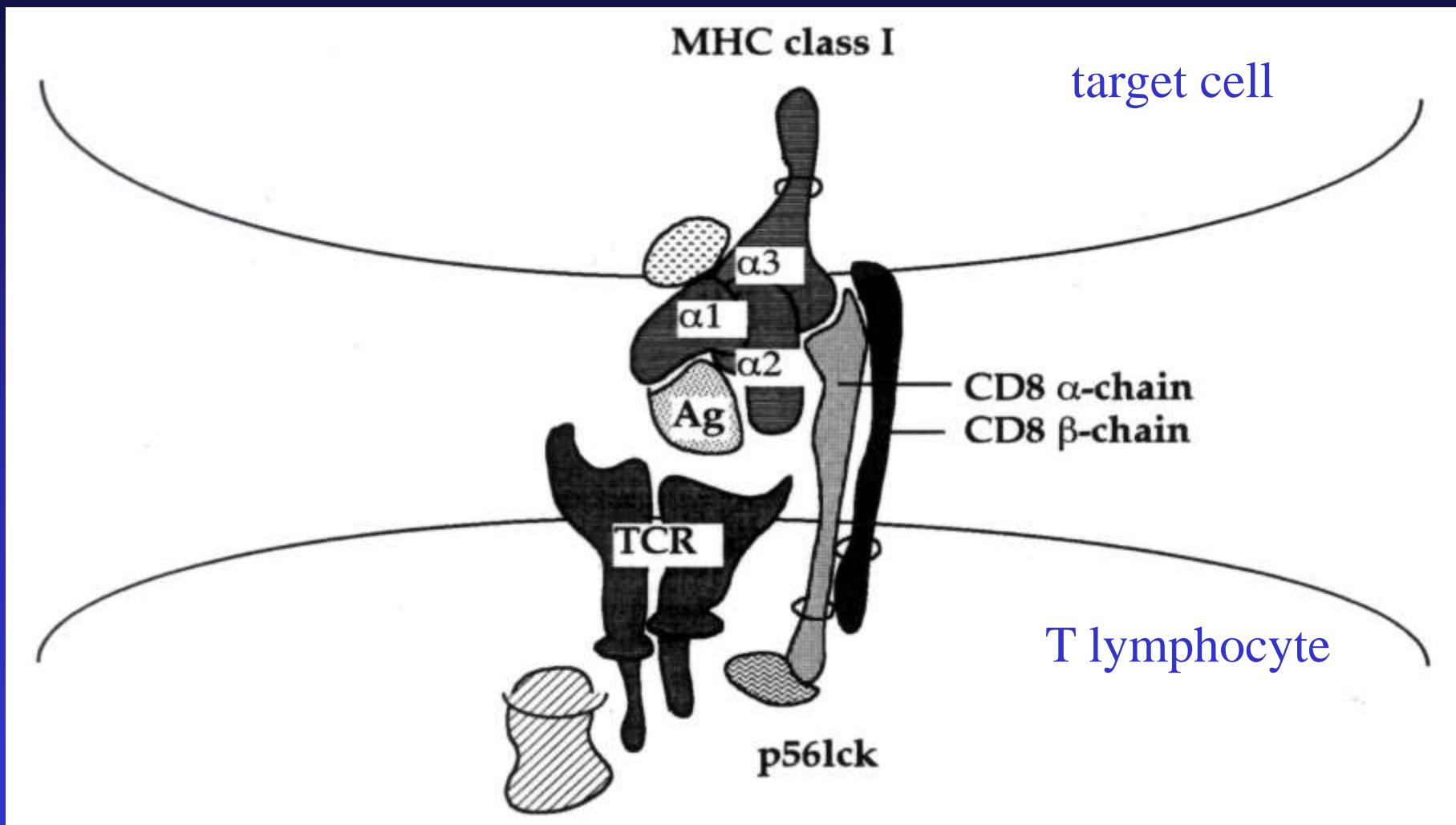
General selection strategy for homologous recombination

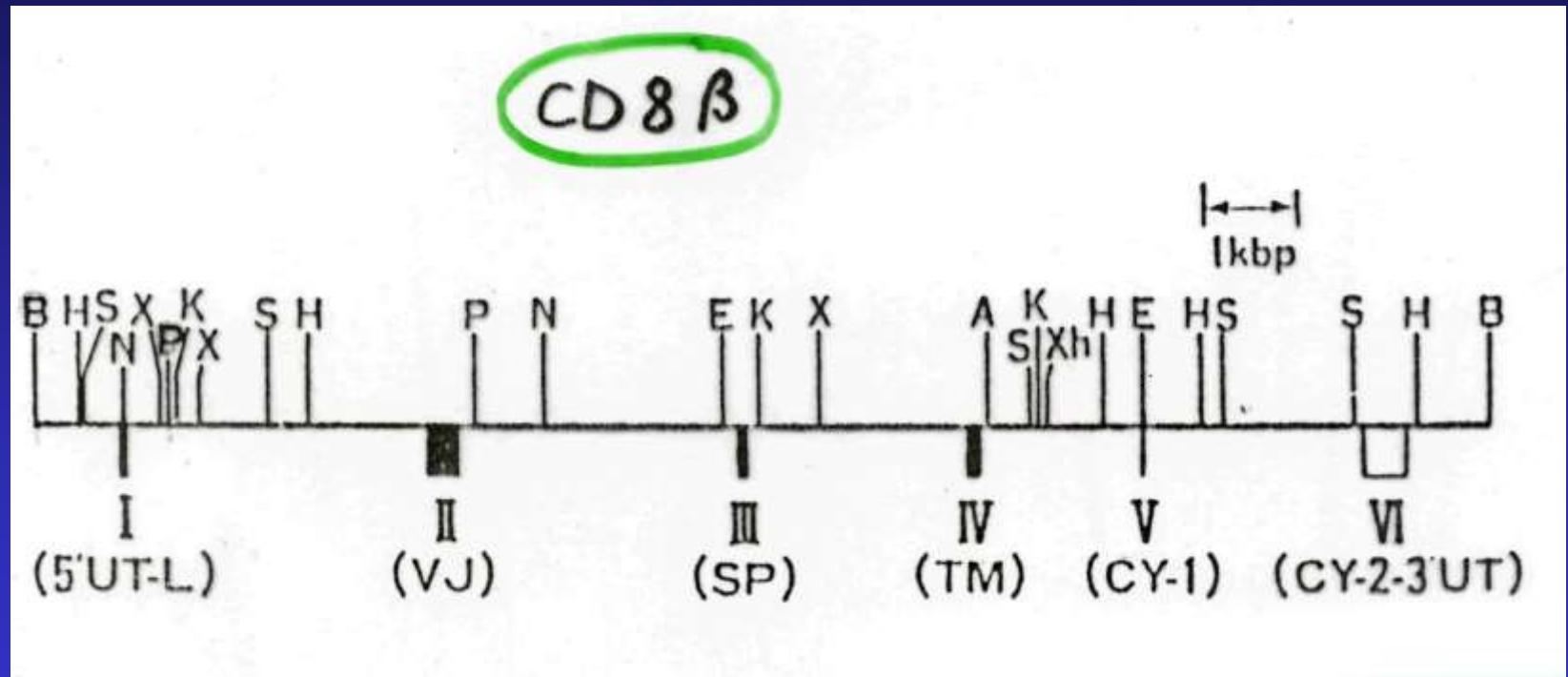


Generation of mouse germ-line chimeras

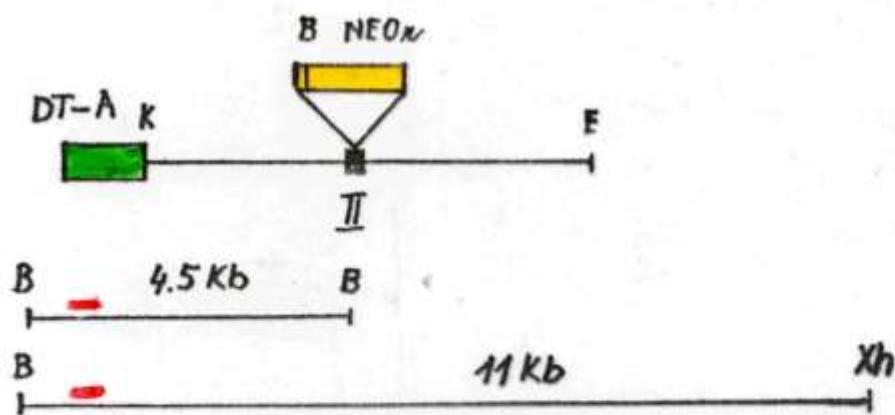
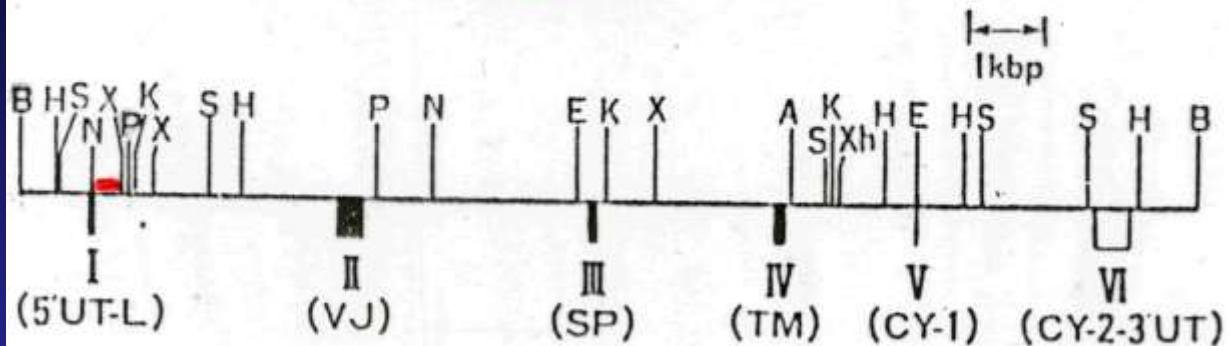


Gene targeting of CD8 beta

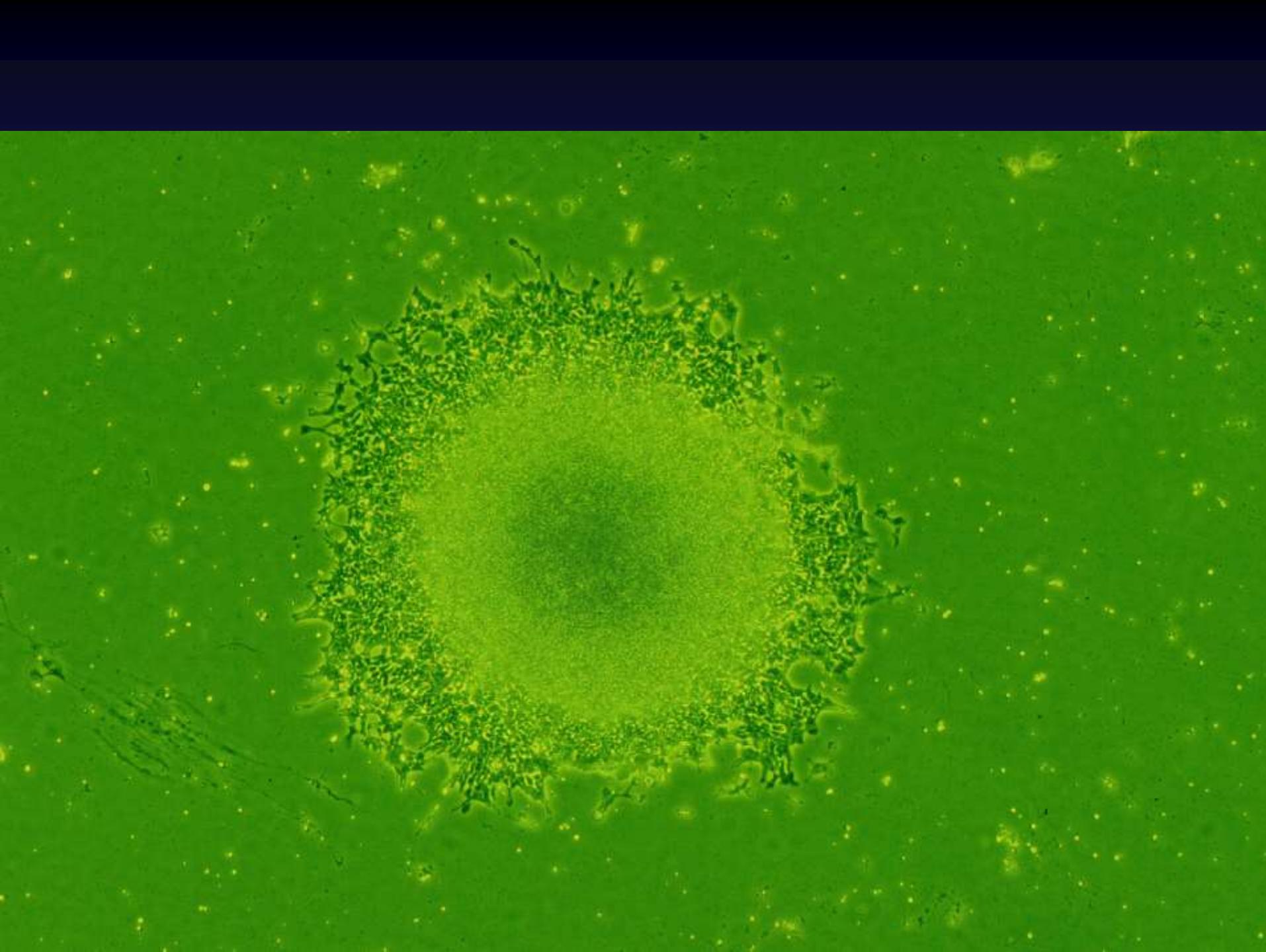


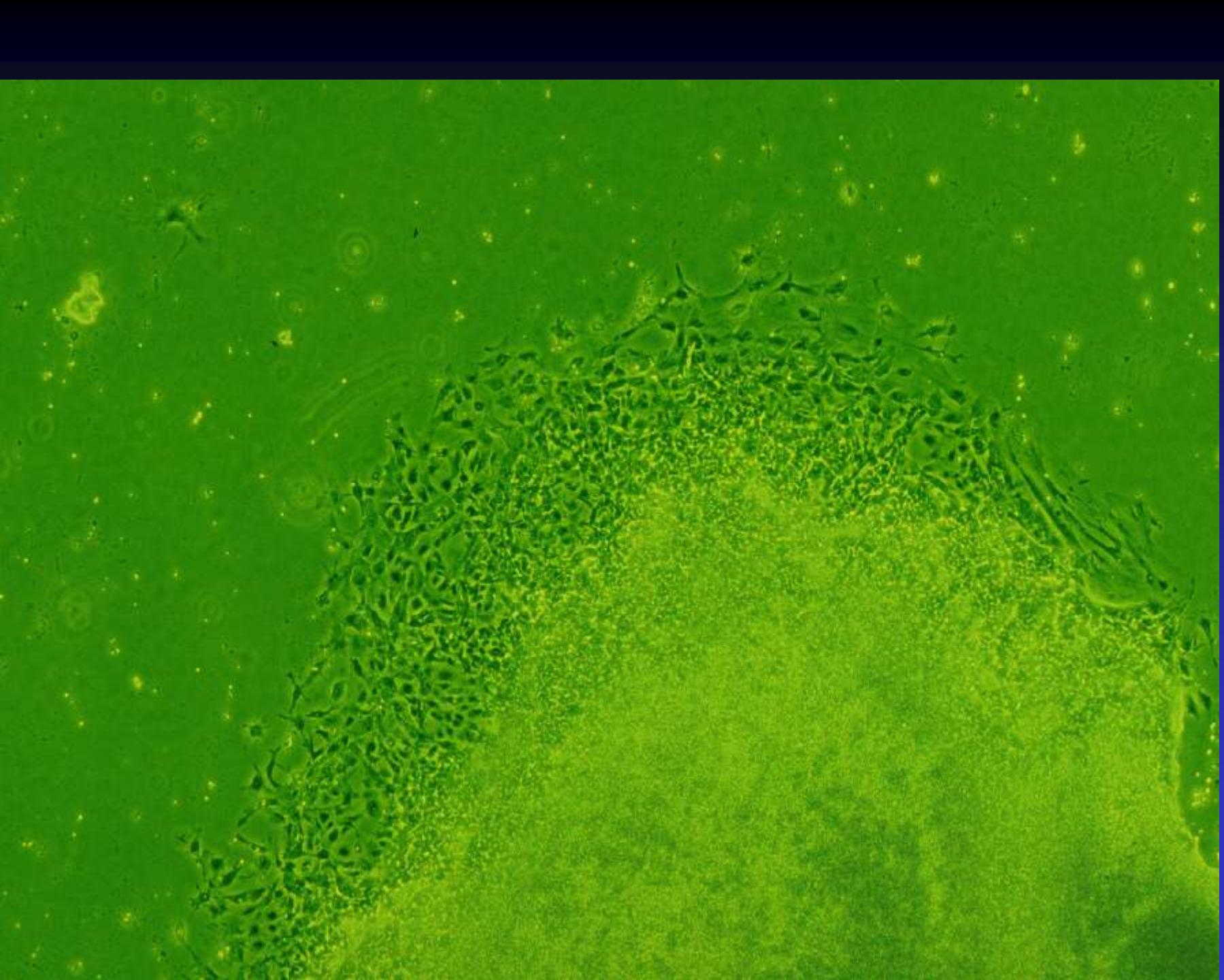


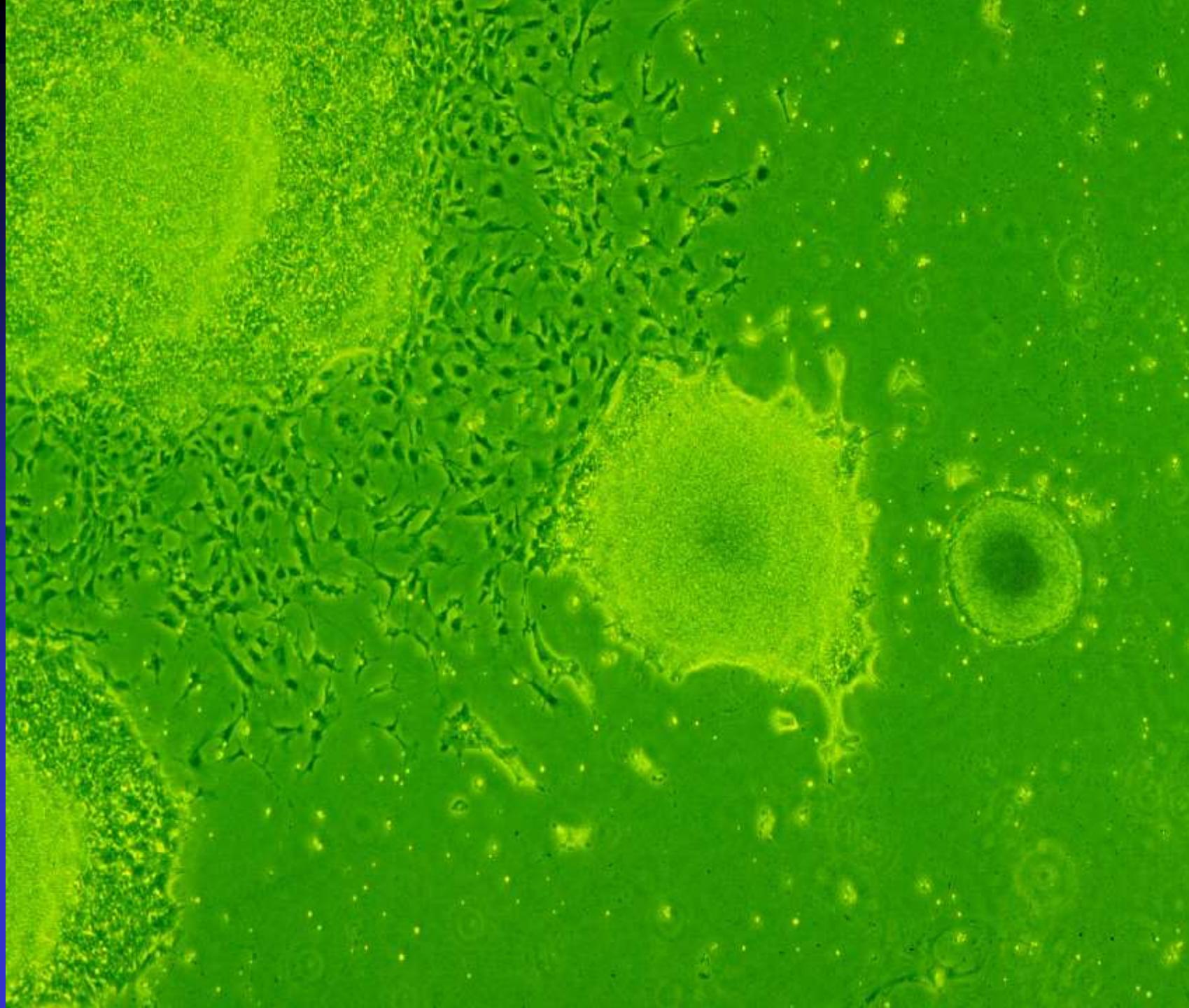
CD 8 β



B, Xh

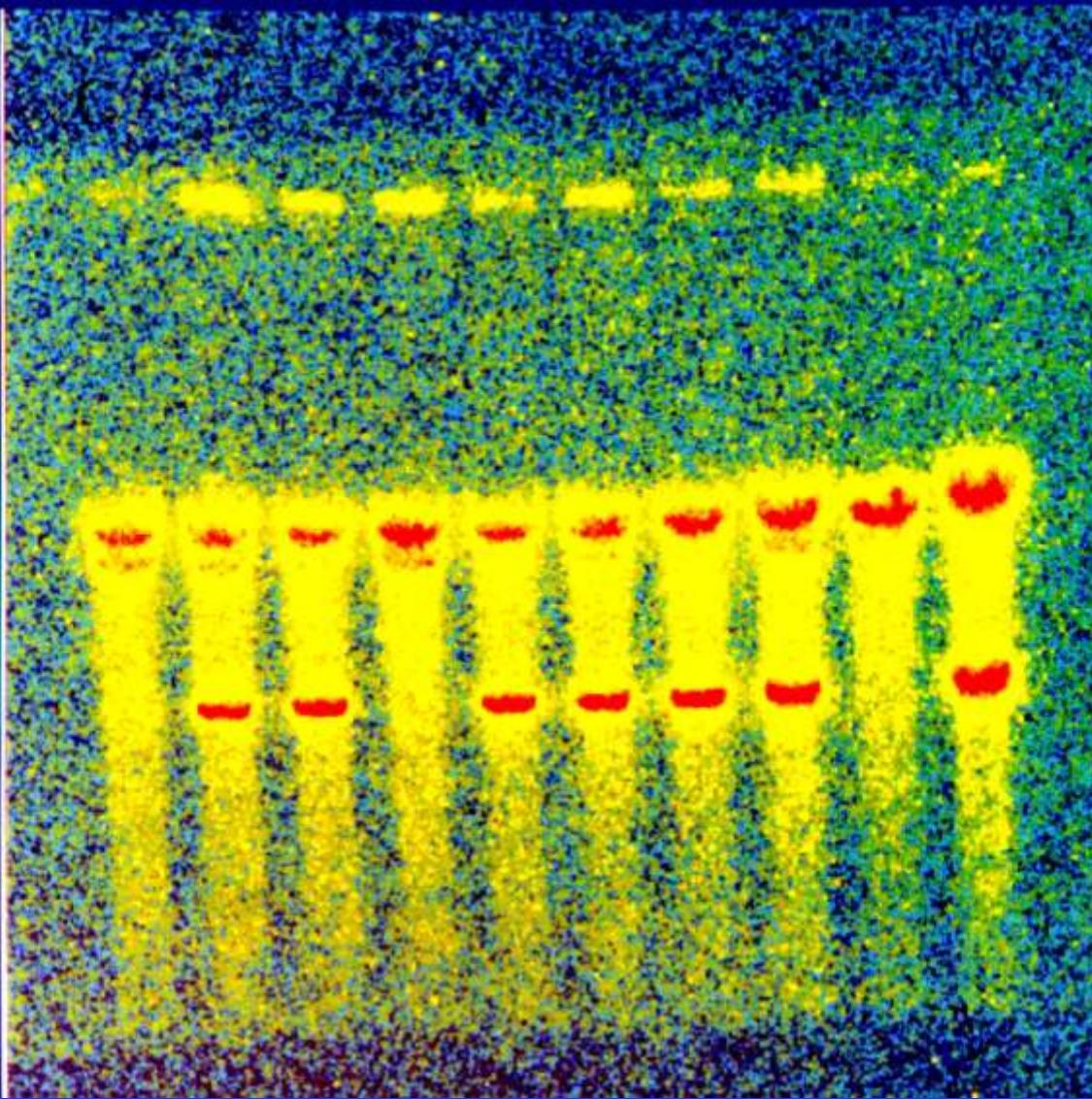


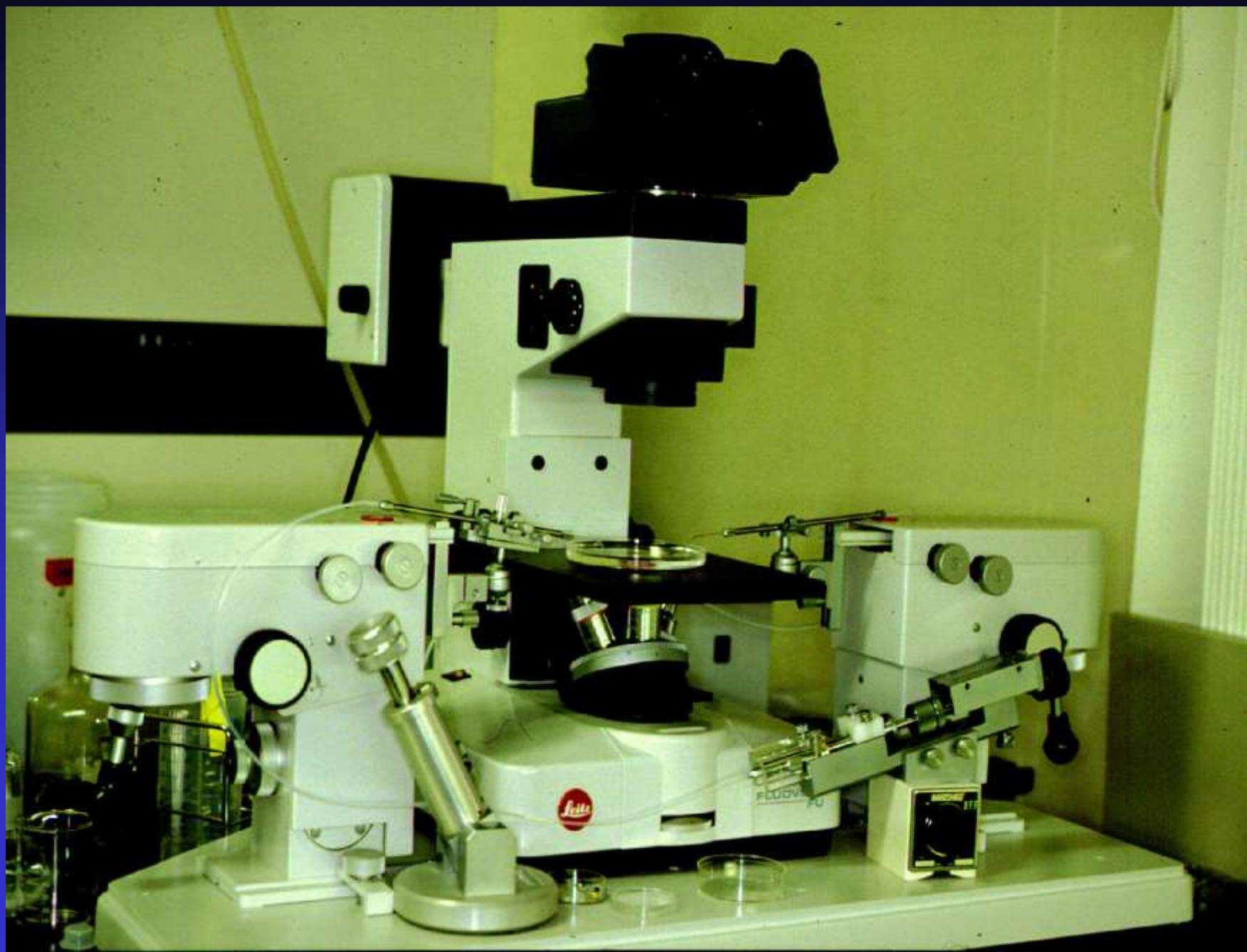




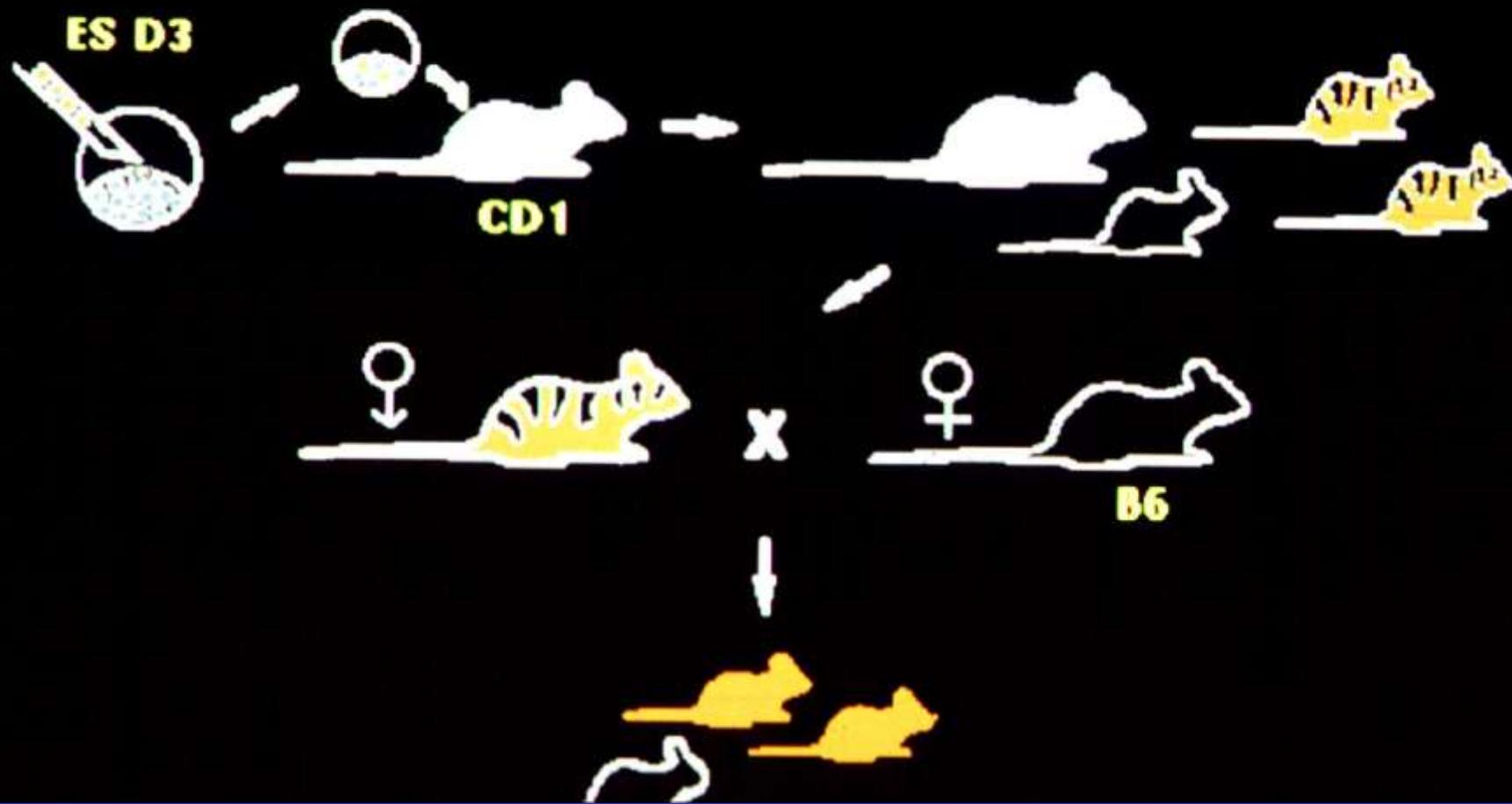
Southern blot analysis of ES E14 cell clones

11 kb →
4.5 kb →





Generation of mouse germ-line chimeras





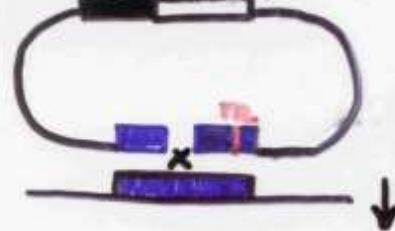




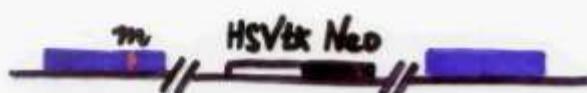




Hit and Run
Neo HSVtk



HOMOLOGOUS
RECOMBINATION



INTRACHROMOSOMAL
RECOMBINATION



HASTY ET AL, 1999
NATURE, VOL 350, 243

HPRT - HYPOXANTHINE PHOSPHORIBOSYL TRANSFERASE
HOX - 2.6

ENHANCER TRAP

P | lacZ | P | neo

GENE TRAP

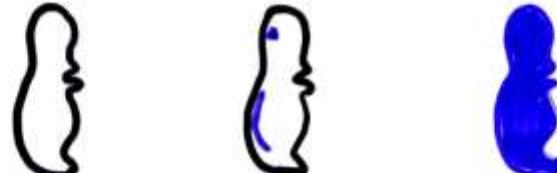
SA | lacZ | P | neo

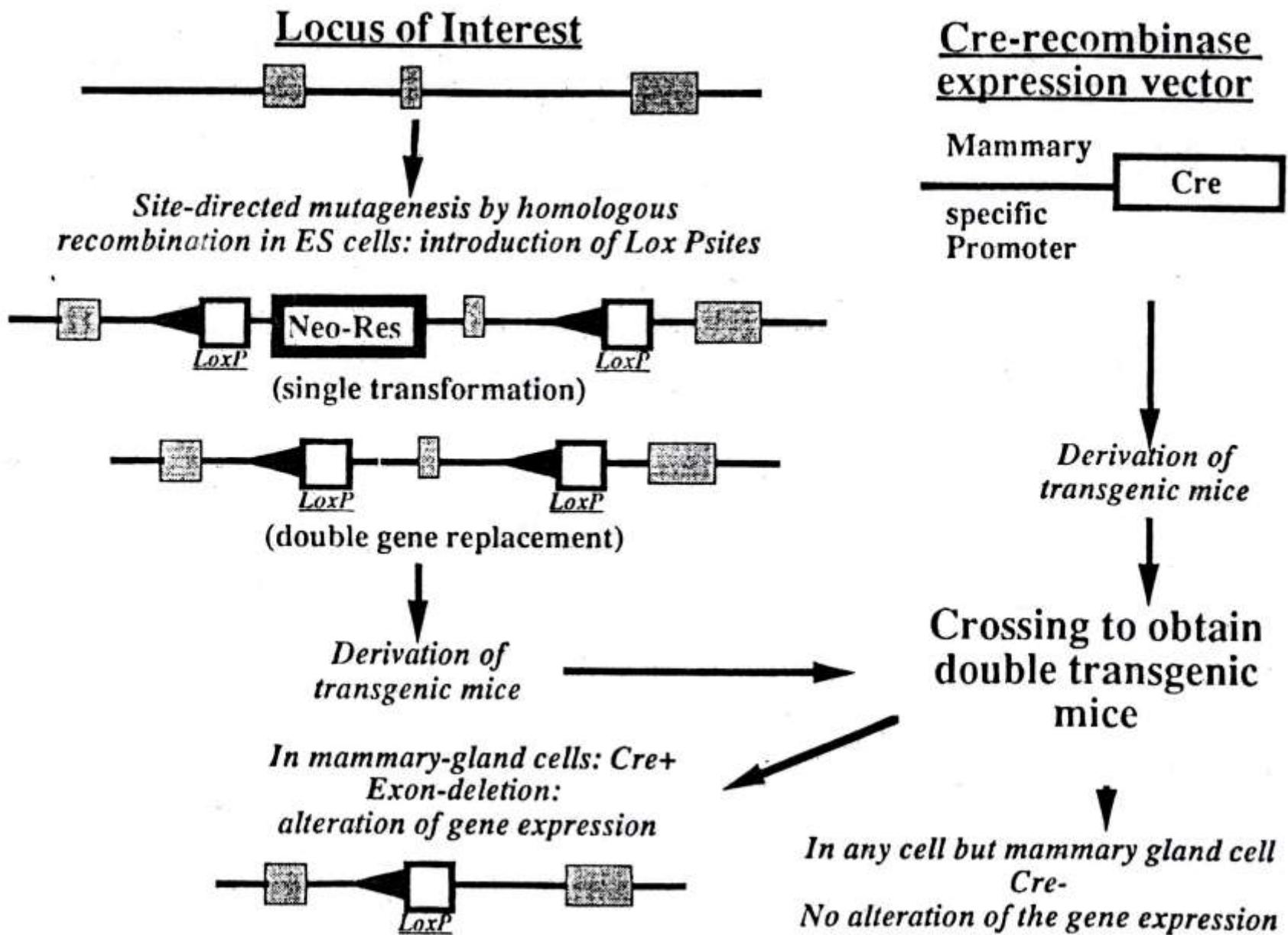
E. coli β -GALACTOSIDASE

L
ELECTROPORATION
G418 SELECTION



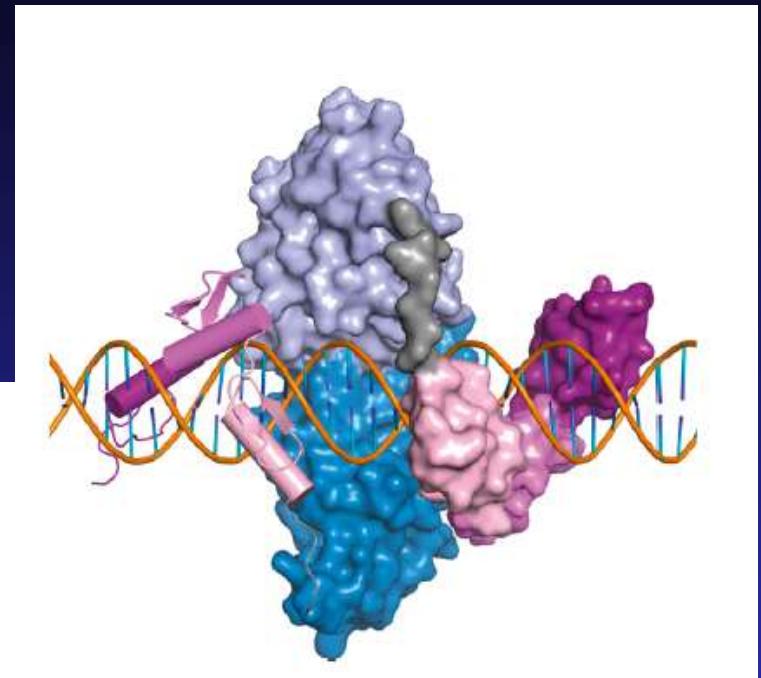
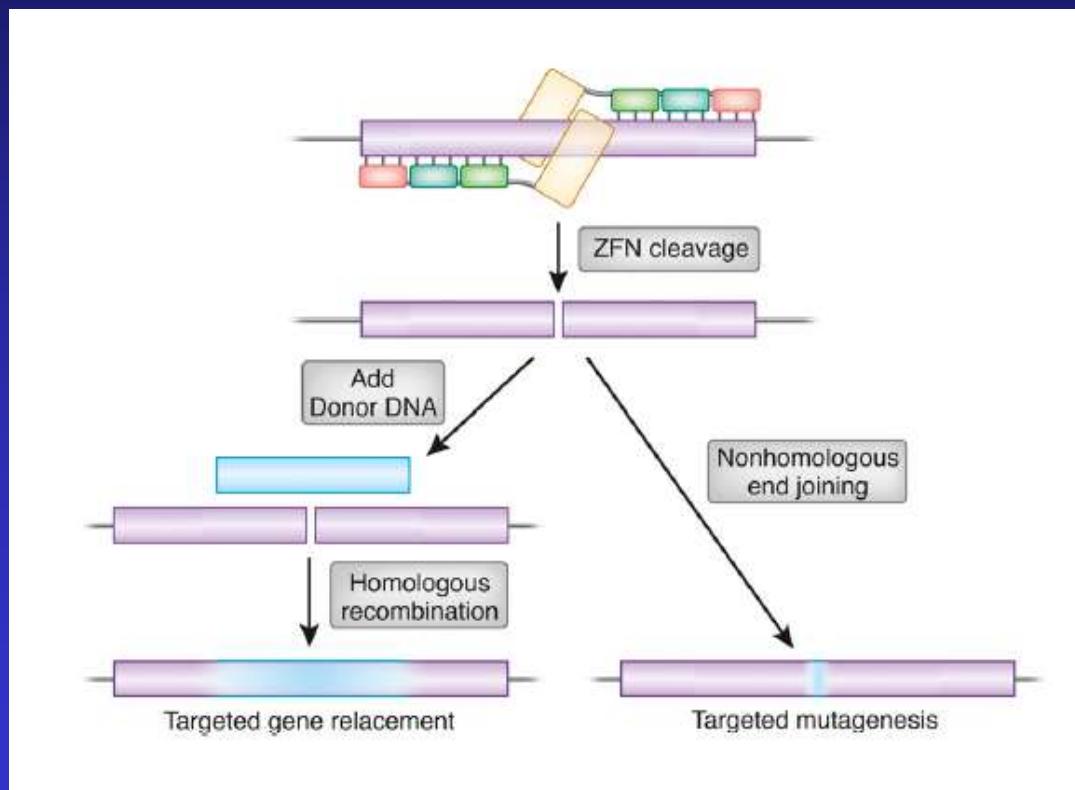
X-GAL STAINING



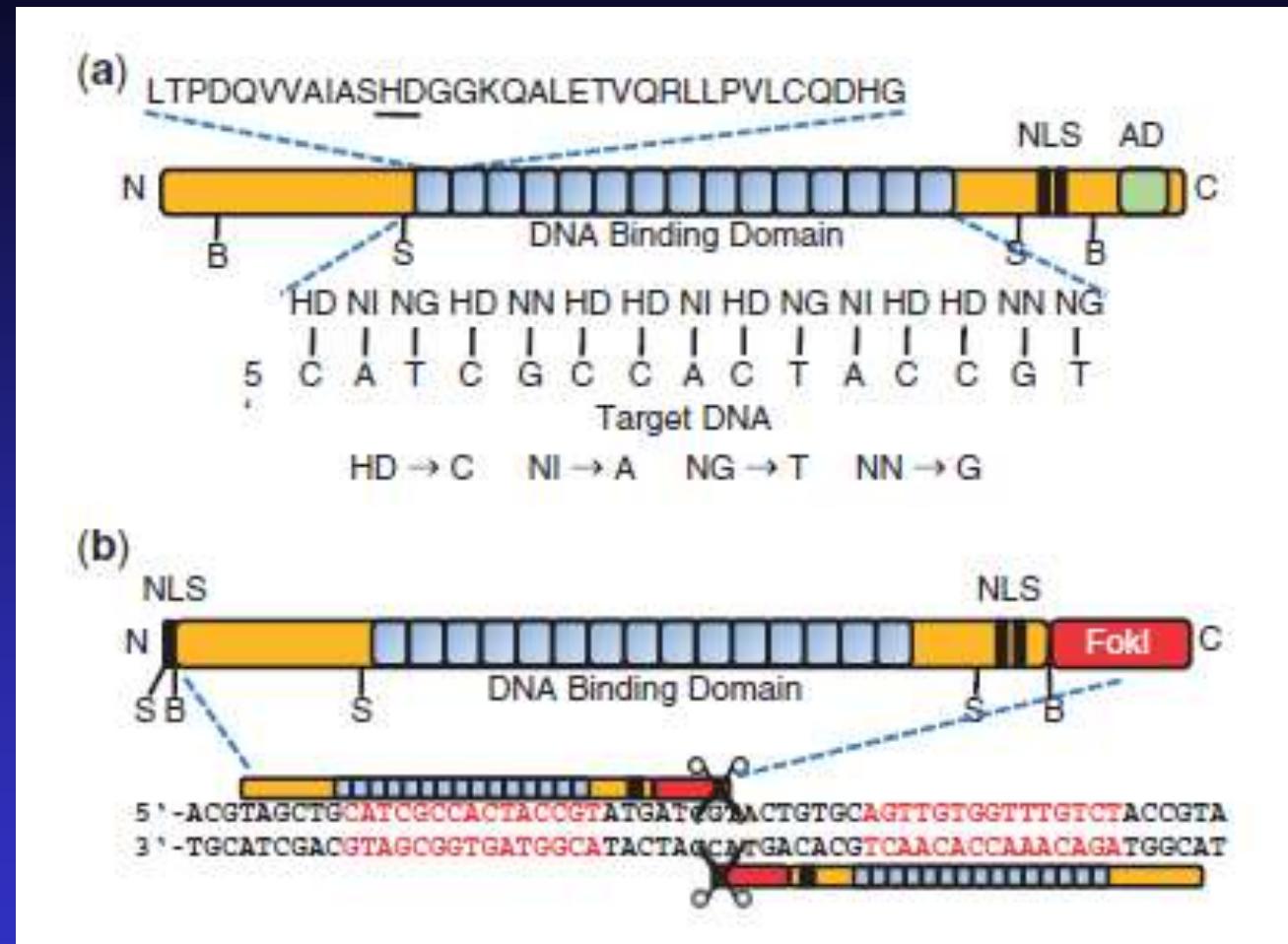


ZFNs – Zinc finger nukleásy – DNA binding domain + Fok I endonuclease monomer

Double-strand break – oprava pomocí non-homologous end-joining, drobné inzerce nebo delece (indels)

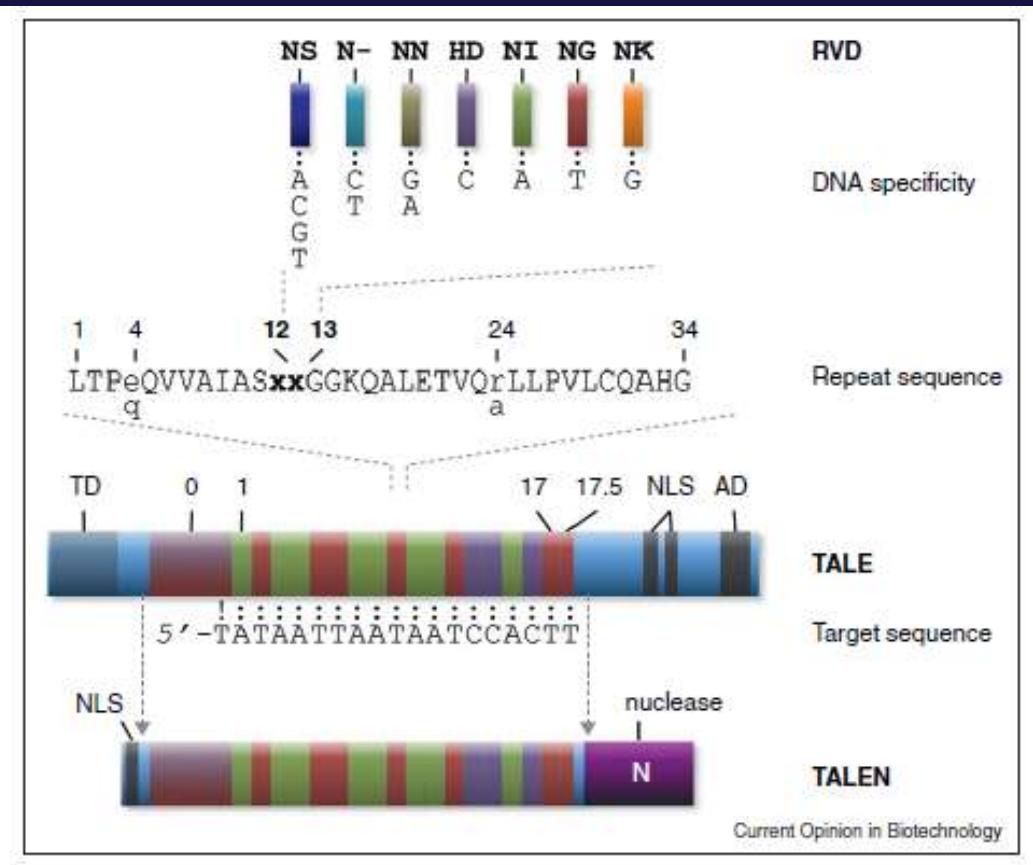


TALENs – transcription aktivátor-like effector nucleases, TALE-based nucleases

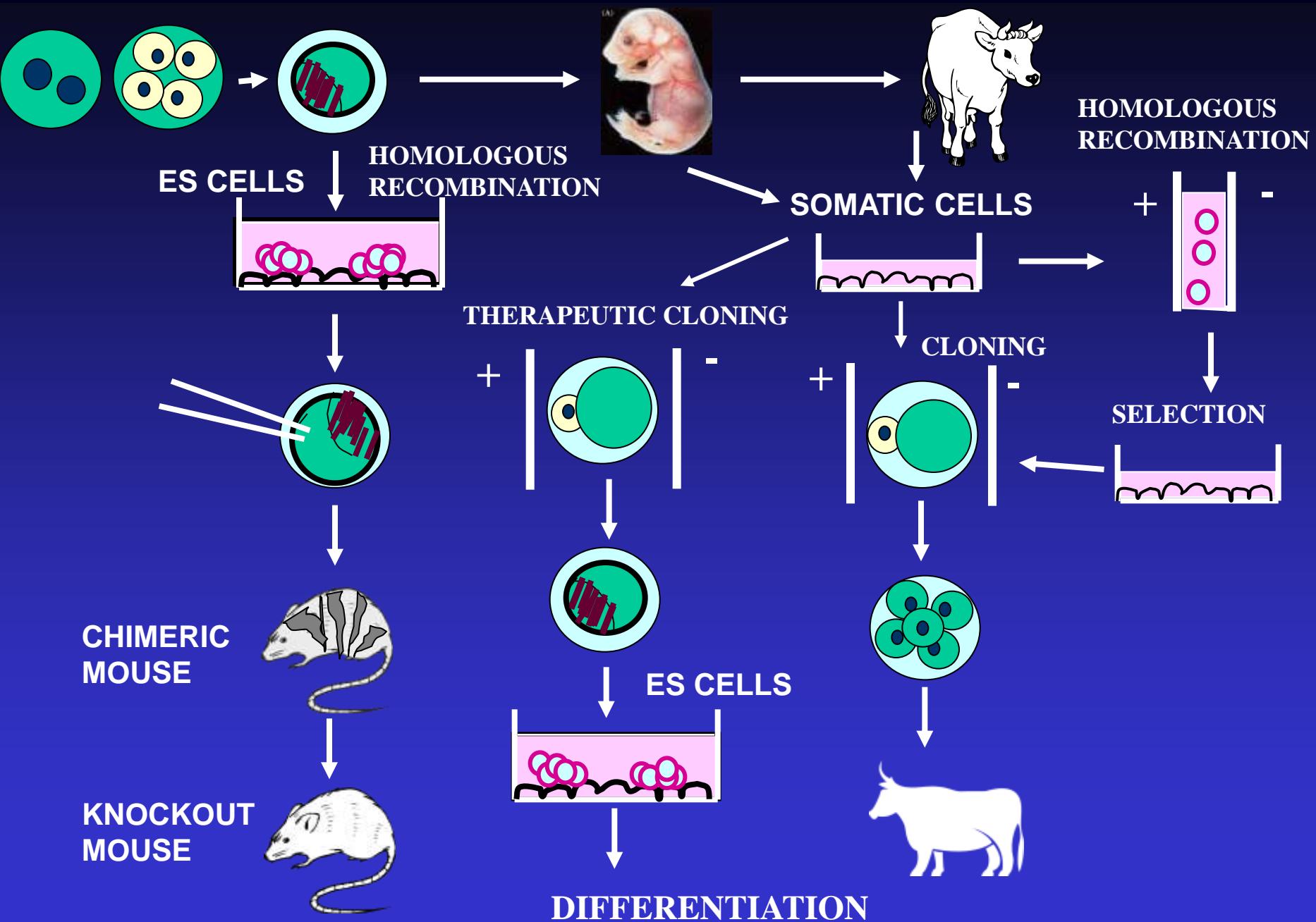


TALE – bakteriální proteiny, pathogen *Xanthomonas* – injikace proteinů do infikovaných rostlinných buněk
Rozpoznání cílové DNA v hostitelském genomu, aktivace exprese genů, nezbytných pro multiplikaci pathogenu

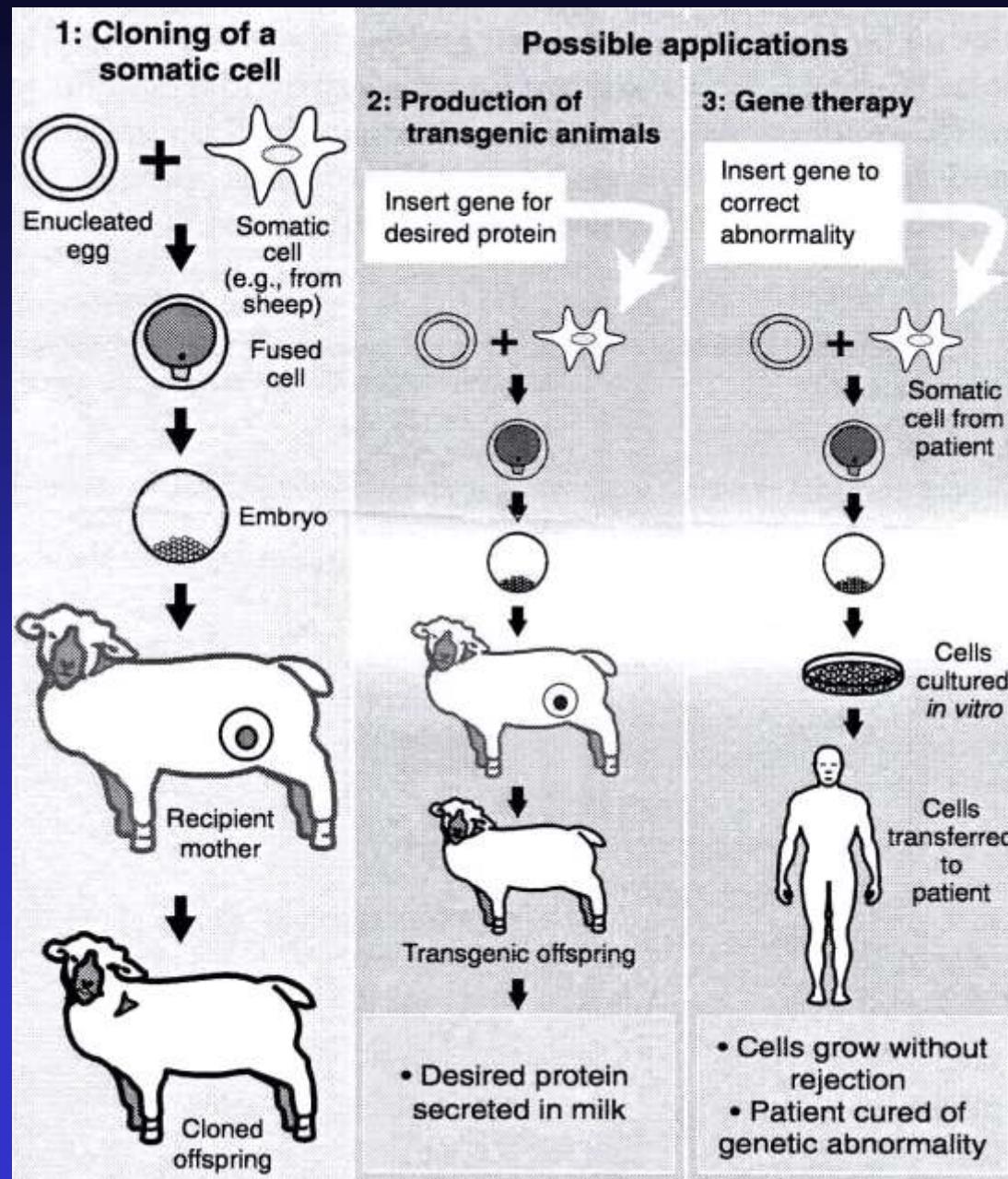
DNA binding domain – skládá se z tandemu 15,5 – 19,5 single repeats, každý se skládá z 34 vysoce konzervovaných zbytků
Carlson D.F. et al., www.pnas.org/cgi/doi/10.1073/pnas.1211446109



PRE-IMPLANTATION EMBRYO



CLONING - POTENTIAL BENEFITS



Trounson, A. ;
MJA 167:568-569
; 1997