

Role of Ribosome Recycling Factor as a Ribosome Releasing Factor

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Abstract

The objective of this presentation is to study the *in vivo* actions of ribosome recycling factor (RRF) and compare them with those found in vitro. RRF is known to catalyze three separate reactions: release of tRNA and mRNA from the post-termination complex (PoTC), and splitting of the ribosome of the PoTC. To study the mechanism of RRF reaction *in vivo*, we used *E. coli* harboring temperature sensitive (ts) RRF and assayed by following downstream reading of translationally coupled ORF. At the non-permissive temperature, ribosomes remain on the termination codon of the junction sequence of coupled ORFs and translate downstream ORF lacking a Shine-Dalgarno (SD) sequence. The readings were in all three frames due to thermal frameshift at the termination codon. When upstream ORF was short, translation of the downstream reading was abolished, suggesting that the **ribosomes released by RRF** are moving toward the SD sequence of the upstream ORF. The thermal frame shift at the stop codon was also stopped by the nearby upstream SD sequence. Our data suggest that the ribosome-bound mRNA may take a secondary structure around the junction sequence. This structure can affect the reading of downstream ORF. For *in vitro* studies, we used mRNA that incorporated different radioactively labeled amino acids based on the frameshift at the junction sequence, UAAUG, of two translationally coupled ORFs. In the absence of RRF, the ribosome stayed on the mRNA and translated in frame with the termination codon UAA. In the presence of RRF, amino acid incorporation occurred in frame with the start codon AUG. This suggests that **RRF releases the ribosome** from UAA and the released ribosome binds to AUG and begins translation. With the use of tethered, unsplittable ribosomes (Ribo-T) in the *in vitro* system, we showed that complete ribosomal splitting is not required for the action of RRF. Therefore, the main role of RRF in the ribosome recycling reaction appears to be the **release of ribosomes** from mRNA.



In vivo studies of RRF action



Figure 1. System used to study the behavior of ribosomes at the end of **ORFs under the influence of RRF/EF-G.** Translation of *LacZ* is a marker for downstream-ORF reading. All d-ORF reading is performed by ribosomes from the u-ORF.











Table 1. LacZ expression at 39°C is dependent on spatial distance between the upstream SD sequence and UAA of the u-ORF ----

Junction Sequence	Spatial Distance (nucleotides) between SD and UAA	LacZ expression (%) at 39°C
plY2100, AUAA	3 (short)	58 (high)
plY2150, AUAA	6 (short)	71 (high)
pIY2180, UAAUG	16 (long)	8 (low)
pTU2200, UAAUG	0 (short)	38 (high)
pIY2200, UAAUG	0 (short)	38 (high)
pIY2300, UAAUG	13 (long)	11 (low)
pIY2400, UAAUG	13 (long)	18 (low)
Short spatial distance b inactivated. Lon	etween UAA and SD gives high % expression g spatial distance gives low % expression wh	when RRF is temperature- en RRF is inactive.

Figure 4. Possible secondary structures of various mRNA used in this study.

mRNA can take on secondary structures on the ribosome in the absence of RRF

In vitro studies of RRF action

AUUUAAUACGACUCACUAUAGGGAAUUCAAAAAUUUAAAAGUUAAC**AGGUA**UACAUACU 17 bases T7 promotor AUG UUU ACG AUU ACU ACG AUC UUC UUU ACG AUC UUC UUU ACG AUU ACU ACG AUC FTITTIFFTIFFTITTI UUC UUU ACG AUU UUC UUU ACG AUU ACU ACG AUC ACU ACG AUC UUC UUU ACG FFTIFFTITTITTI FFT In the presence of RRF (0 frame) - - - - **UAA UG** CGU CUG CAG GCA UGC AAG CUA A₂₄ AGC $M \quad R \quad L \quad Q \quad A \quad C \quad K \quad L \quad K_8 \quad S$ In the absence of RRF (+1 frame) - - - **UAA UG**C GUC UGC AGG CAU GCA AGC UAA AAA₂₁AGC C V C R H A S

Figure 5. mRNA sequence used for the *in vitro* study of the role of RRF









Conclusion

All data (*in vivo* and *in vitro*) support the concept that RRF releases ribosomes from mRNA of the PoTC without necessarily splitting the ribosome into subunits.

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Acknowledgments: We thank Mr. Hal Chen for his help in preparing this presentation. Supported by funding from Creative Biomedical Research Institute.



