Commentary

INDUCED STRUCTURAL TRANSITIONS IN tRNA

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Received 11 April 1978

As stated in [1], we have presented experimental evidence that upon codon–anticodon recognition the tRNA undergoes a conformational change exposing the T–ψ–C–G sequence for binding to complementary oligonucleotides ([2–4] in [1]). Initial experiments with $tRNA^{Phe}$ and (uridylyl-3′,5′)$_7$-uridine (U_8) have been confirmed with $tRNA^{Lys}$/poly(A) and $tRNA^{Val}$/GUUU. We were not able to detect a difference in using either tRNA or aminoacylated tRNA, but our experiments were never planned to investigate this aspect in detail. The specific radioactivity of CGAA was low and the different components, like Phe-$tRNA^{Phe}$, were placed into both compartments in order to show that the binding of CGAA to the tRNA is only due to the codon. Furthermore, it should be noted that at codon concentrations where a stoichiometric tRNA·codon complex is expected only about 10% of the complexed tRNA is active in CGAA binding [2]. This could explain the negative findings in NMR measurements [3].

There is some agreement regarding the effect of aminoacylation; we see a definite difference between $tRNA^{Phe}$ and the ternary complex EF-T_u·GTP·Phe-tRNA. To stimulate CGAA binding to the latter a lower U_8 concentration is needed (0.3 mM versus 0.7 mM) and the optimal Mg^{2+} concentration is reduced. This could indicate that either the association constant for codon–anticodon complex formation is increased, or that EF-T_u·GTP stabilises the binding type structure of the tRNA. An increased association between an oligonucleotide and the cognate tRNA does not always result in stabilising the binding type structure of the tRNA. In the case of UUCA/$tRNA^{Phe}$, AAAA/$tRNA^{Lys}$ and GUAA/$tRNA^{Val}$ the K_a values are 10-fold higher as compared with the corresponding trinucleotides [4]. All 3 tetranucleotides are, however, inactive in stimulating the binding of their cognate tRNA to 30 S ribosomes. We believe that the tetranucleotides terminating in adenosine at the 3′-end stabilise a non-binding type tRNA conformation by interacting with the invariant U33 of the tRNA. The addition of CGAA, however, shifts the nonbinding type tRNA structure to the active one in this assay system [5].

Thus, it seems to us that tRNAs show a structural flexibility and that a defined conformation exists only when the tRNA is a part of a nucleic acid–protein complex like aminoacylsynthetase·tRNA, EF-T_u·GTP·AA-tRNA, 70 S·mRNA·EF-T_u·GTP·AA-tRNA, or 70 S·mRNA·Pep-tRNA. All ligands, either small ones like Mg^{2+}, oligonucleotides, and the aminoacyl residue, or high molecular weight ones like aminoacyl synthetases or EF-T_u·GTP act as either inducers or stabilisers of a defined tRNA conformation [6].

References

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