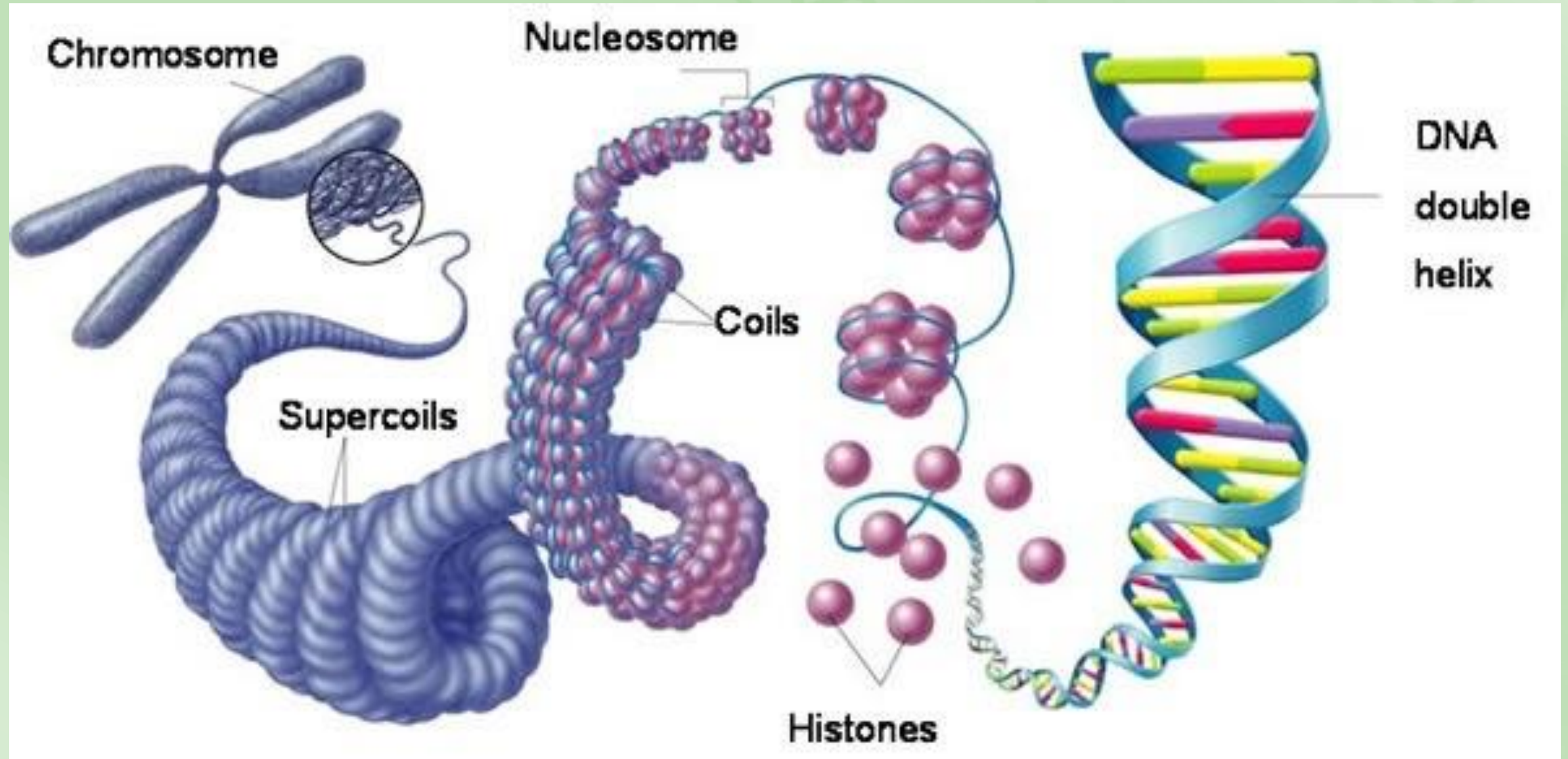


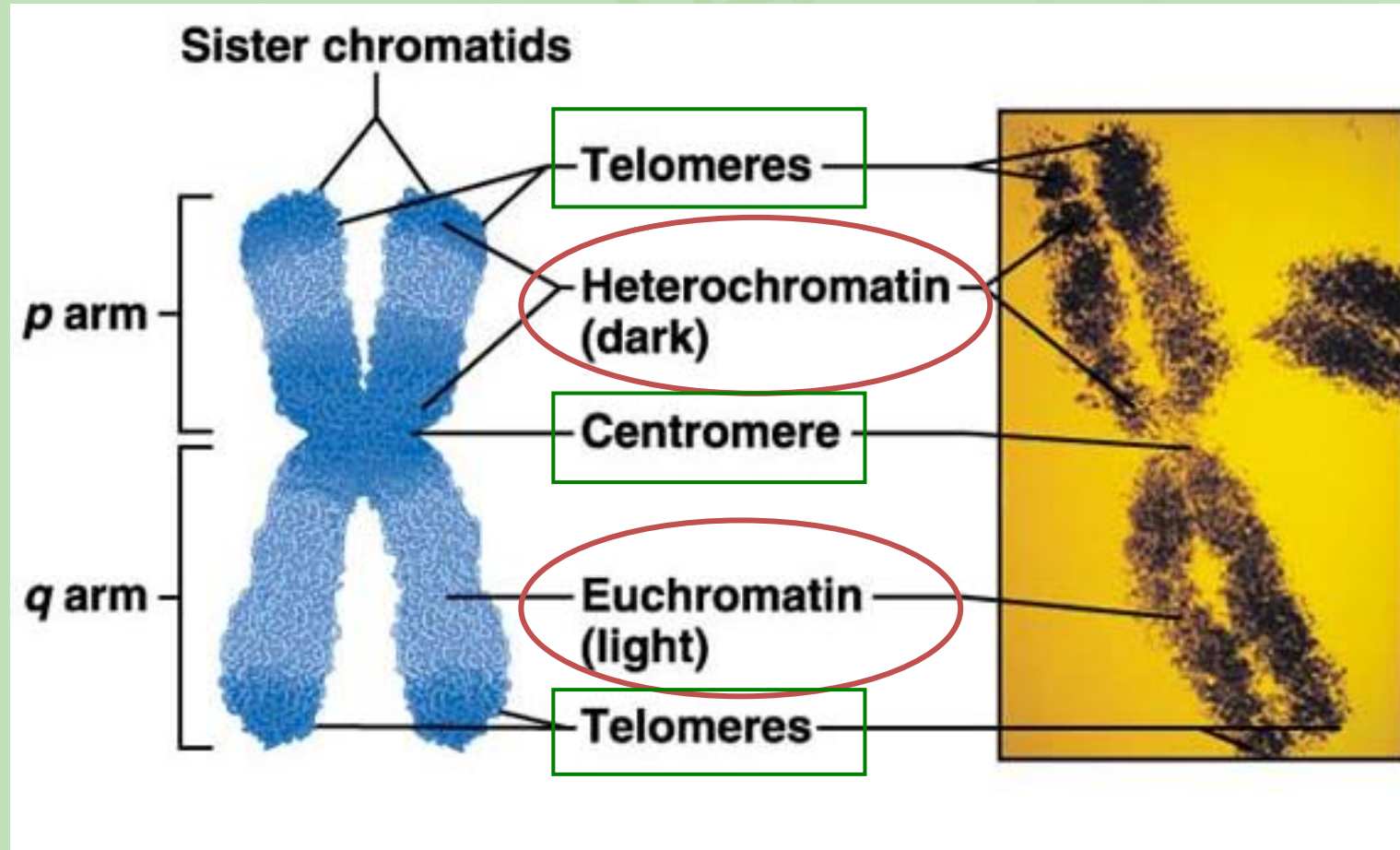
Organização de genomas fúngicos

Profa. Dra. Chirlei Glienke
BIOGEMM-UFPR

Genomas eucarióticos - Conceitos básicos



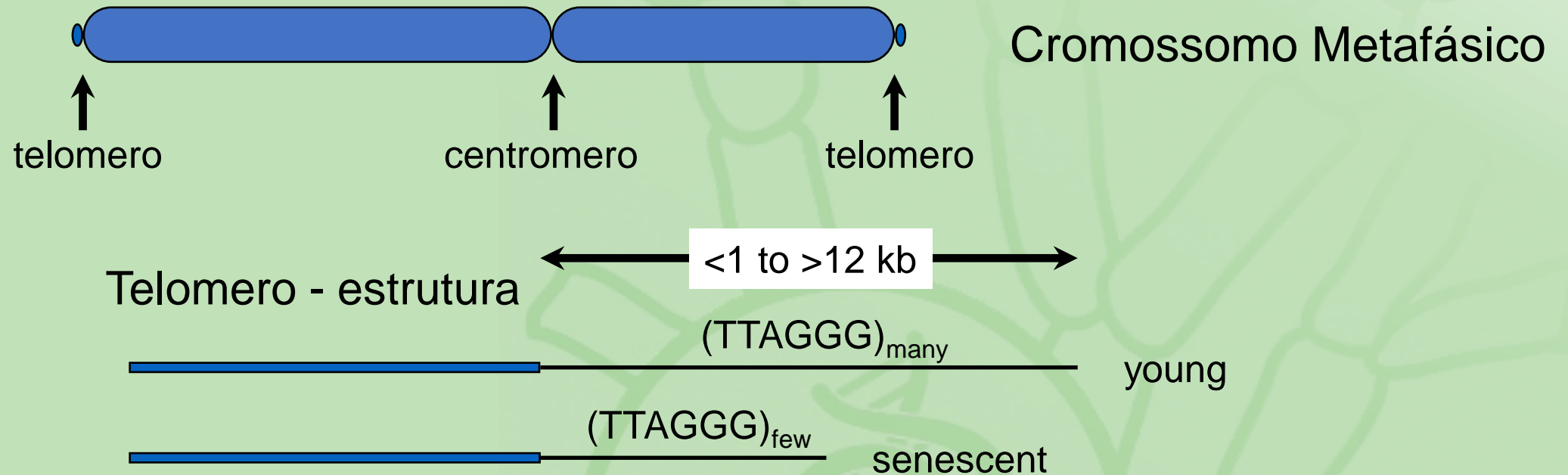
Anatomia de um cromossomo eucariótico



Heterocromatina: cromatina densa

Eucromatina: cromatina menos densa

Telômeros e centrômeros



Sequencia telomérica de muitos eucariotos incluindo muitos fungos: TTAGGG

Sequencia telomérica de *Sacharomyces cerevisiae*: TG1-3/C1-3A)

Species	Sequence	Reference
<i>Neurospora crassa</i>	TTAGGG	Schechtman 1990
<i>Fusarium oxysporum</i>	TTAGGG	Powell and Kistler 1990
<i>Histoplasma capsulatum</i>	TTAGGG	Woods and Goldman 1992
<i>Cladosporium fulvum</i>	TTAGGG	Coleman et al. 1993
<i>Podospora anserina</i>	TTAGGG	Javerzat et al. 1993
<i>Ustilago maydis</i>	TTAGGG	Guzman and Sanchez 1994
<i>Magnaporthe grisea</i>	TTAGGG	Farman and Leong 1995
<i>Pneumocystis carinii</i>	TTAGGG	Underwood et al. 1996
<i>Aspergillus nidulans</i>	TTAGGG	Bhattacharyya and Blackburn 1997
<i>Aspergillus oryzae</i>	TTAGGGTCAACA	Kusumoto et al. 2003
<i>Cryptococcus neoformans</i>	TTAG ₃₋₅	Edman 1992
<i>Schizosaccharomyces pombe</i>	T ₁₋₂ ACA ₀₋₁ C ₀₋₁ G ₁₋₆	Matsumoto et al. 1987
<i>Saccharomyces cerevisiae</i>	TG ₂₋₃ (TG) ₁₋₆	Shampay et al. 1984
<i>Saccharomyces exiguus</i>	TG ₂₋₃ (TG) ₁₋₆	Cohn et al. 1998
<i>Saccharomyces castellii</i>	TCTGGGTG	Cohn et al. 1998
<i>Saccharomyces dairenensis</i>	TCTGGGTG	Cohn et al. 1998
<i>Saccharomyces kluyveri</i>	GACATGCGTACTGTGAGGTCTGGGTG	Cohn et al. 1998
<i>Candida albicans</i>	TCTAACTTCTTGGTGTACGGA TG	McEachern and Hicks 1993
<i>Candida guilliermondii</i>	TACTGGTG	McEachern and Blackburn 1994
<i>Candida glabrata</i>	CTGTGGGGTCTGGGTG	McEachern and Blackburn 1994
<i>Candida maltosa</i>	CAGACTCGCTTGGTGTACGGA TG	McEachern and Blackburn 1994
<i>Candida tropicalis</i>	TCACGATCATTGGTGTA(A/C)G GATG	McEachern and Blackburn 1994
<i>Candida pseudotropicalis</i>	TGATTAGTTATGTGGTGTACG GATT	McEachern and Blackburn 1994
<i>Kluyveromyces lactis</i>	TGATTAGGTATGTGGTGTACG GATT	McEachern and Blackburn 1994

The sequence corresponding to the template region of the *S. cerevisiae* telomerase RNA, ACCACACCCACACA, is also found in the *Saccharomyces* species *S. paradoxus*, *S. cariocanus*, *S. mikatae*, *S. kudriavzevii*, *S. bayanus*, and *S. pastorianus* (Dandjinou et al. 2004).

Sequências teloméricas em fungos

Topics in Current Genetics, Vol. 15

P. Sunnerhagen, J. Piškur (Eds.): Comparative Genomics

DOI 10.1007/4735_108 / Published online: 11 October 2005

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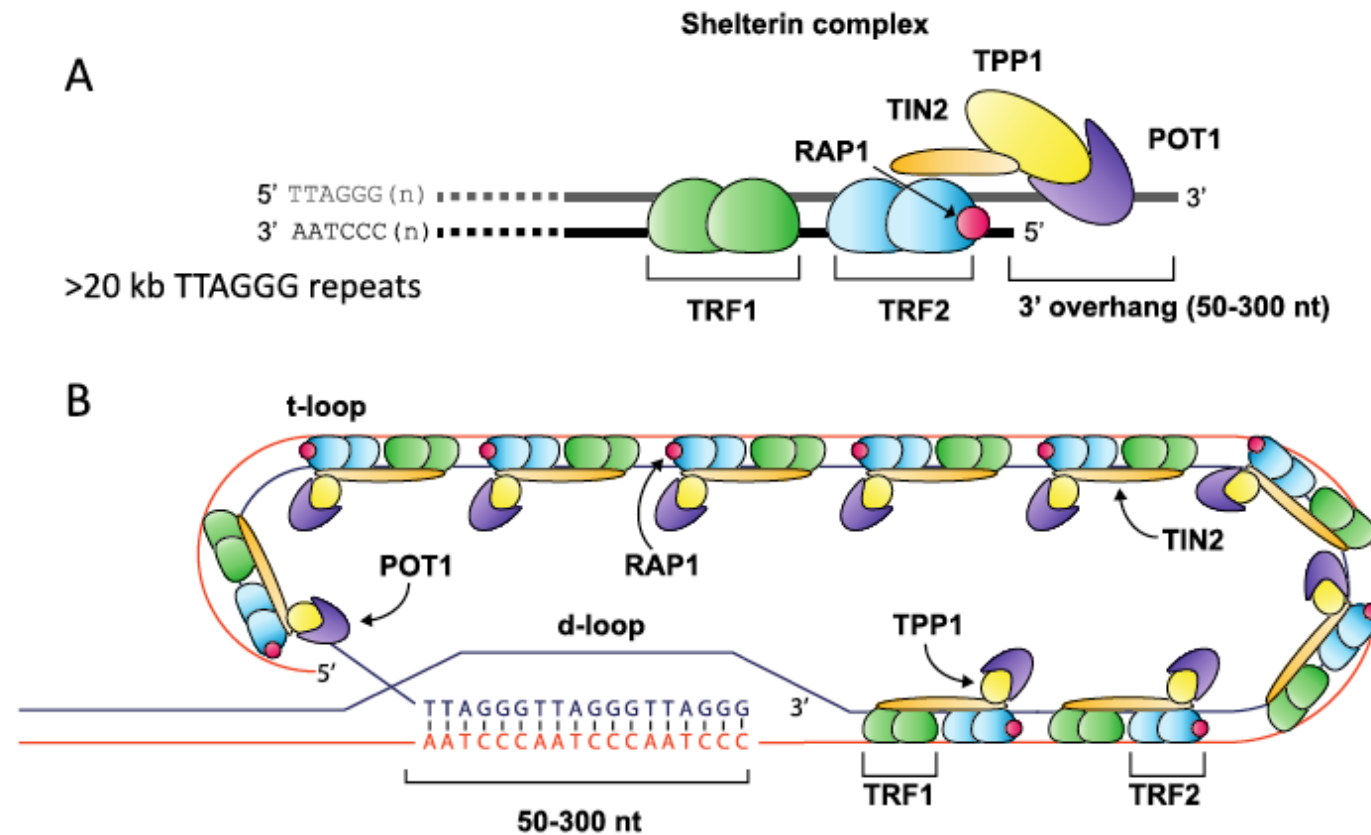
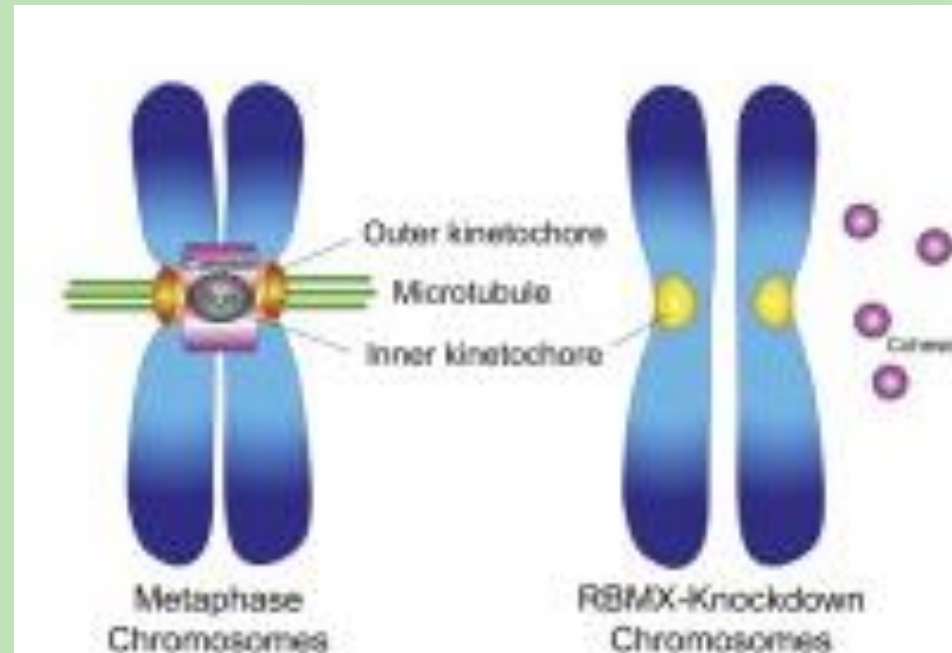


Figure 1. Overview of telomere structure. The terminal ends of mammalian chromosomes consist of an array of (TTAGGG)_n repeats ending with a 3' overhang of between 50 and 300 nt in length (A). This array is bound by many protein components including members of the shelterin complex, which anchors to the repeat array through Telomere Repeat binding Factors 1 & 2 (TRF1 and TRF2), binding repeats as a homodimer, and forming a complex with TIN2 (TRF1-interacting factor), RAP1 (Repressor Activator Protein 1), TPP1 and POT1 (Protection of Telomere 1) (A). The repeat array folds into a higher-order t-loop structure where the 3' overhang displaces a portion of the forward strand to create a d-loop, thereby sequestering the free chromosome end from the DNA repair machinery (B).



A

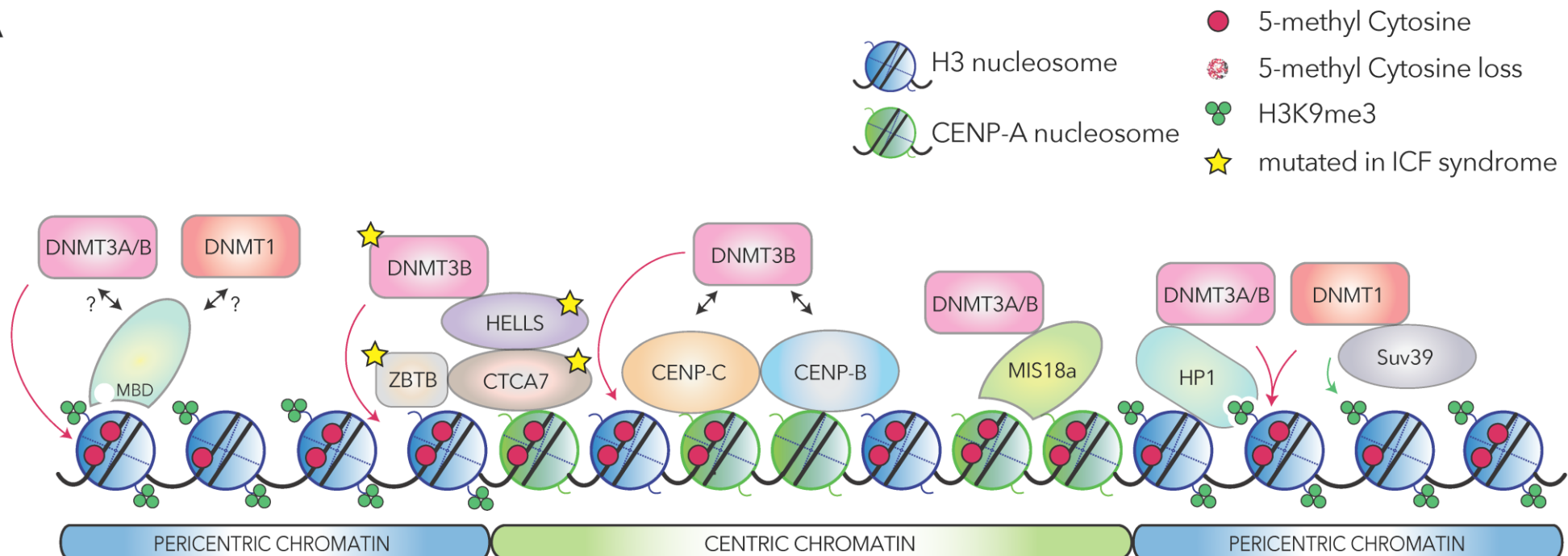
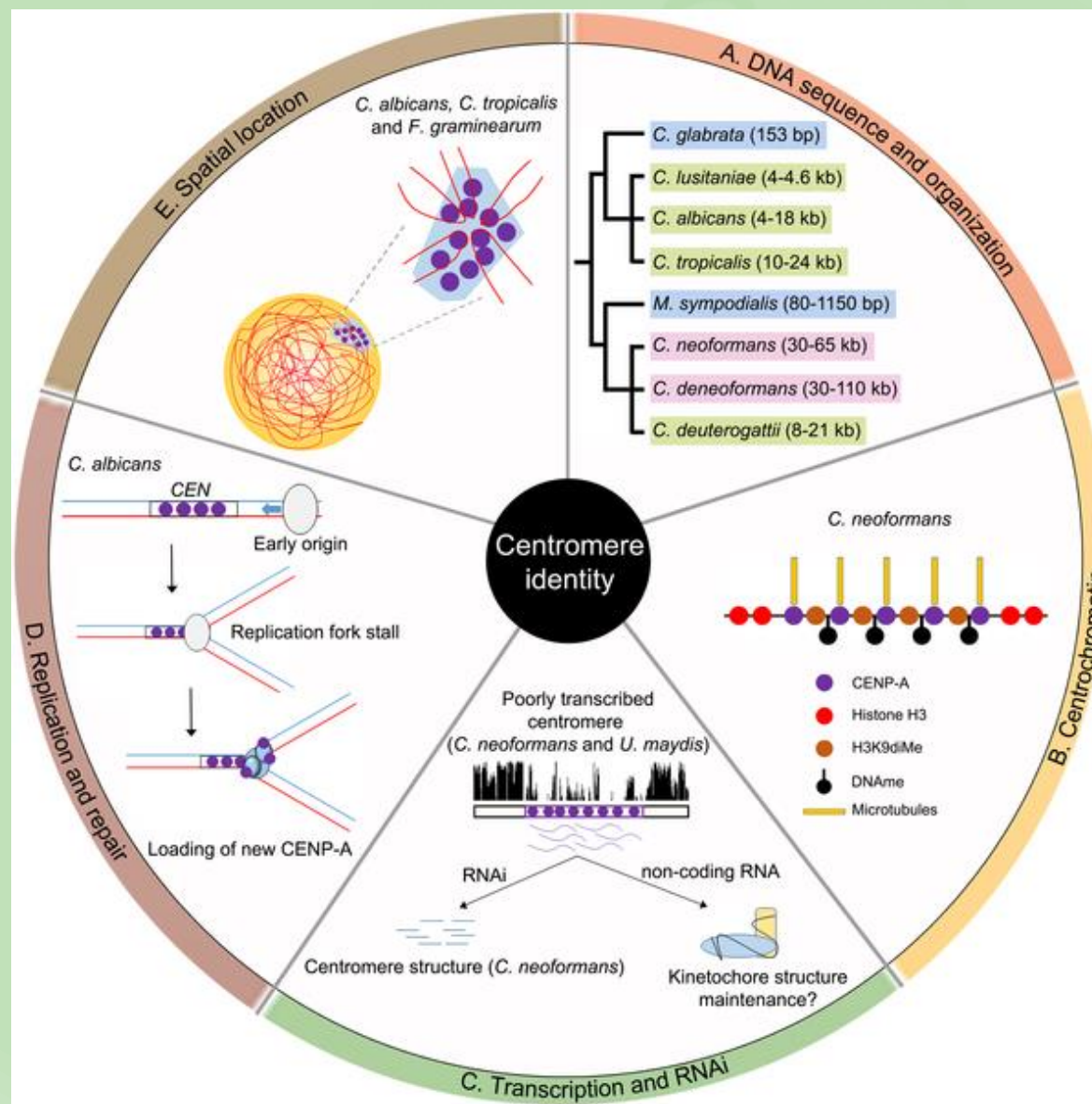
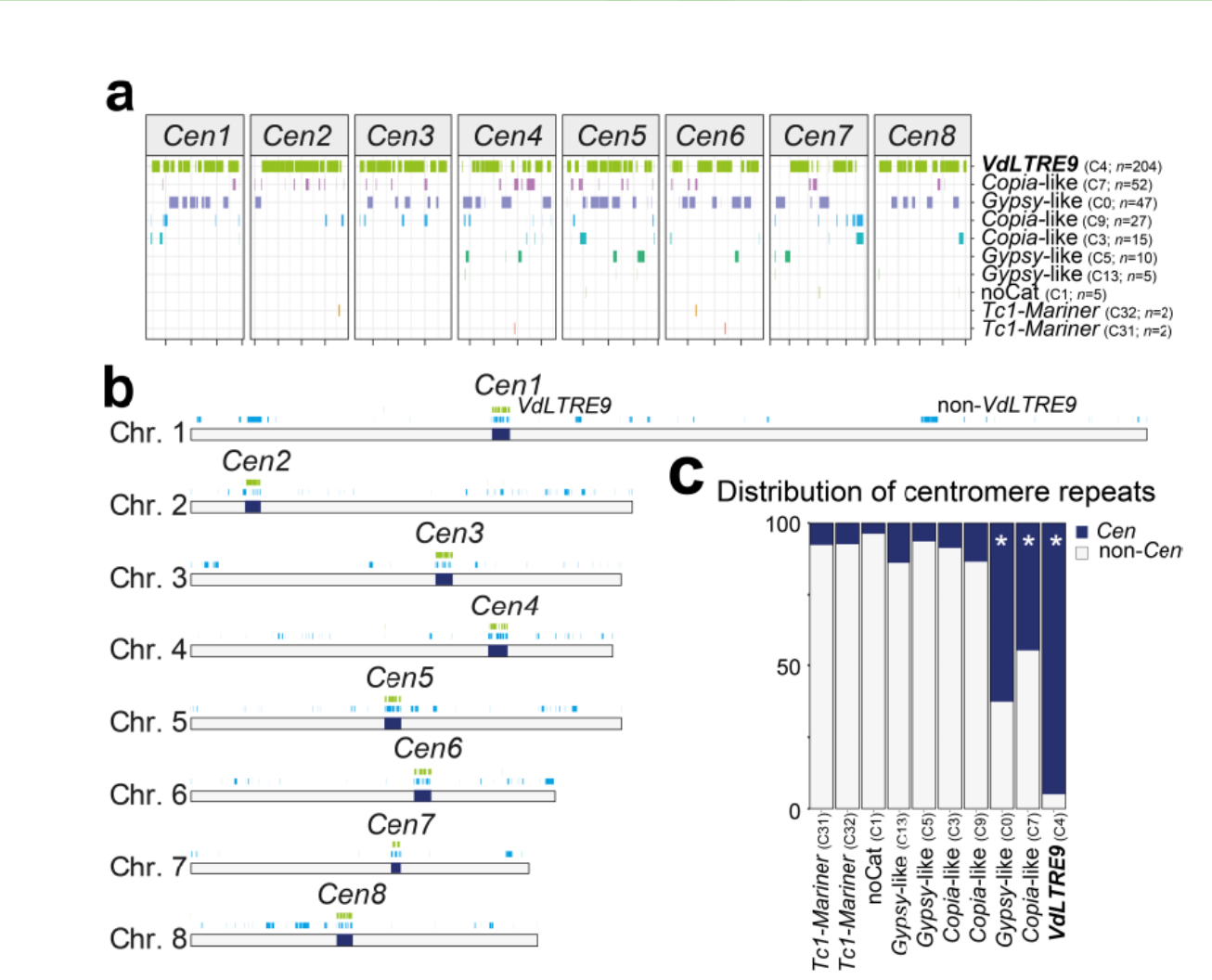


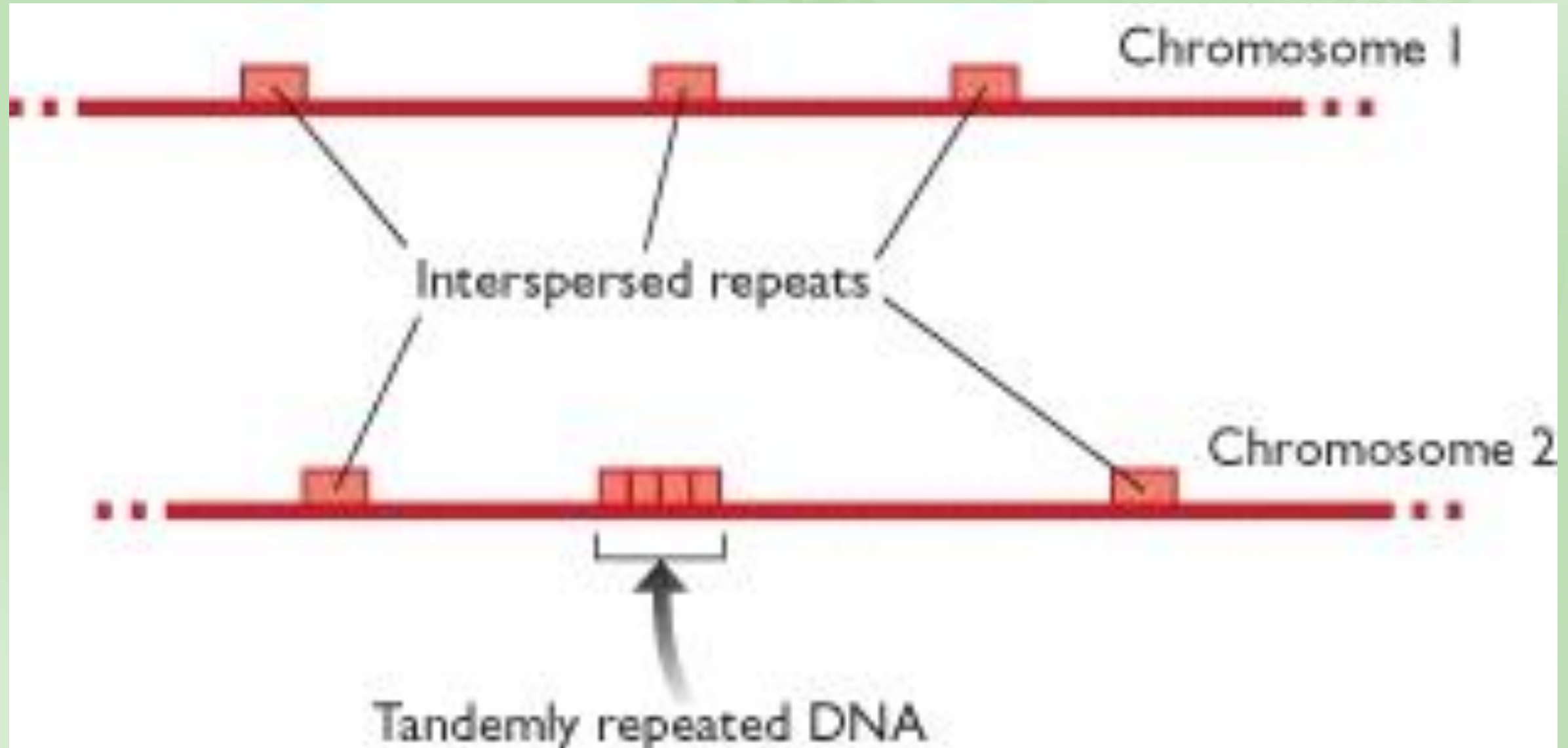
Fig 1. Five key determinants of centromere identity in pathogenic fungi.



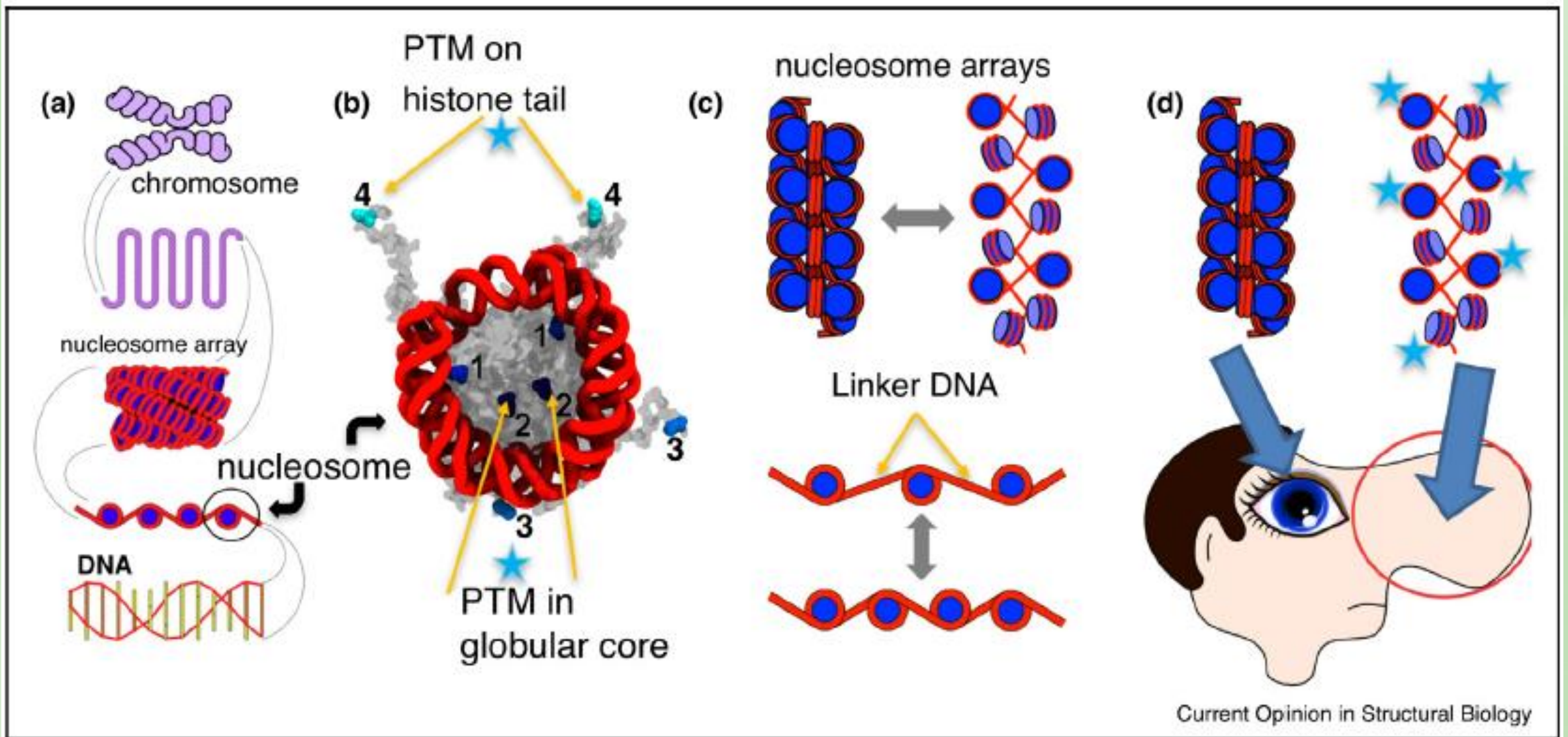
Sequências repetitivas em centrômeros de *Verticillium dahliae*

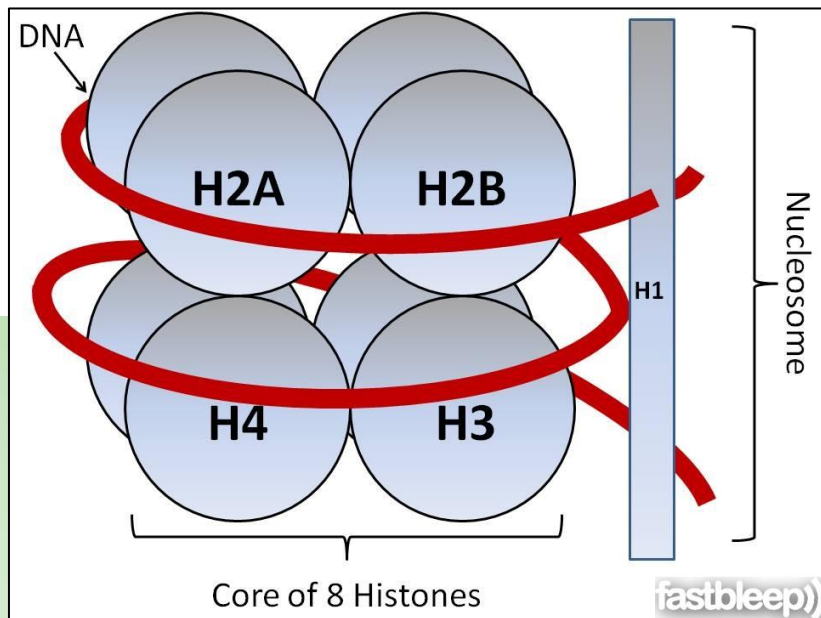
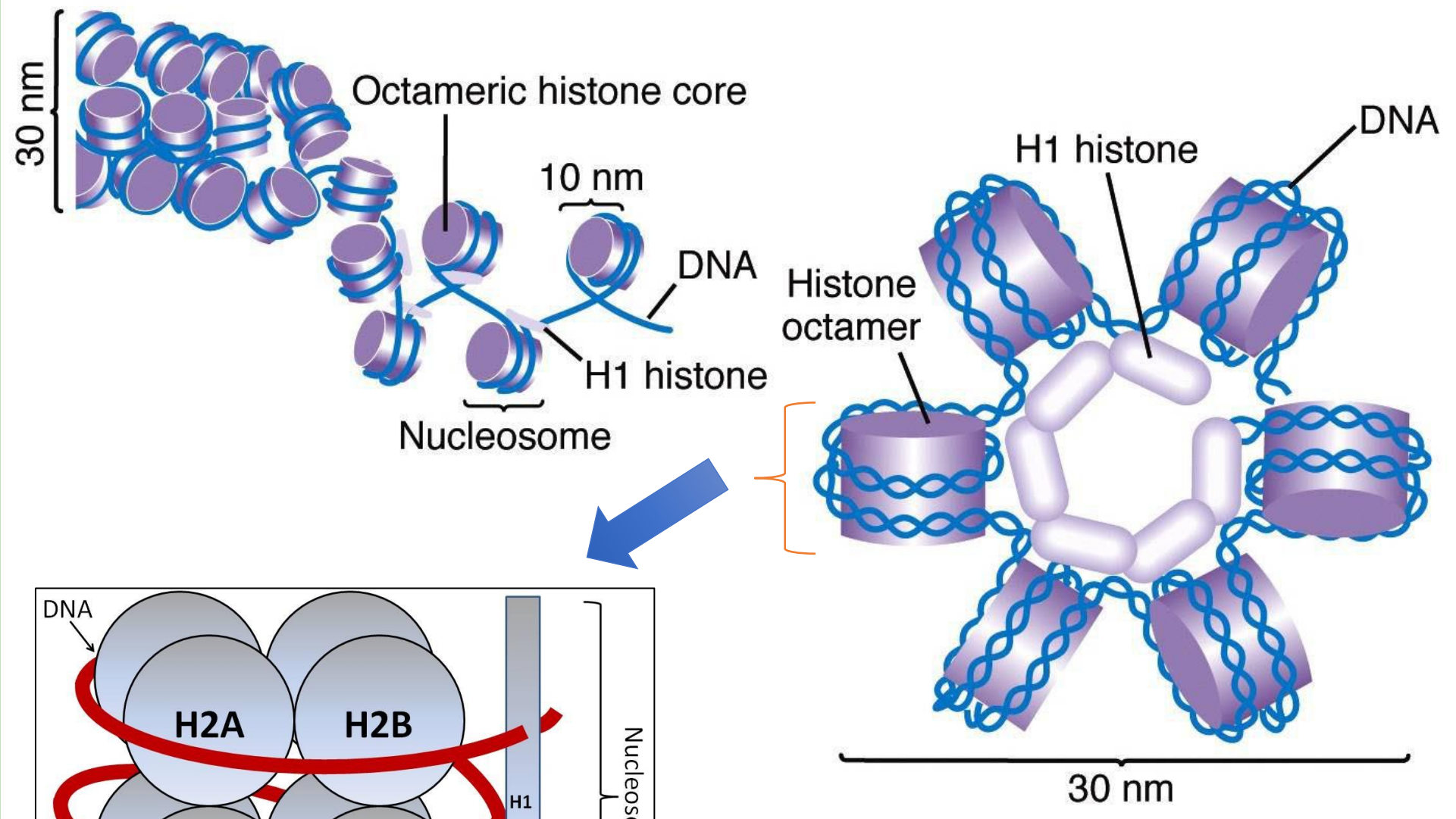


Sequencias repetitivas: dispersas e *in tandem*



Organização da cromatina de eucariotos – estrutura e função





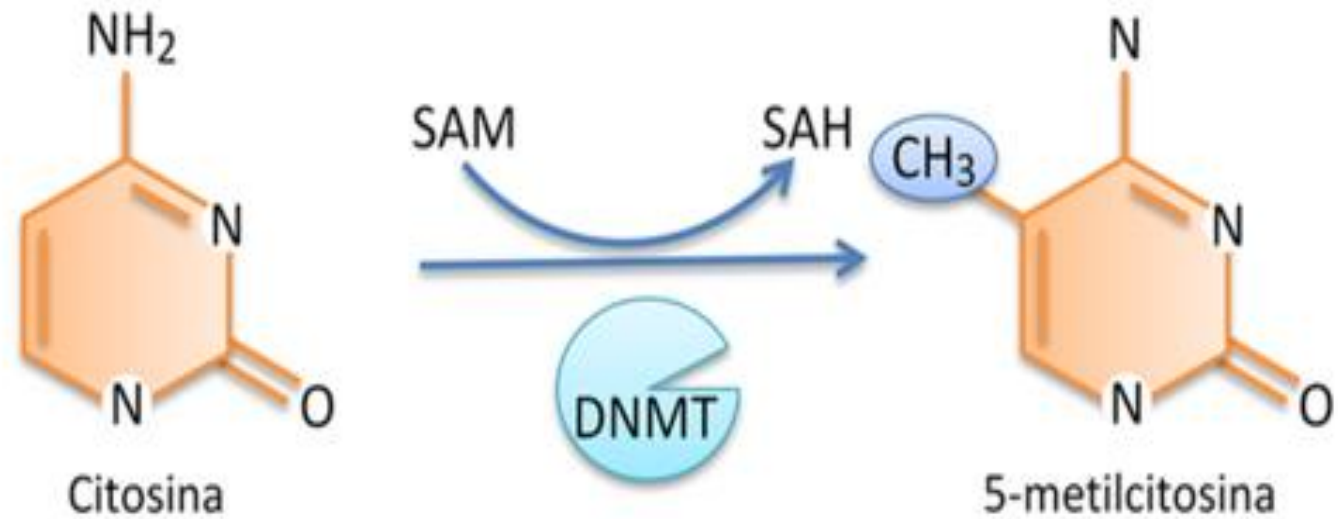
Nucleossomos e histonas

Mecanismos epigenéticos

1. Metilação do DNA
2. Modificação das histonas
3. Modificação por RNAi



Metilação de DNA



SAM: S-adenosil-metionina (doador do grupo metil)

SAH: S-adenosil-homocisteína

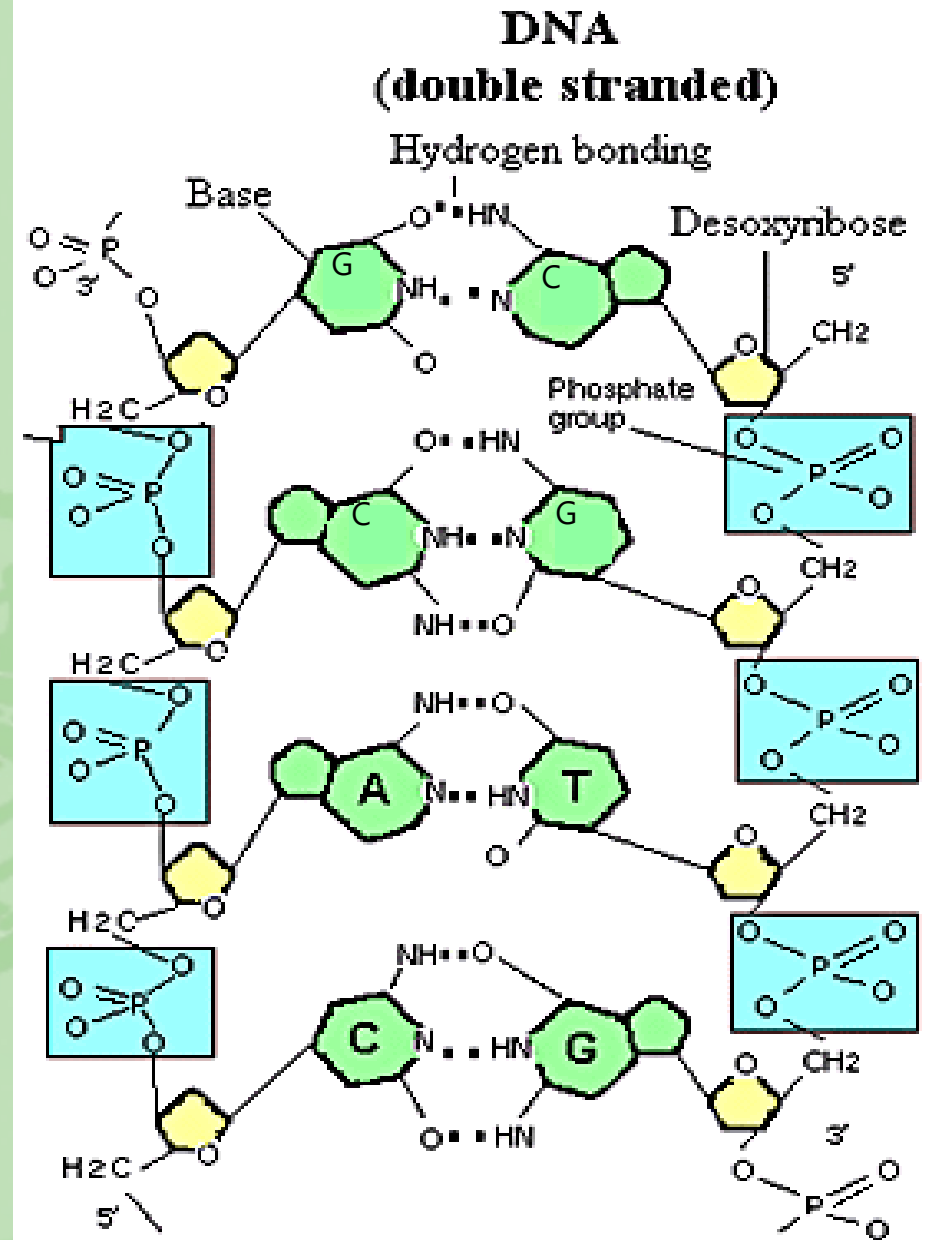
DNMT: **DNA metiltransferase**

Metilação do DNA

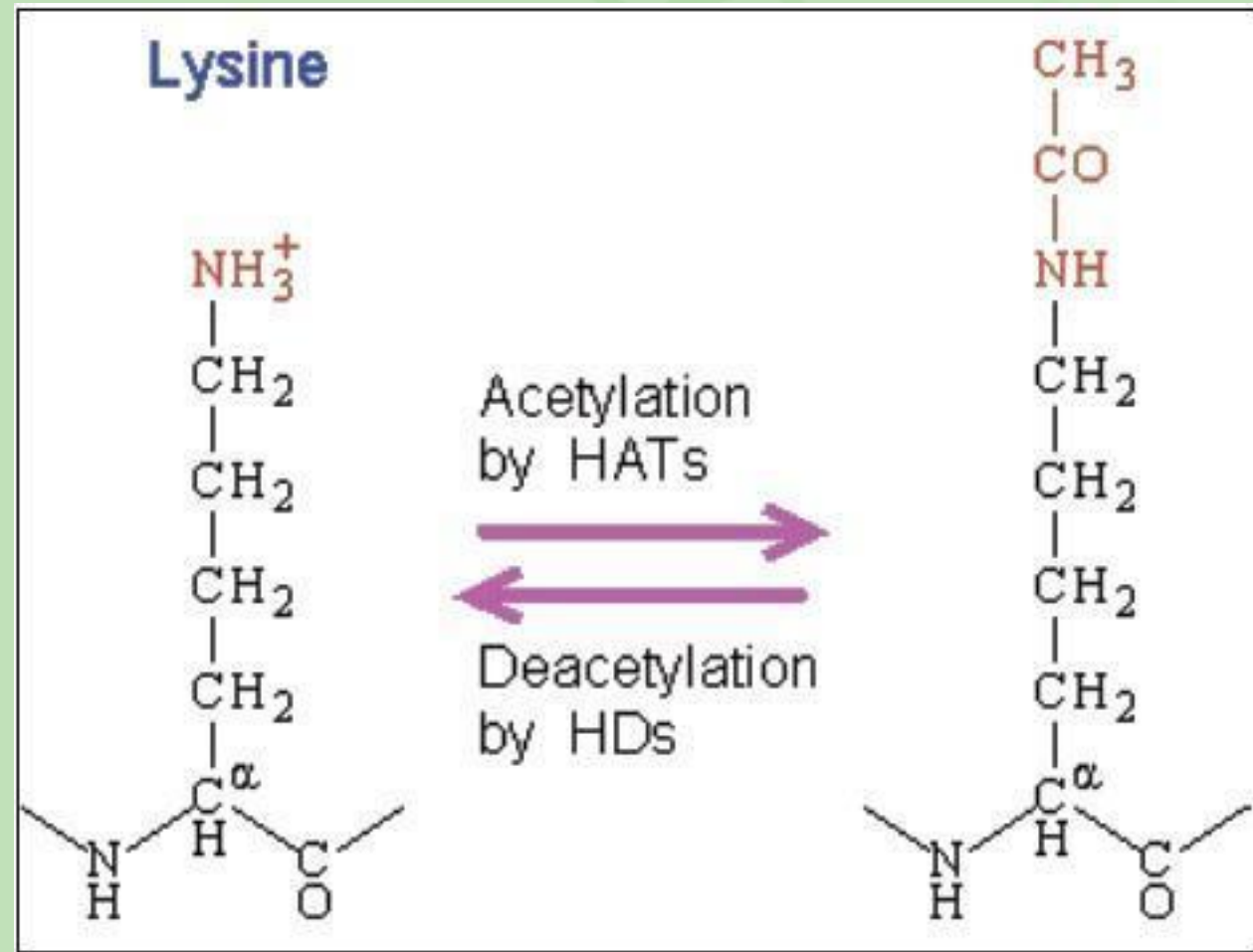
- Ocorre no carbono 5 de uma citosina que geralmente precede uma guanina (CpG)

5' - CpG - 3'

ligação —
fosfodiéster

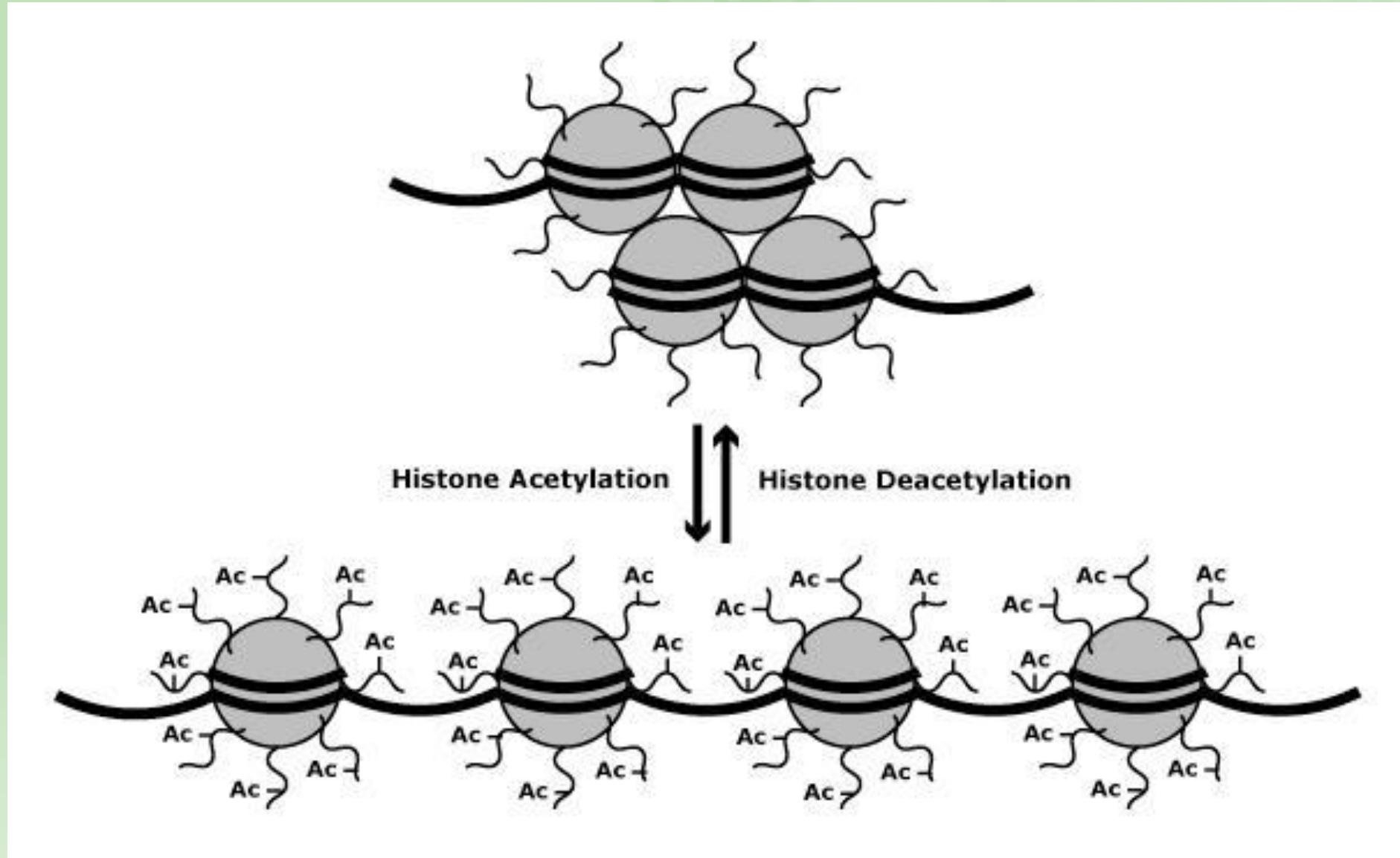


Modificação de histonas

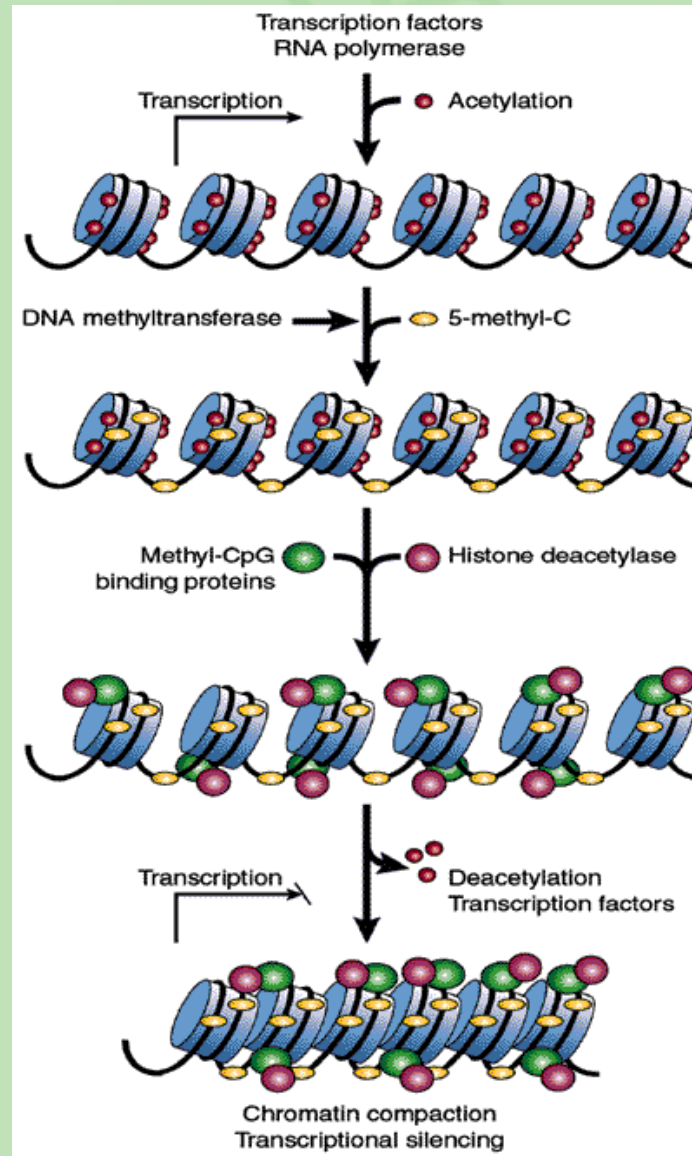


Enzimas: histonas acetilases (HATs)
histonas desacetilases (HDs ou HDACs)

Modificação de histonas

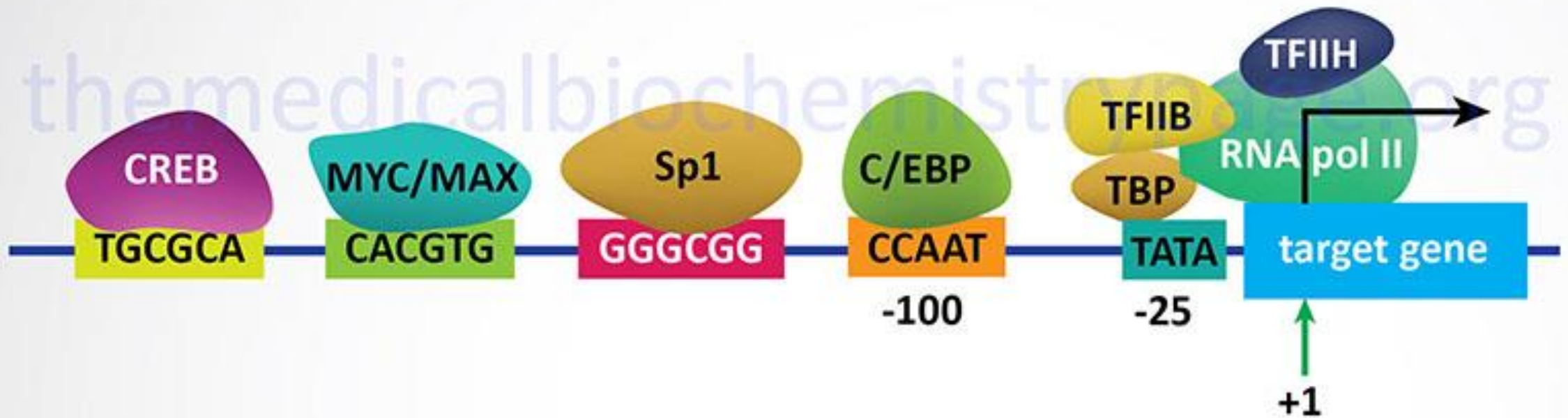


Modificação de histonas

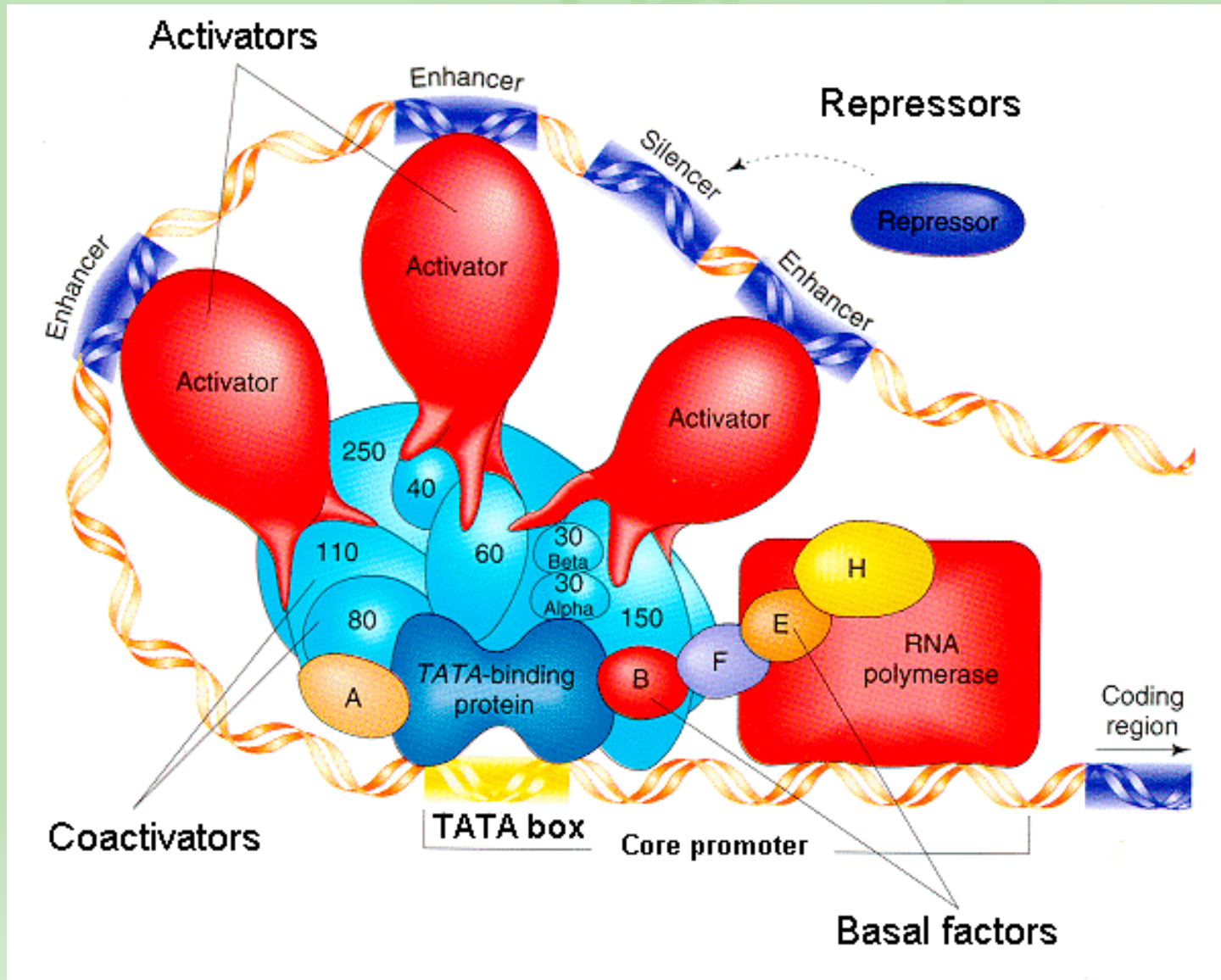


Regiões da cromatina transcritionalmente ativas tendem a estar hiperacetiladas e hipometiladas.

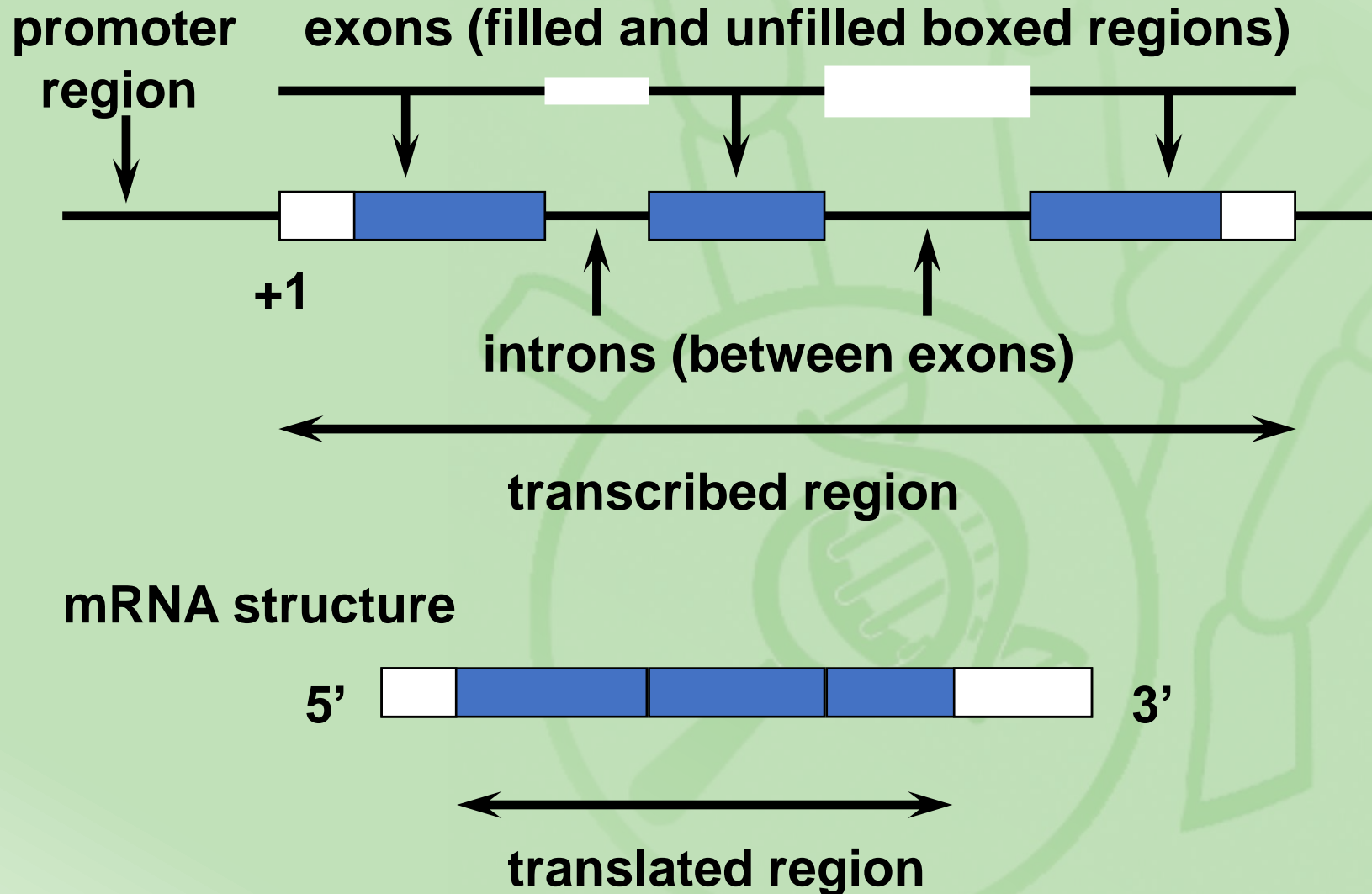
Organização de genes eucariotos



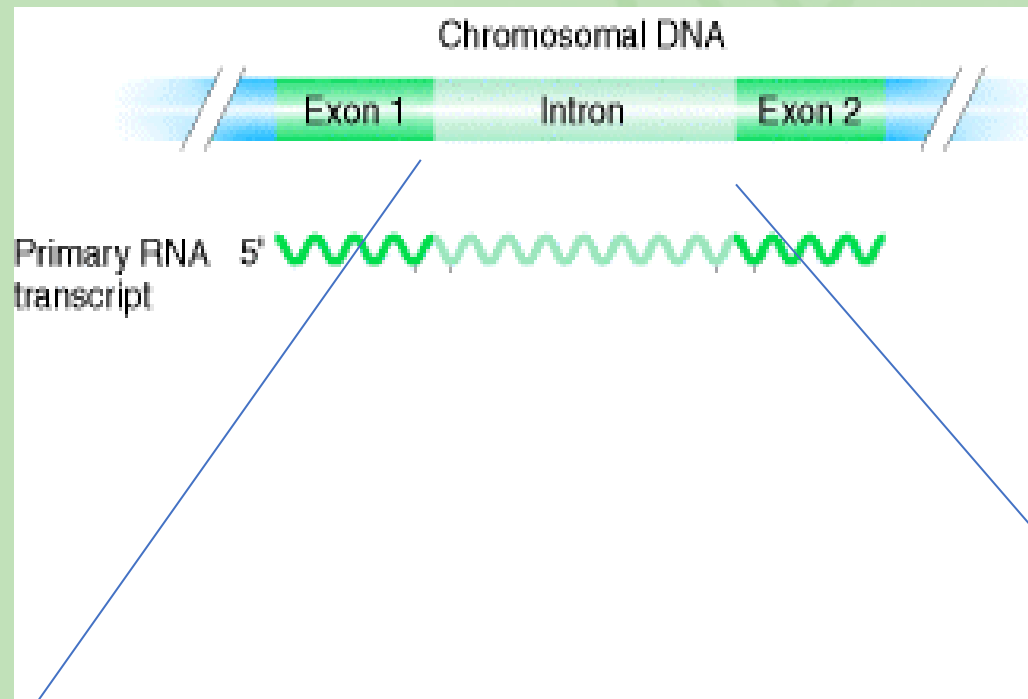
Organização de genes eucariotos



Estrutura de genes eucarióticos

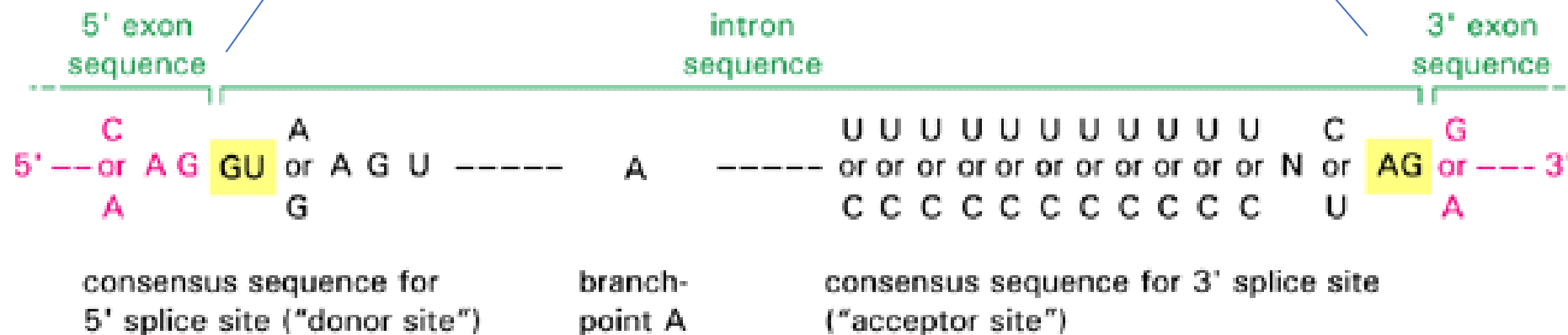


Recomposição de mRNA – remoção de íntrons



DNA molde

Pré-mRNA



Sítios canônicos e não canônicos de splicing em animais, fungos e plantas

Table 1. Splice site combination frequencies in animals, fungi, and plants. Only the most frequent combinations are displayed here, and all minor non-canonical splice site combinations are summarized as one group (“Others”). A full list of all splice site combinations is available (Files S1 and S2).

	GT-AG	GC-AG	AT-AC	Others
Animals	98.334%	0.983%	0.106%	0.577%
Fungi	98.715%	1.009%	0.019%	0.257%
Plants	97.886%	1.488%	0.092%	0.534%
All	98.265%	1.074%	0.101%	0.560%

Sítios adjacentes ao sítio de splicing GA-AG

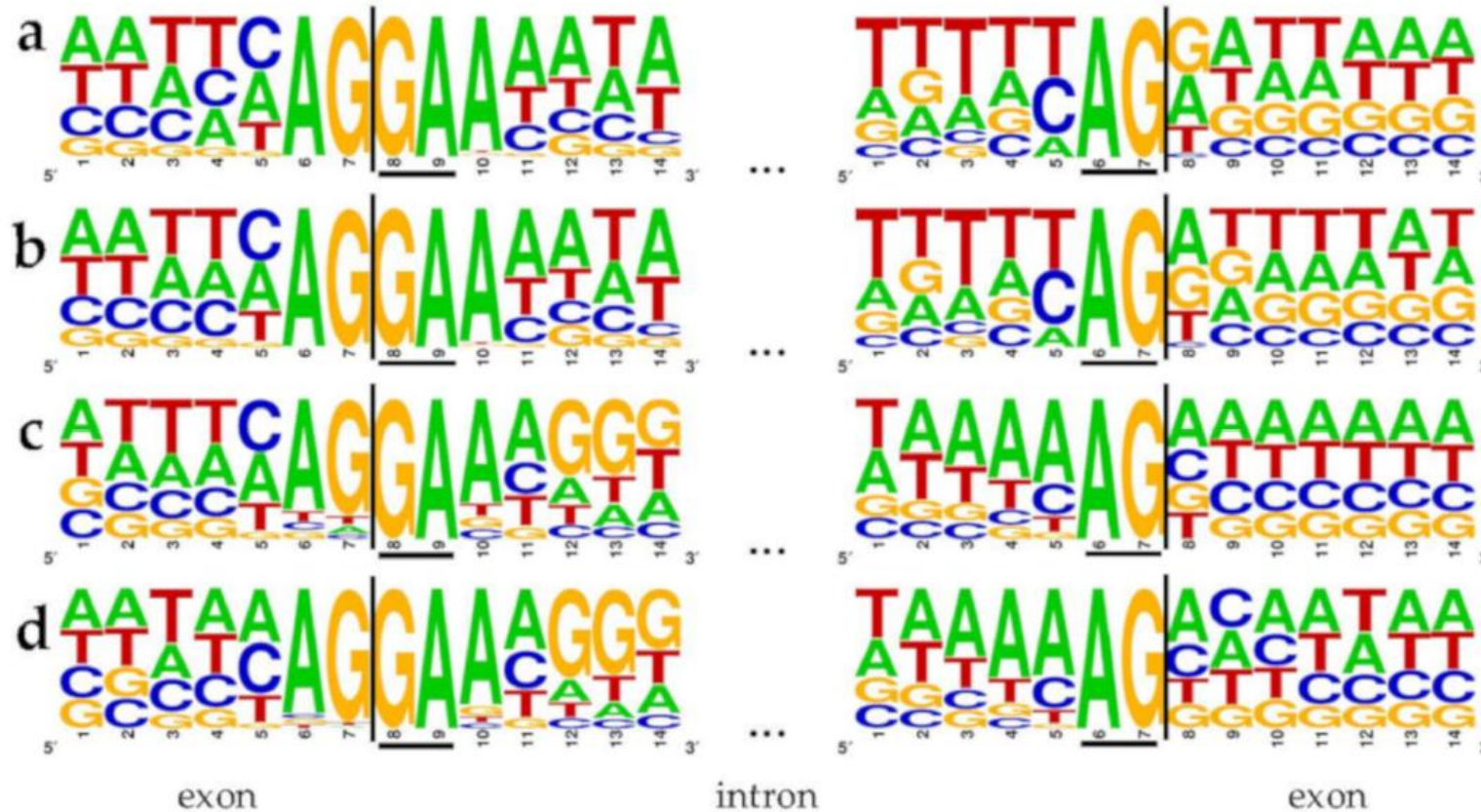
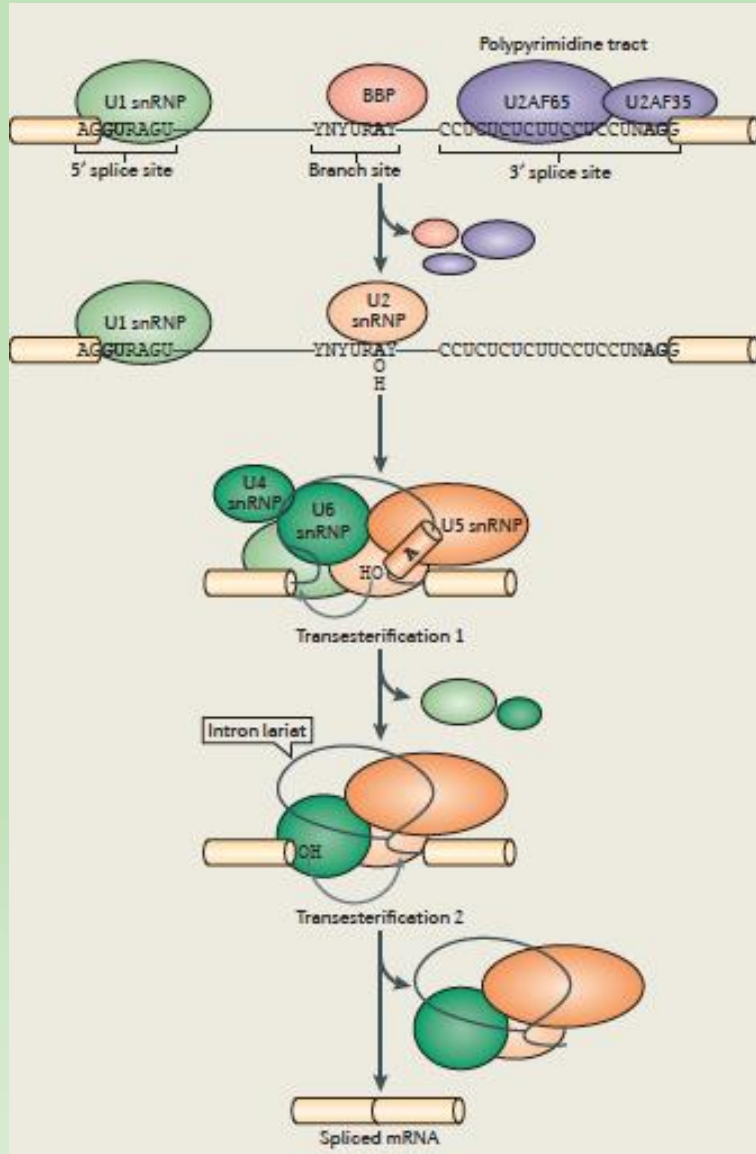


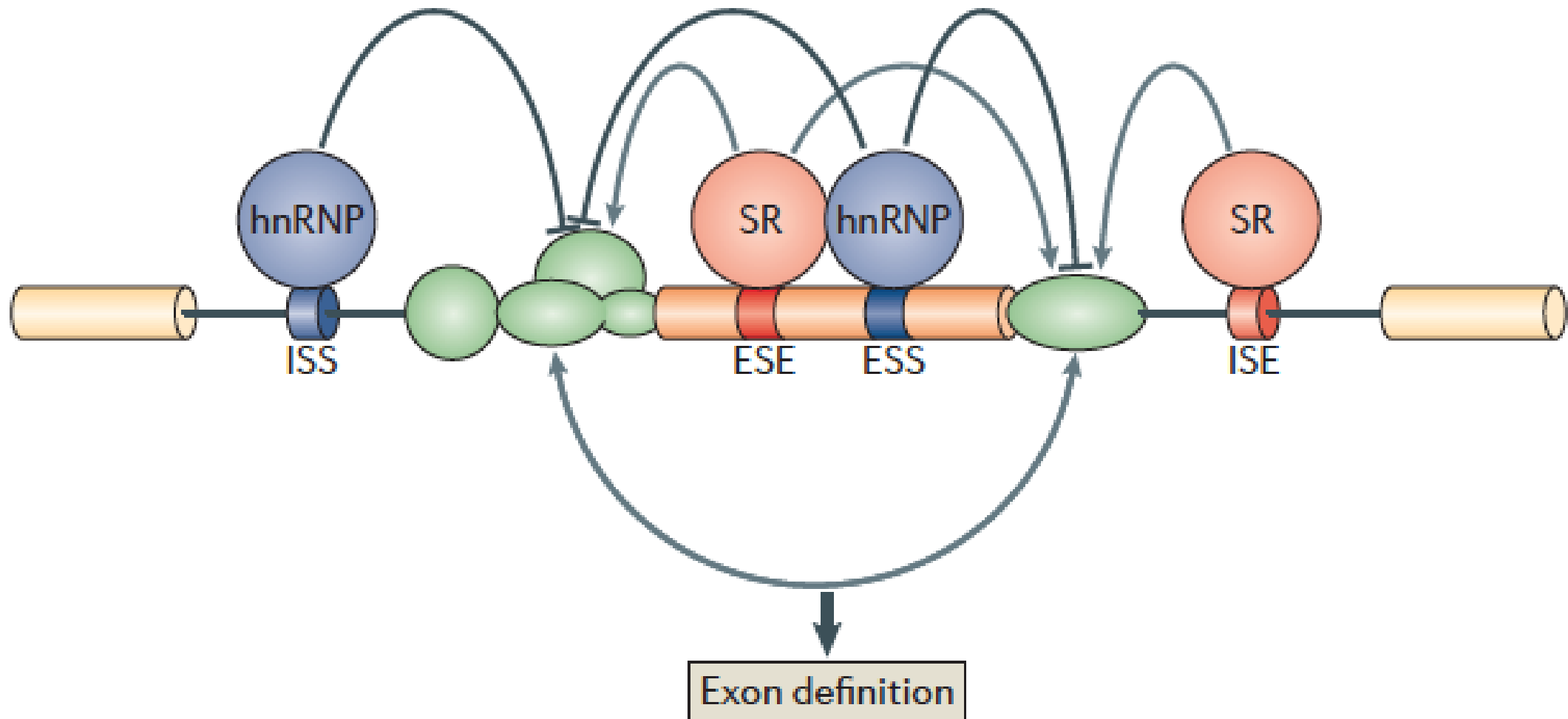
Figure 2. Flanking positions of GA-AG splice site combinations in *Eurytemora affinis* (a,b) and *Oikopleura dioica* (c,d). All splice site combinations (a,c) as well as all 5795 with RNA-Seq data supported splice site combinations (b,d) of these two species were investigated. Seven exonic and seven intronic positions are displayed at the 5' and 3' splice sites. Underlined bases represent the terminal dinucleotides of the intron, i.e., the 5' and 3' splice site.

Recomposição de mRNA – remoção de íntrons

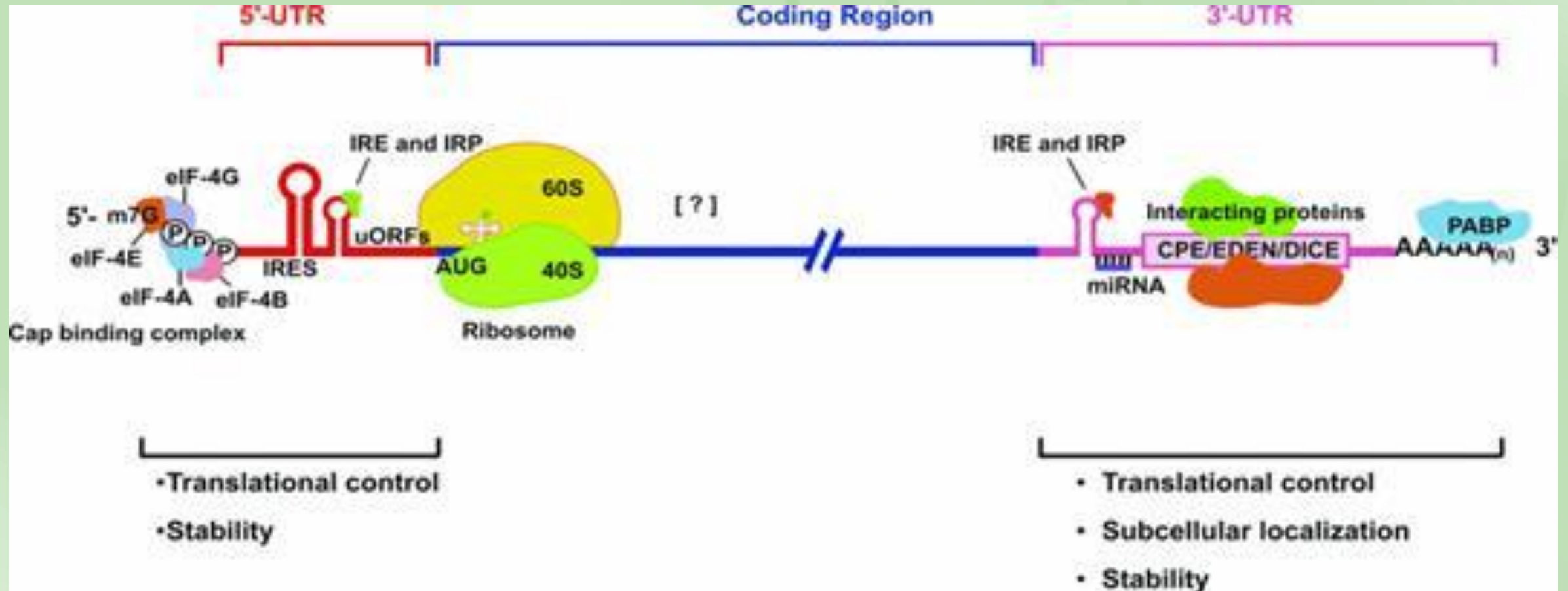


- Ocorre no núcleo
- Mediado pelo spliceosomo
- Unidades do spliceosomo:
 - Ribonucleoproteínas
 - Proteínas e RNAs

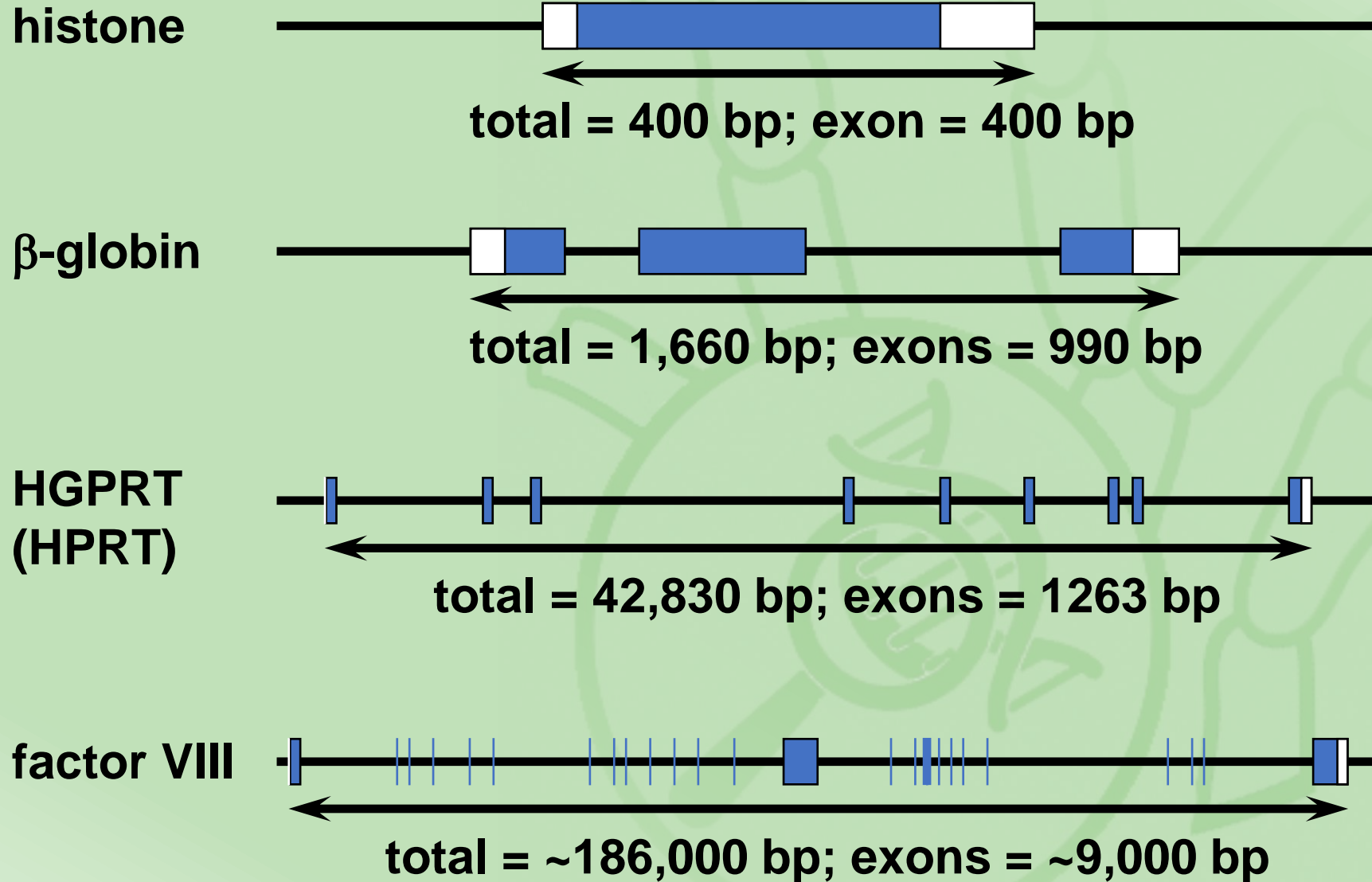
Recomposição de mRNA – remoção de íntrons



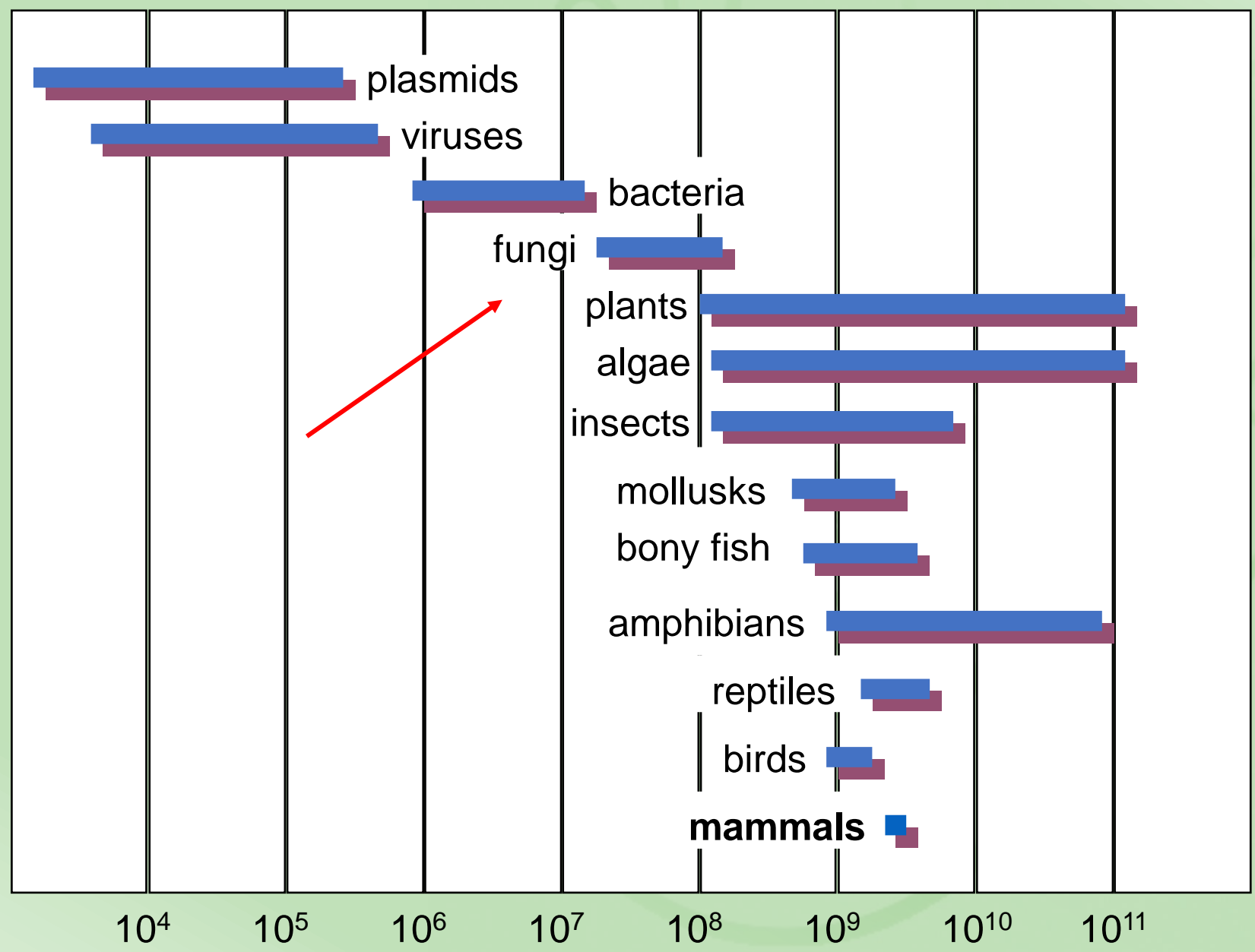
Estrutura e organização de mRNA



Variação entre genes do mesmo organismo



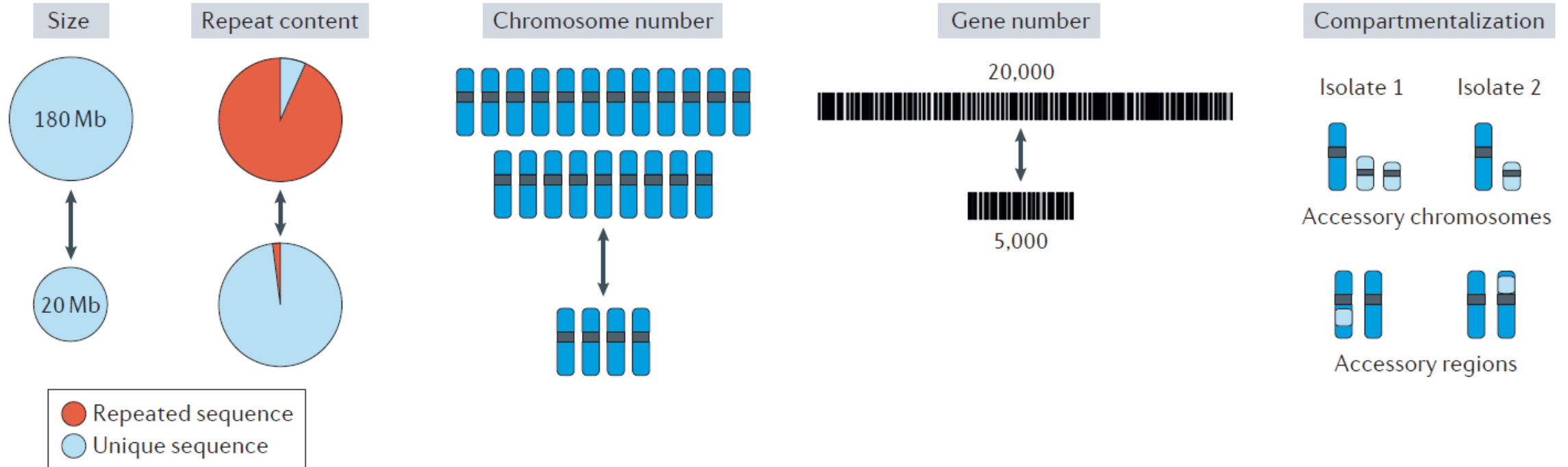
Genomas – variação inter e intra grupos taxonômicos



Genomas de fungos fitopatogênicos

Variação em tamanho de genoma, sequências repetitivas, número de cromossomos, número de genes e compartimentalização

a Fungal plant pathogen genomes are highly diverse



Diversidade de TEs entre genomas de fungos

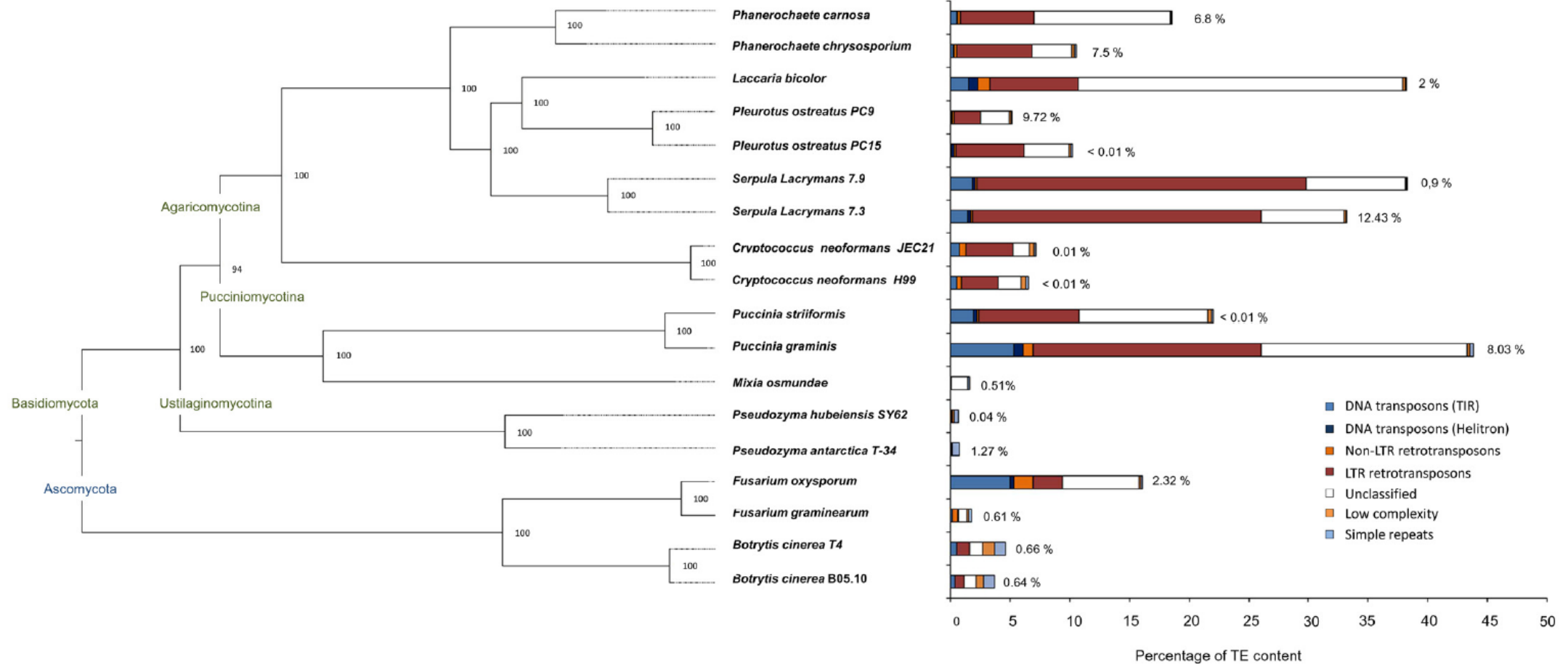
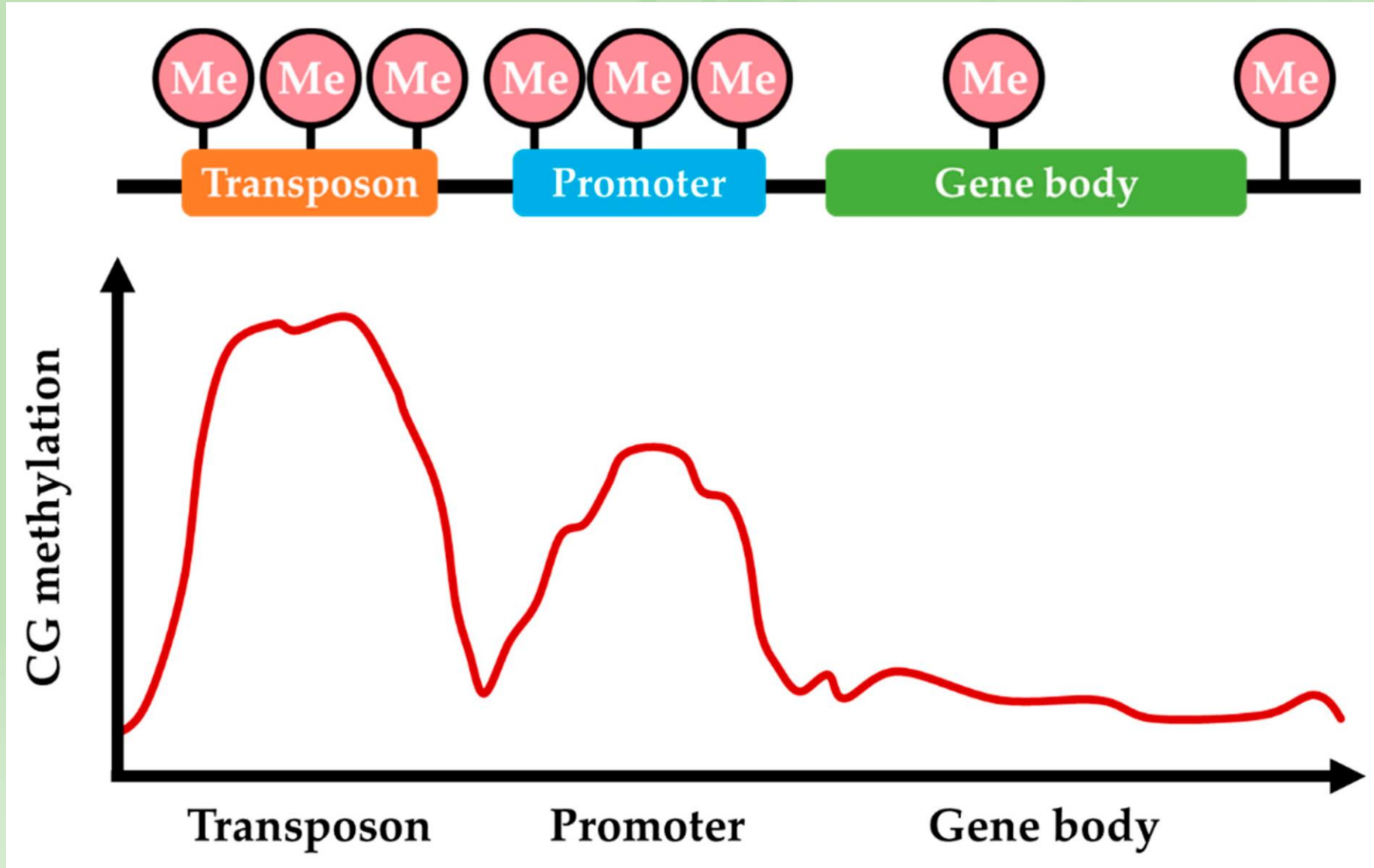


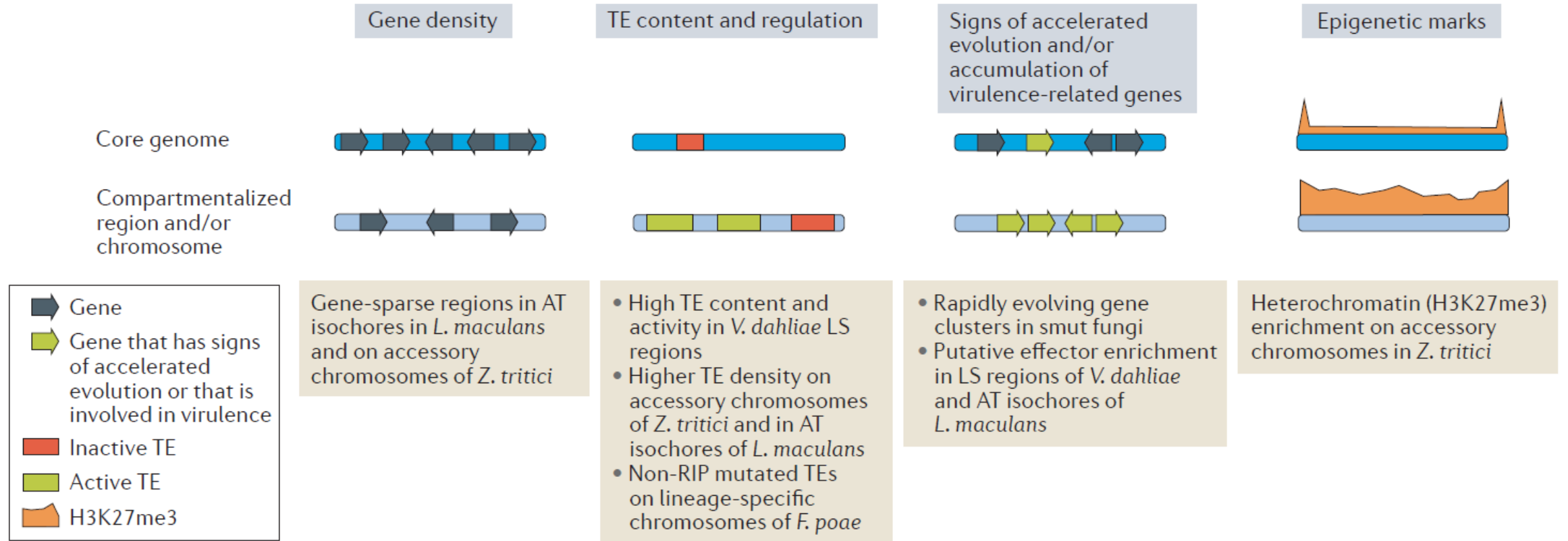
Fig 7. Phylogeny and repeat content of eighteen fungal species. Maximum-likelihood phylogeny inferred with RAxML based on 551 genes and 100 bootstraps. Percentages of assembly gaps are shown near to each bar. Dashed lines are used to align each branch to the tip.

Silenciamento de transposons



Compartimentos do genoma x core genoma

b Characteristics of genome compartments



Compartimentalização de genomas - Efetores

- Podem ser encontrados:
 - dispersos no genoma – associação com elementos repetitivos
 - organizados em clusters no genoma em regiões específicas - compartimentalização
- Compartimentalização do genoma – implicações:
 - Em nível funcional: co-regulação
 - Sequências regulatórias compartilhadas
 - Regulação epigenética
 - Em nível evolutivo
 - Clusters podem ser co-transferidos horizontalmente como uma unidade de função
 - Co-segregação de alelos
 - Alta taxa de mutação

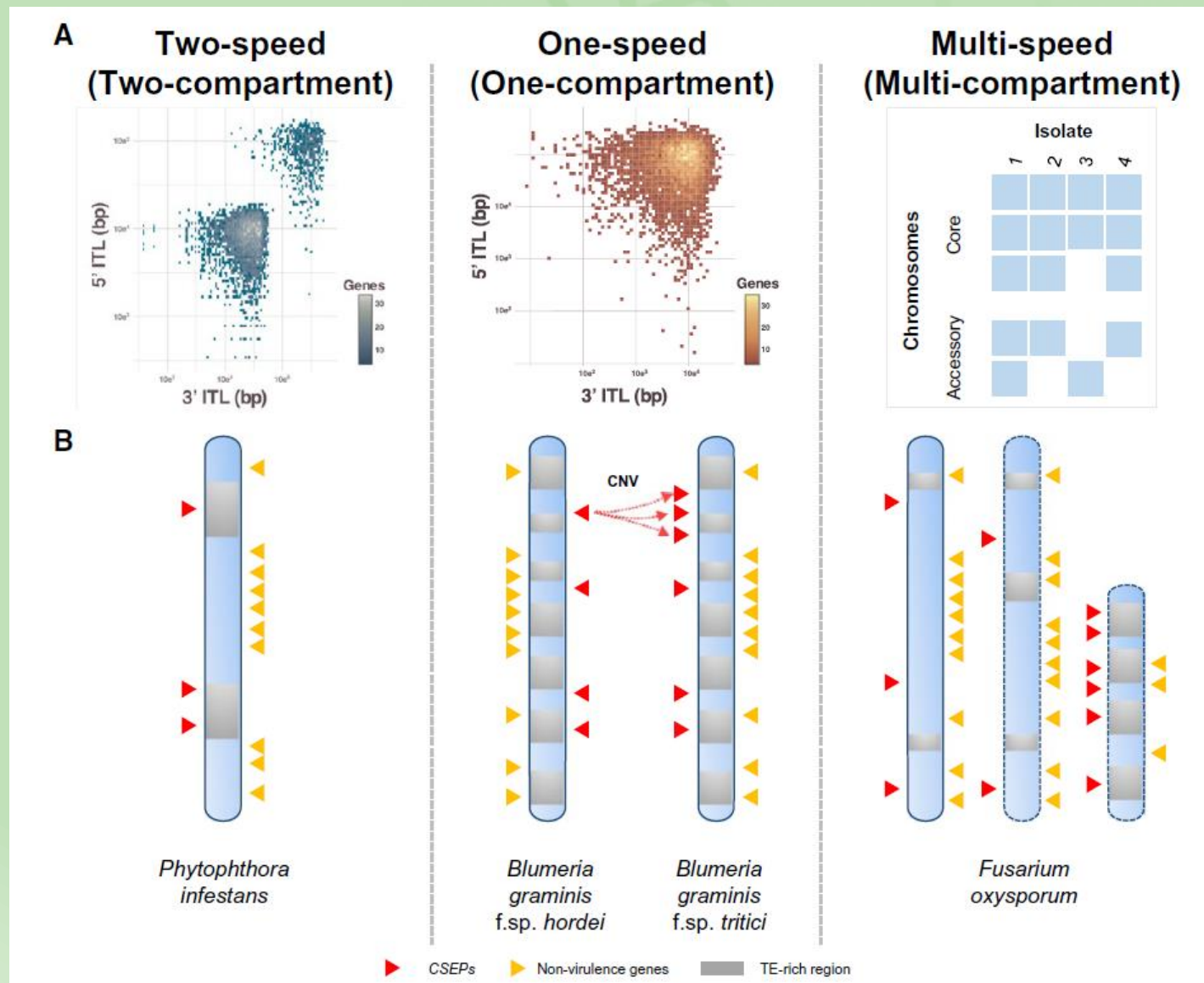
Conceito two-speed

- Housekeeping genes (HG)
 - Conservados - seleção
- Não HG
 - Exemplos:
 - efetores
 - metabolismo secundário
 - Rápida evolução - Isolados da mesma espécie:
 - Apenas moderada sintonia (colinearidade de genes)
 - Frequente polimorfismo gênico e cromossômico

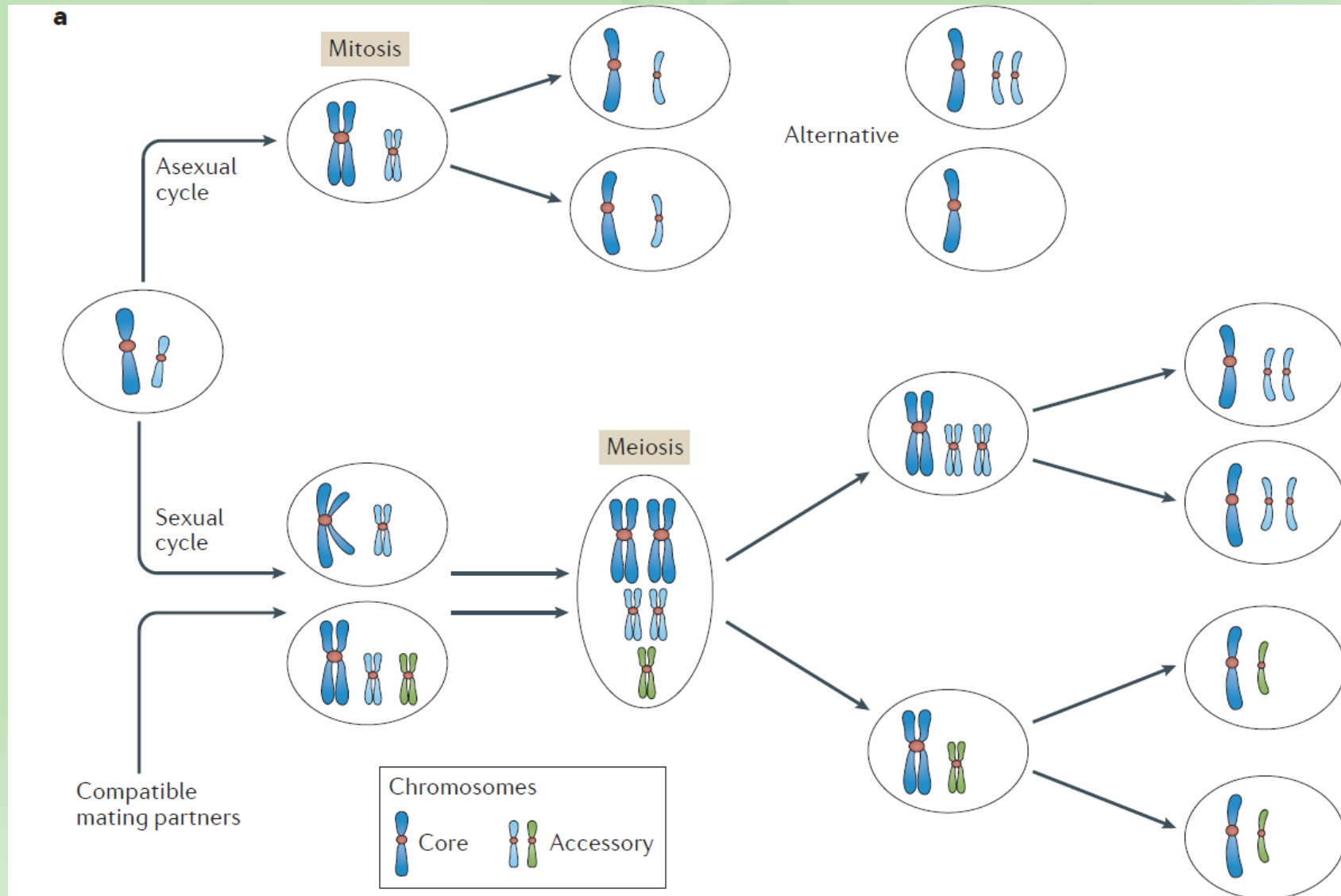
Conceito Genomas two-speed (Doing et al., 2015)

- Presença de compartimentalização física do genoma
- Diferentes taxas de evolução nos dois compartimentos
 - Taxa de mutação por unidade de tempo
- Genomas de fungos fitopatogênicos:
 - Compartimentalizados
 - Arquitetura de genoma mosaico – regiões:
 - densas em genes (genes housekeeping conservados) e pobres em sequências repetitivas
 - Esparsas em genes e ricas em regiões repetitivas, contendo genes associados a virulência de rápida evolução
 - Presença de AT-rich isochores e cromossomos acessórios

Variações do conceito



Dinâmica de cromossomos acessórios



Exemplo de região acessória e de core genoma no mesmo cromossomo

c Chromosome 7 of *Z. tritici* has characteristics of core and accessory chromosomes

