STUDY OF RNA FOLDING RESULTING FROM HIGH Z^+ INTAKE USING CRYSTALLOGRAPHIC DATA

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This prime objective of the present work is to study the RNA folding resulting from high Z^+ intake using latest crystallographic data. An RNA fold is the result of packing together two or more coaxial helical stacks. The four RNA folds have been determined at near-atomic resolution by X-ray crystallography:

(i) Transfer RNA

(ii) The Hammerhead ribozyme

(iii) The P4-P6 domain of the Tetrayhymena group I intron, and

(iv) The hepatitis delta virus ribozyme.

All four folds resulting RNAs that are considerably more compact than isolated A-from duplexes. These structures illustrate, to varying degrees, three modes of fold stabilization of close RNA packing by binding of cations, and stabilization through pseudoknotting.

Keywords: Z^+ intake, BIS intake, Bisology, LSFAO, alcoholic drinks. Coaxial stack, helix packing, strand crossover, tertiary interaction, cation binding site pseudo-knotting.

INTRODUCTION :

Twenty-five years ago, the structure determinations of $tRNA^{Phe}$ demonstrated that ribonucleic acid can adopt a compact, globular fold. In the last five years, the structures of the new RNA folds have been determined at near atomic resolution: the hammerhead robozyme, the P4-P6 domain of the *Tetrahymena* group I nitron (4), and the hepatitis delta virus (HDV), ribozyme (18a). Side-by-side comparison of the four known RNA folds shows that they all are constructed by packing together coaxially stacked helices. To different extents in the four folds, the packing appears to be stabilized by nonhelical or tertiary hydrogen bonding network, coordination of metal ions, and by the connectivity of the RNA backbone.

We compare and contrast the size, complexity, and inferred or experimentally verified modes of fold stabilization for four known RNA folds. The growth of structural information on RNA is extremely useful in understanding the biochemical roles and capabilities in biosystems

BIS LOADS ON THE HUMAN GENOME AND GENETIC DISEASES :

On the basis of our own investigations and those of earlies worker, we have found that following CHROMOSOME AND GENETIC DISEASES ARE INDUCED BY BIS MECHANISM:

Chromosome 1: Faulty gene for GBA an enzyme, which breaks down certain fats. This leads to *Gaucher's disease.* This is created by taking high BIS diet

Chromosome 2: *Faulty PAX-3 gene* is associated with deafness. Each eye is a different colour. This causes *Waadenburg syndrome.* This is created by taking high BIS diet.

Chromosome 3: When the high BIS intake succeeds in attacking the VHL gene Chromosome 3, becomes faulty. This faulty gene causes abnormal blood vessel formation. This leads to the von Hippel-Lindau disease.

Chromosome 4: Faulty gene causes dementia. This leads to *Huntington's diseases.* This is created by taking high BIS diet.

Chromosome 5: Faulty gene causes malformed hands and feet. This leads to diastrophic dysplasia. This is created by taking high BIS diet.

Chromosome 6: When the resistive, inductive and capacitive BIS intakes make the SCA1 gene faulty, then the cerebellum is withered and one gets climsiness. This leads to spinocerebellar atrophy. Chromosome 6 is a biggest structure of genes. There are 2190 genes in the 166 million letters of DNA. Out of 2190 genes, there are 633 non-active genes and cannot be activated. Rest 1557 genes are completely active. This is created by taking high BIS diet.

Chromosome 7: Faulty gene causes ultimately fatal build-up of mucus in lungs and pancreas. This leads to Cystic fibrosis. This is effecting by taking high BIS diet. The use of beta carotene supplements by smokers, increased risk of lung cancer and death.

Chromosome 8: Defective gene in chromosome 8, generated by high BIS intake causes premature ageing. This leads to Werner's syndrome.

Chromosome 9: When the high BIS intake succeeds in making the faulty CDK2 tumour repressor gene, skin cancer emerges. This leads to Malignant melanoma.

Chromosome 10: When high BIS intake creates defects in MEN2A gene, tumours of thyroid and adrenal glands are created. This leads to multiple endocrine neoplasia. This is also responsible for coronary artery disease and heart attacks.

Chromosome 11: Harvey RAS oncogene predisposes to common cancers. This leads to cancer. This is created by the consumption of high BIS diet.

Chromosome 12: Defects in PAH gene created by high BIS intake cause mental retardation by blocking digestion of common amino acid in food. This leads to Phenyl-ketonuria.

Chromosome 13: Defects in BRCA 2 gene raises risk of breast cancer. This is created by high BIS diet.

Chromosome 14: Faulty AD3 gene in linked with the development of plaques in the brain. This leads to Alzheimer's disease. AD3 gene becomes defective by the excessive consumption of resistive, inductive and capacitive BIS intakes.

Chromosome 15: Abnormal FBN1 gene weakness, connective tissue, potentially rupturing blood vessels. This leads to Marfan's syndrome (position unknown). This is created due to the consumption of high BIS diet.

Chromosome 16: Falty PkD1 gene causes cysts to form, which trigger kidney failure. This leads to Polycystic kidney diseases. High BIS diet is responsible for abreeations at Chromosome 16.

Chromosome 17: Mutations in p53 gene increase vulnerability to cancer, BRCA pre0disposes to breast cancer. This is caused by high BIS diet.

Chromosome 18: Damage to DPC4 gene accelerates pancreatic cancer. This is created due to consumption of high BIS diet.

Chromosome 19: Defective gene for apolipoprotein E raises blood cholesterol, predisposing to artery blockage. This leads to Coronary heart diseases. This is created by taking high BIS diet.

Chromosome 20: Abnormal adenosine deaminase (ADA) gene destroys immunity. Correctable by gene therapy. This leads to Severe combined immunodeficiency. This is created by taking high BIS diet.

Chromosome 21: Wasting disease linked with defective superoxide dismutase I (SODI) gene. This leads to Lou Gehrig's disease. This is caused by high BIS diet.

Chromosome 22: Abnormal DGS gene triggers heart defects and facial changes. This leads to DiGeorage syndrome. This is created due to consumption of high BIS diet.

Chromosome 23: Abnormal DMD gene triggers muscle degeneration. This leads to Duchenne muscular dystrophy. This also known as X chromosomes. This is created by taking high BIS diet.

Chromosome 24: Governed by the gene for testis-determining factor. This leads to Testicle development. This is also known as Y chromosomes. This is affected by (high Z_{BIS} diet).

The HDV ribozyme fold is perhaps the most suggestive of the function of the RNA because of the resemblance of this RNA fold to that of many protein enzymes. The presence of a deep catalytic site cleft between the two helical stacks of the fold where the 5-hodroxyl leaving group is snugly placed between potentially with protein enzyme active sites, where substrates are bound positioned, and activated for catalysis.

CONCLUSION:

As discussed above, some modes of stabilization of RNA folds might result in weakly formed structures. This suggests that whereas many RNAs could in principle have intramolecular or interstack interfaces that are conducive to folding, the free energy of folding might be small enough to require the binding of a protein to drive the equilibrium in the folded direction (la). If this is true, it would be expected that many RNA fold within ribonucleoproteins (RNPs) would-be similar to those of RNAs that fold spontaneously. Such a role for proteins is also consistent with most biologically important RNAs present-day cells occurring as RNPs (e.g. ribosomes, spliceosomes, sihnal recognition particle, mobile group II introns, etc.). In the case of group I introns, two studies imply that proteins can play precisely such a role in stabilizaing RNA folds that, ion other contexts, are stable by themselves.

How many RNA folds exist? If there is a finite, relatively small numberof folds, is this a consequence of the intrinsic chemical stability of the folds, or a reflaction of the numbers of RNA folds present at the origin of life? The a reflection of the number of RNA folds present at the origin of life? The discovery that the GNRA utetraloop motif, common in biological RNAs, forms part of the substrate binding pocket in an artificially selected molecule, argues that some RNA motifs are prevalent due to their intrinsic chemical stability. Only the determination of more structures will tell whether this holds for RNA folds as well.

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