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III. MACROMOLECULAR POLARITIES

A. Free Macromolecules

1. a) *Deoxyribonucleic acid (DNA)*

a[1] *Structure.* As noticed in **I** (Fig. 5) the two polynucleotide strands of the DNA double helix have opposite polarities and transcription only occurs from the sense strand (+) in the 5'→3' direction.

The bipolar pattern of the DNA double helix has important consequences on DNA recombination processes which involve restriction enzymes (Arber, 1974; Nathans and Smith, 1975). The recognition sequence for representatives of these site-specific endonucleases such as *Eco*RI and *Hind*III is a palindrome, i.e. a sequence of six inverted repeat base pairs showing a twofold rotational symmetry. The inverted polarity of the two DNA strands imposes a positioning of the cleavage sites outside the axis of palindromic symmetry. The ensuing asymmetric cutting produces single-stranded ends containing four bases of complementary sequences.

Seemingly, small variations in molecular structure or electrostatic potential at specific sites can make a critical difference in how the nucleic acid is organized and how it is recognized by other molecules in the intracellular environment. This is becoming increasingly clear from scanning tunnelling microscopy studies of calf thymus DNA and poly(rA)·poly(rU) which have shown that the helical pitch and periodic alternation of major and minor grooves can be visualized and reliably measured (Arscott *et al.,* 1989).

a[4] *Mutations.* Those causing variegation are due to the action of transposons, a group of genetic elements known to move from one location in the genome to another. Certain strains of *Saccharomyces cerevisiae* contain an intron endowed with the ability for transposition in the gene coding for mitochondrial RNA which is absent from the corresponding gene of other strains; most of the progeny between intron plus and intron minus are positive (Dujon *et al.,* 1974). This phenomenon, termed "polarity of recombination" by Bolotin *et al.* (1971) resembles a duplicative transposition which is characteristic for prokaryotic transposons.

As recently outlined by crystallographic structural studies of contacts in repressor-operator complexes, "positioning contacts" appear to be important conserved features within families of helix-turn-helix proteins (Pabo *et al.,* 1990).

b) *Ribonucleic acid (RNA)*

Antisense RNA molecules can selectively turn off genes and be used as antisense expression vectors to produce pigment variegations in flowers (Weintraub, 1990).

2. Proteins

As one of the recently described DNA-binding motifs, the zinc finger protein coordinates with a Zn^{2+} ion through paired cysteine and histidine residues along the amino-to-carboxyl protein dipole (Johnson and McKnight, 1989).

The thermodynamics of membrane-located proteins containing large (hundred of Debye units) permanent dipoles has been outlined by Schwarz (1978). Ordered water molecules can contribute directly to the properties of proteins by influencing their interaction with ligands. In their studies of atomic structures of the complexes of the L-arabinose-binding protein with sugars, Quiocho *et al.* (1989) have found that "two hydrogen-bonded water molecules in the site contribute further to tight binding of L-arabinose but create an unfavourable interaction with a methyl group of D-fucose".

5. Enzymes

The distribution of charges within the charge-relay system (or "catalytic triad") at the active site of the serine proteinases has been further investigated. An Asp--Asn mutant in rat trypsin has been engineered by Craik *et al.* (1987). As reported by (Blow, 1990), this mutant showed that "the polarization of the histidine by the buried aspartate enhanced the reactivity of the serine". Warshel *et al.* (1989) have used the technic of computational chemistry "to estimate the effect of the charged carboxylate group and the polarized histidine on the reactivity of the serine side-chain surrounded by water".

B. Aggregates

2. c) *Polar viral morphopoiesis*

Packaging of bacteriophage λ DNA involves polarity of chromosome entry into the prohead (**I**, p.70) from the *Nu1* end to the *R* end (Becker and Murialdo, 1990).