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Empowering Communities...

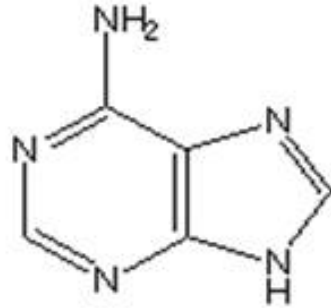
TOPIC-7: NUCLEIC ACIDS



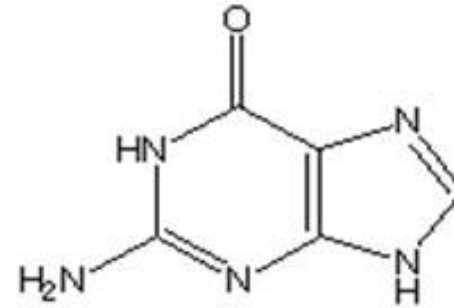
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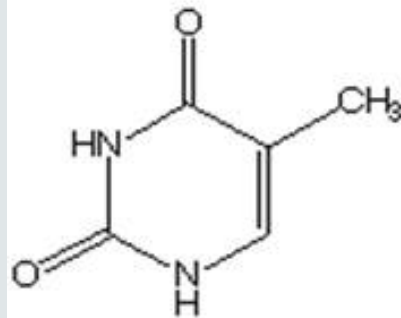
NITROGENOUS BASES



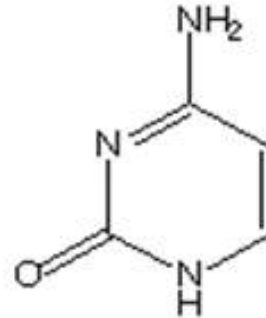
Adenine (DNA/RNA)



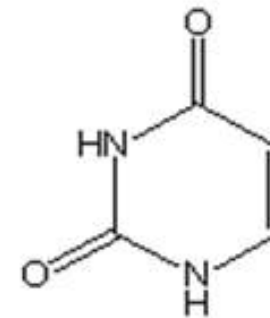
Guanine (DNA/RNA)



Thymine (DNA)



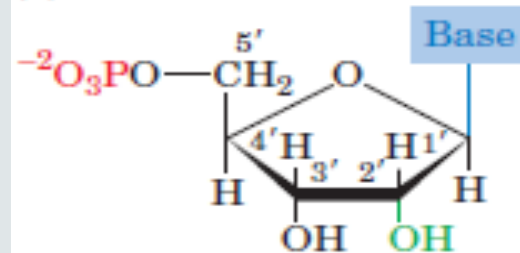
Cytosine (DNA/RNA)



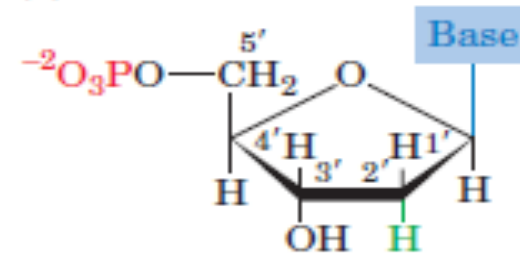
Uracil (RNA)

(a)

(b)



Ribonucleotides



Deoxyribonucleotides



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Chargaff *et al.*, 1940

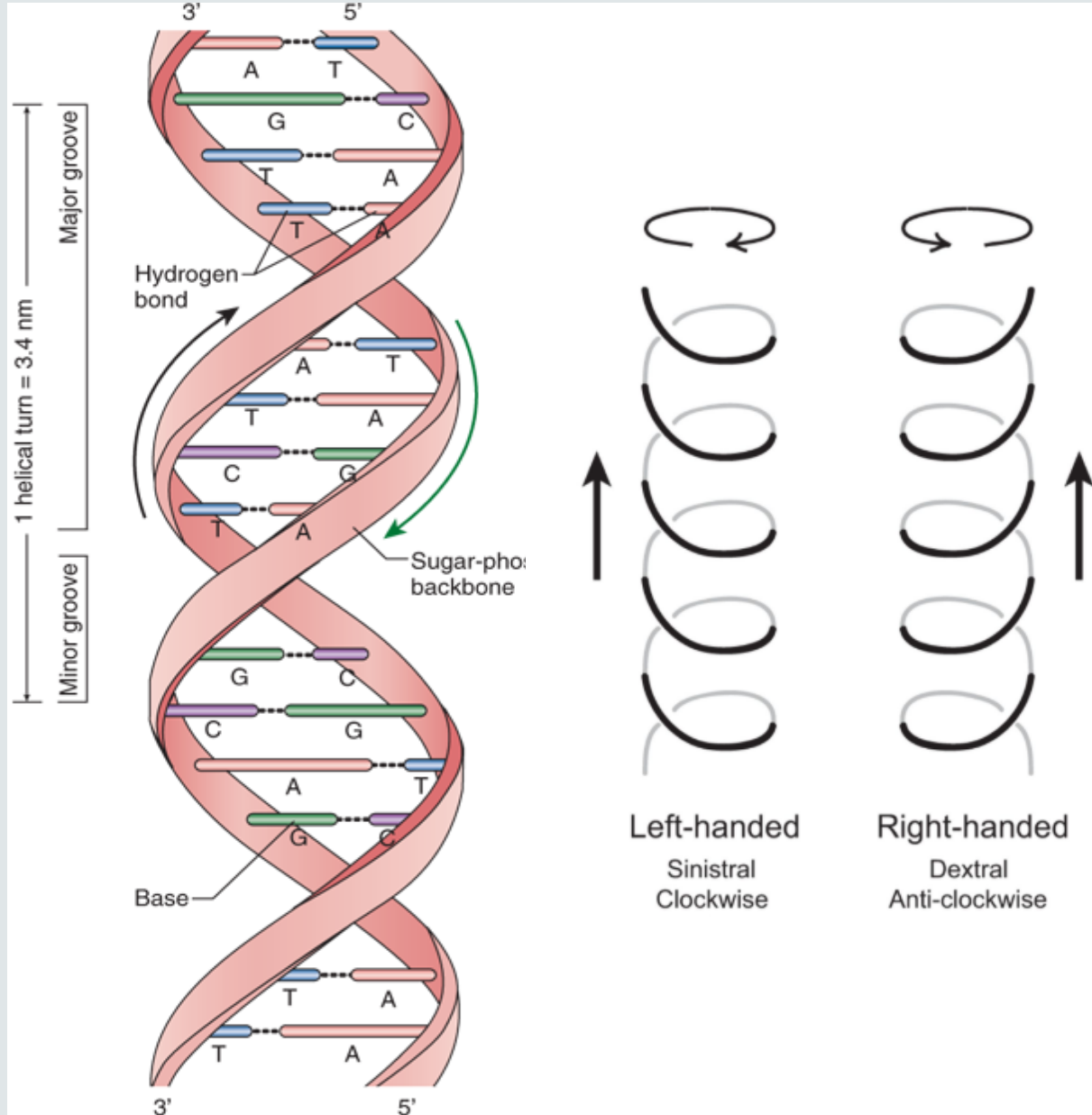
1. The base composition of DNA generally varies from one species to another.
2. DNA specimens isolated from different tissues of the same species have the same base composition.
3. The base composition of DNA in a given species does not change with an organism's age, nutritional state, or changing environment.
4. In *all* cellular DNAs, regardless of the species, the number of adenosine residues is equal to the number of thymidine residues (that is, $A = T$), and the number of guanosine residues is equal to the number of cytidine residues ($G = C$). From these relationships it follows that the sum of the purine residues equals the sum of the pyrimidine residues; that is, $A + G = T + C$.



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Structure of B-DNA: Watson & Crick, 1953



Source: Karen C. Carroll, Stephen A. Morse, Timothy Mietzner, Steve Miller: Jawetz, Melnick, & Adelberg's Medical Microbiology, 27th Edition. www.accessmedicine.com
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DNA: Key Points

- ❖ Absorbance of DNA at 260 nm increases as DNA becomes denatured – Hyperchromic shift.
- ❖ Temperature at which 50% of DNA is melted is called Melting Temperature (T_m) and depends on nature of DNA.
- ❖ Denaturation: At 90°C or above, ds DNA is denatured and strand separation takes place. Absorbance measured at 260 nm.



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DNA: Key Points

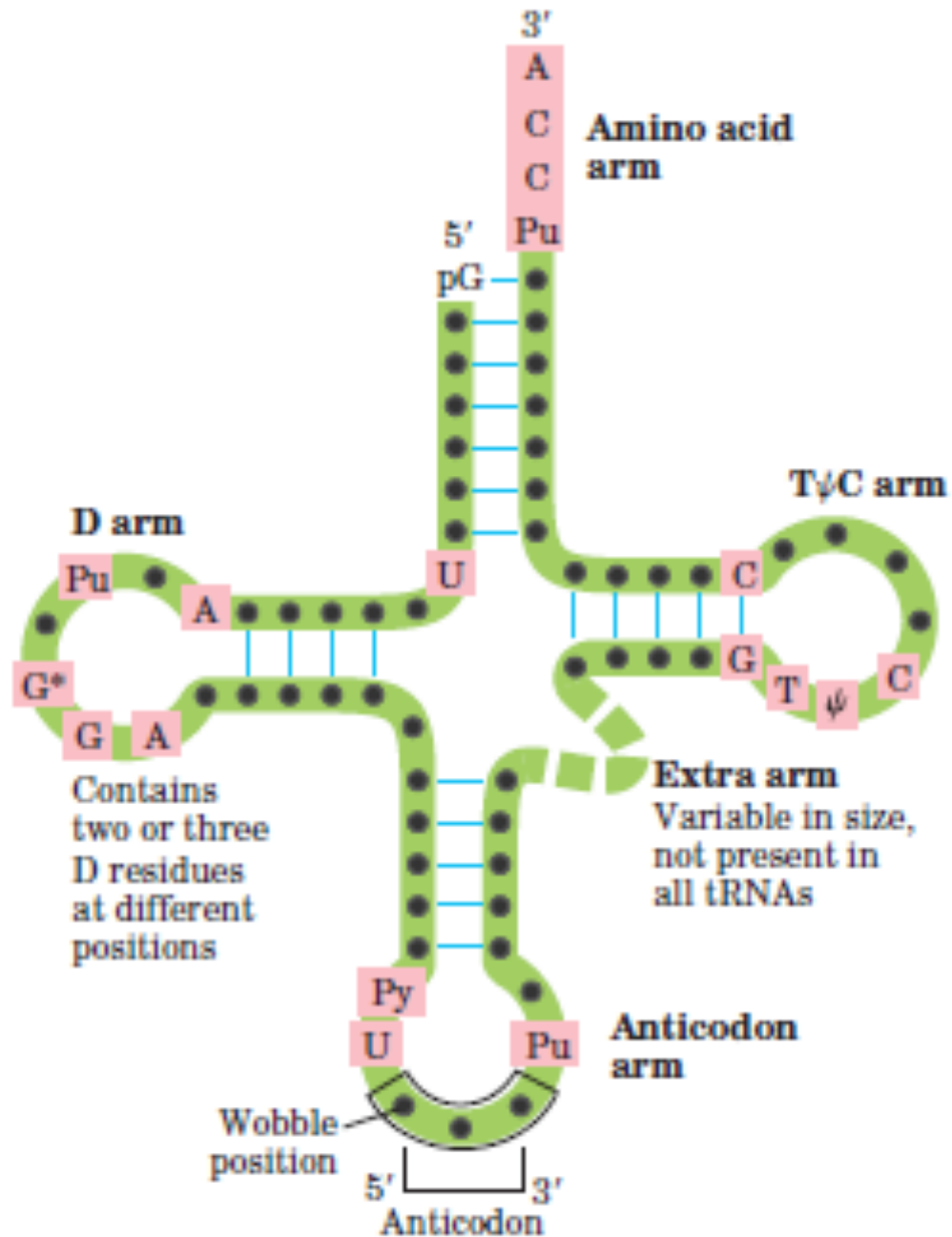
- ❖ T_m is highest for those DNA molecule consisting highest proportion of C, G residues and T_m actually be used to estimate percentage of C+G in DNA sample.
- ❖ Renaturation: If melted DNA is cooled, it is possible for the separated strands to re-associate, a process reverse to denaturation.
- ❖ Annealing: Small ss fragments of DNA (oligonucleotides, upto 40 bases in length) can hybridize to a denatured sample of DNA, pending on base sequence of oligontd. and salt concentration of sample.



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tRNAs





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GENETIC CODE

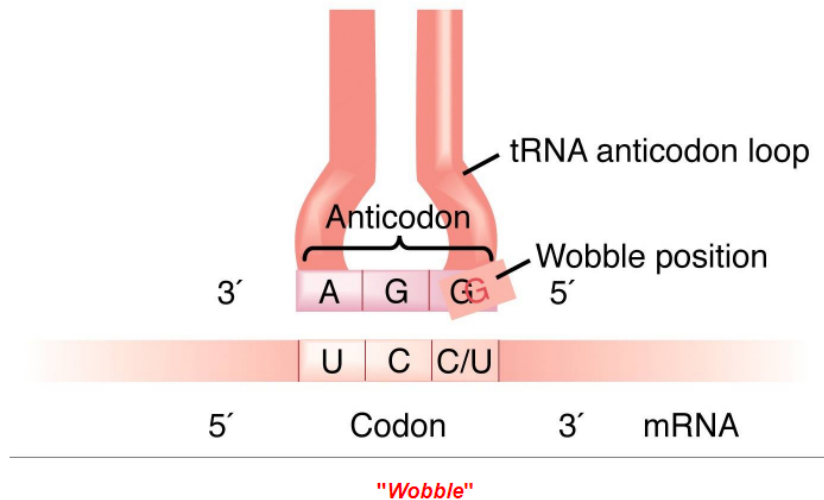
		Second Letter										
		U		C		A		G				
1st letter	U	UUU Phe	UCU	UAU Tyr	UGU Cys	3rd letter	U	UUC	UCC Ser	UAC	UGC	C
	UUA Leu	UCA	UAA Stop	UGA Stop	A							
	UUG	UCG	UAG Stop	UGG Trp	G							
1st letter	C	CUU Leu	CCU	CAU His	CGU	3rd letter	U	CUC	CCC Pro	CAC	CGC Arg	C
	CUA	CCA	CAA Gln	CGA	A							
	CUG	CCG	CAG	CGG	G							
1st letter	A	AUU	ACU	AAU Asn	AGU Ser	3rd letter	U	AUC Ile	ACC Thr	AAC	AGC	C
	AUA	ACA	AAA Lys	AGA Arg	A							
	AUG Met	ACG	AAG	AGG	G							
1st letter	G	GUU Val	GCU	GAU Asp	GGU	3rd letter	U	GUC	GCC Ala	GAC	GGC Gly	C
	GUA	GCA	GAA Glu	GGA	A							
	GUG	GCG	GAG	GGG	G							



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Wobble HYPOTHESIS



Pairing of the **tRNA anticodon** with the **mRNA codon** proceeds from the **5' end of the codon**. Once the first two positions are paired, exact base pairing of the third position is less critical. The third (**5'**) base of the anticodon can typically pair with either member of the purine or pyrimidine pair in the codon as appropriate: it "**wobbles**". In this example, the double-ringed **G** can pair with either a single-ringed **U** or **C**. This allows **mRNA** to be translated with fewer than the **64 tRNAs** that would be required without wobble. Some wobble positions can pair with any of the four bases.