EMBO EUROPEAN MOLECULAR BIOLOGY ORGANIZATION

FIFTH EMBO ANNUAL SYMPOSIUM

NUCLEIC ACID-PROTEIN INTERACTIONS

12-15 October, 1979

Programme and Abstracts for the Poster Sessions

12, 13, 14, and 15 October

RELATONSHIP BEITTEEN PROTEIN AND NUCLEIC ACID SEQUENCES IMPLICATED IN SPECIFIC BINDING INTERACTIONS

G.V.Gursky, A.S.Zasedatelev, V.G.Tumanyan, A.L.Zhuze, S.L.Grokhovsky, S.A.Streitsov, A.A.Khorlin, A.N.Surovaya and B.P.Gottikh
Institute of Molecular Biology, Academy of Sciences of the USSR, Moscow 117984, USSR

Arguments are summarised which support the existence of a certain correspondence (code) between the protein and nucleic acid sequences implicated in specific binding interactions. Recognition protein sites are assumed to contain pairs of antiparallel poly-peptide chain segments which form a right-hand twisted antiparallel 0-sheet, Uoon complex formation between a protein and SNA the sheet undergoes a structural transition allo.ving for the backbone amide groups in the two polypeptide chain segments to form hydrogen bonds with DNA base pairs. The binding is stereospecific in the sense that N-C-C' sequence in the polypeptide chain segments coincides with C3' - C5' direction in the adjacent polynucleotide chains. According to the code proposed by us the side chains of amino acid residues present in the outward-pointing positions in a */3*-sheet control hydrogen binding interactions between the peptide groups of recognition protein site and DNA base pairs. These re-sidues can be. divided in two groups those coding for AT pairs -(Sen, Thr, Asm, Gln, His, Cys, in some cases, presumably, Lys and Arg) and those coding for GC pairs (Gly, Ala, Leu, Yal, Ile, Phe, Met, Trp, Tyr, Asp, Glu, in certain cases Lys and Arg).[1,2] These rules are strongly supported by the fact that for a number of specific protein nucleic acid complexes there is a remarkable correspondence between the protein and nucleic acid sequences (lac repressor-lac operator, ^ repressor- ^ operator, Cro protein — ^ operator,

CI protein and its interaction site in cY region of λ genome, ribosomal S8 protein and its interaction site on ribosomal 16S SNA). *These* rules are also supported by our observations that ρ polypeptides bind to synthetic DNA's with defined sequences and exhibit base sequence preferences predicted by our code rules. For example, oligo (L-threonine) binds more strongly to poly(dA)*poly(dT) than to poly(dG)*poly(dC), whereas oligo (L-valine) exhibits an opposite order of binding preferences. The binding is accompanied by spectral changes in the UV spectral region 190-240 nm thereby indicating That amide groups of the oligopeptide molecules are implicated in the cindihg interactions. Ologopeptides in a single-stranded form exhibit a low affinity for BNA as compared with the affinity of dimeric .species. Binding isotherms were obtained by a number of technique and interpreted on the basis of statistical mechanical theory developed by us earlier.[3,4]

References

1. Gursky,G.V., Tumanyan,V.G., Zasedatelev,A.S., Zhuze,A.L., Grokhovsky, S.L., Gottikh,B.P. (1977) in Nucleic Acid-Protein Recognition, Vogel H.J., ed. pp. 189-217, Academic Press, New York
2. Gursky,G.V., Zasedatelev,A.S., Tumanyan.V.G., Zhuze,A.L., Grokhovsky, S.L., Gottikh,B.P. (1979) in FEBS Federation of European Biochemical Societies 12th Meeting Dresden 1978, volume 51 Gene functions, S.Rosenthal et al., Eds., pp. 23-32
3. Gursky G.V., Zasedatelev A.S. (1978) Biophysics 23, 932-946
4. Livshitz,M.A., Gursky,G.V., Zasedatelev,A.S., Volkenstein M.V. Nucleic Acids Research in press