Nonsense-Mediated Decay – Molecular Bases



Quality control mechanisms ensure fidelity to mRNA biogenesis



The life cycle of mRNA





The relative amount of a mRNA is regulated by a balance between properly synthesized (thus exported and translated) and degraded transcripts

Quality control mechanisms ensure fidelity to mRNA biogenesis



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Premature Stop Codon (PTC)-containing mRNA

1. Recognition of the stop codon as a PTC

2. Tagging of PTC-containing mRNA

3. Degradation and/or isolation of the tagged mRNA



The road to degradation

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The Exon-Junction Complex (EJC) as a splicing hallmark

Multi-protein complexes deposed during splicing at <u>20-24 nucleotides</u> upstream of each exon-exon junction



Experimental data indicate that **elF4AIII**



Represents a scaffold for other proteins such as those involved in mRNA transport

| | OIE4AIII | 123 | | |
|------|----------|---------|---------------|--|
| ore | | 1,2,0 | pre-mRNA | |
| ō | Magon | 1, 2, 3 | | |
| ä | Y14 | 1, 2, 3 | | |
| - | MLN51 | 1, 2, 3 | | |
| | UAP56 | 1, 2 | intermediates | |
| | REF | 0, 1, 2 | | |
| tors | | 2 | | |
| fac | p15 | 2 | nuclear | |
| Ba | | 1.2 | Spliced MRINA | |

EJCs as splicing markers and scaffolds for protein effectors

(EJCs are multi-protein complexes deposed during splicing at 20-24 nucleotides upstream of each EJ)



EJCs are *cis*-acting key components \rightarrow NMD is splicing-dependent

Protein effectors involved in Nonsense-Mediated Decay are conserved

| Organism | 30 | 0 | Marc | | |
|-----------|--|---|--|--|--|
| | Yeast (Saccharomyces cerevisiae) | Nematodes (<i>Caenorhabditis</i> elegans) | Fruitfly (<i>Drosophila</i> melanogaster) | Mammals (<i>Mus musculus</i>) | Plant (<i>Arabidopsis</i> thaliana) |
| Effectors | Upf1 Upf2 Upf3 | SMG-2(UPF1) SMG-3(UPF2) SMG-4(UPF3) SMG-1 SMG-5 SMG-6 SMG-7 | UPF1 UPF2 UPF3 SMG1 SMG5 SMG6 | UPF1(RENT1) UPF2 UPF3a/b SMG1 SMG5 SMG6 SMG7 | UPF1(IBA1) UPF2 UPF3 nd nd nd nd |

NMD effectors are *trans*-acting proteins able to recognize and bind EJCs (*cis*-acting signals)

Protein effectors involved in Nonsense-Mediated Decay are conserved



hUpf proteins in HeLa cells - immunocytochemical staining

Lykke-Andersen et al., Cell, 2000



SMG7 SMG5 b SMG6

Proteins containing a 14-3-3-like domain for binding to phosphorylated residues

eIF4AIIII (part of the EJC core) is required for NMD in mammalian cells

Experimental model: HeLa cells transfected with two different minigene constructs and RNAi technique followed by Northern blot analysis



Result: Depletion of either hUpf1 or eIF4AIII stabilizes PTC+ mRNA to a similar extent

 \rightarrow NMD is splicing-dependent

Quality control mechanisms ensure fidelity to mRNA biogenesis



eIF4E binds the 5'cap <u>before</u> the steady-state translation of mRNA

Evidence for a <u>Pioneer Round of mRNA Translation</u>: mRNAs Subject to Nonsense-Mediated Decay in Mammalian Cells Are Bound by CBP80 and CBP20

Yasuhito Ishigaki,² Xiaojie Li, Guillaume Serin, and Lynne E. Maquat¹

The EMBO Journal Vol. 21 No. 13 pp. 3536–3545, 2002

The exon junction complex is detected on CBP80bound but not elF4E-bound mRNA in mammalian cells: dynamics of mRNP remodeling

Fabrice Lejeune, Yasuhito Ishigaki¹, Xiaojie Li and Lynne E.Maquat²

The <u>PIONEER ROUND</u> of translation – Normal Stop Codon



Normal Termination Codon



Ribosome scanning of the mRNA in a first round of translation

Displacement of EJCs from mRNA



The exon junction complex is detected on CBP80bound but not elF4E-bound mRNA in mammalian cells: dynamics of mRNP remodeling

Experimental model: Nuclear (N) and Cytoplasmic (C) CBP80 co-immunoprecipitation and western blotting analysis with antibodies specific for other complexed proteins



CBP80 but not eIF4E co-immunoprecipitates with EJC components

The exon junction complex is detected on CBP80bound but not eIF4E-bound mRNA in mammalian cells: dynamics of mRNP remodeling



The <u>PIONEER ROUND</u> of translation – <u>Premature</u> Stop Codon



The <u>PIONEER ROUND</u> of translation – <u>Premature</u> Stop Codon



When the distance between a stop codon and the downstream exon-exon junction is more than 55 nt \rightarrow stop codon = PTC

Interplay between EJCs and ribosomes \rightarrow NMD is translation-dependent

The relative position of a PTC influences the efficiency of NMD

Experimental model:

Minigenes containing PTCs at different positions, transfected in cells displaying normal (+) or suppressed (-) translation and Northern blot analysis with a specific exon 3 probe



Target protein

Results:

- i) Translation suppression decreases the NMD \rightarrow NMD is translation-dependen
- ii) NMD efficiency is influenced by PTC position

The relative position of a PTC influences the efficiency of NMD

Experimental model:

Minigenes containing PTCs at different positions, transfected in cells displaying normal (+) or suppressed (-) translation and Northern blot analysis with a specific exon 3 probe



Target protein

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The relative position of a PTC influences the efficiency of NMD

Experimental model:

Minigenes containing PTCs at different positions, transfected in cells displaying normal (+) or suppressed (-) translation and Northern blot analysis with a specific exon 3 probe

7

100

6

100

96

control

Target protein 8

100



Results:

- Translation suppression decreases the i) NMD \rightarrow NMD is translation-dependen
- NMD efficiency is influenced by PTC position ii)

Premature Stop Codon (PTC)-containing mRNA

1. Recognition of the stop codon as a PTC

- EJCs
- Protein effectors (UPF3, UPF2, UPF1)
- Splicing-dependent
- Translation-dependent
- Influenced by position of PTCs



Binding of a novel <u>SMG-1–Upf1–eRF1–eRF3</u> complex (SURF) to the exon junction complex triggers Upf1 phosphorylation and nonsense-mediated mRNA decay

Isao Kashima, Akio Yamashita, Natsuko Izumi, Naoyuki Kataoka, Ryo Morishita, Shinichi Hoshino, Mutsuhito Ohno, Gideon Dreyfuss and Shigeo Ohno

Genes & Dev. 2006 20: 355-367



Mammals (Mus musculus)

UPF1(RENT1) UPF2 UPF3a/b SMG1 SMG5 SMG6 SMG7

Upf1 is recruited within the so-called SURF complex



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Upf1 is recruited within the so-called SURF complex



mRNA is comitted to decay after phosphorylation of UPF1 by SMG1



UPF1 is regulated by phosphorylation/dephosphorylation cycles



Recruitment of SMG6 and/or SMG5-SMG7 via the phosphate tags on UPF1



Recycling of UPF1 and
other effector proteins involved in NMD

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Degradation of the tagged mRNA comitted to NMD



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Experimental model: Lysates of HeLa cells transfected with siRNAs and western blotting analysis on phospho-UPF1 levels after silencing



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Experimental model: Lysates of HeLa cells transfected with siRNAs and western blotting analysis on phospho-UPF1 levels after silencing



Result: SMG-1-mediated phosphorylation of UPF1 requires UPF2, UPF3, and Y14

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mRNA Processing bodies (P-bodies) contain enzymes involved in mRNA degradation



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Also known as mRNA-decay foci, DCP bodies or GW bodies

Specialized cytoplasmic regions enriched with degrading enzymes such as XRN1, DCP1, DCP2 e Lsm1-7



The image shows the co-localisation of the mRNA decapping protein DCP1 with the <u>GW182</u> antigen, <u>a P-body marker</u> in multicellular organisms.



Involved in <u>storage</u>, <u>repression</u> or <u>degradation</u> of mRNAs

 \rightarrow mRNAs in P-bodies can move back to the cytoplasmic pool

eIF-4E

P-bodies (mRNA-processing bodies)





Premature Stop Codon (PTC)-containing mRNA

- 1. Recognition of the stop codon as a PTC EJCs and effector proteins (Upf and SMG family)
- 2. Tagging of PTC-containing mRNA **Phosphorylation of the Upf1 effector protein**
- 3. Degradation and/or isolation of the tagged mRNA
 - a) SMG6- and/or SMG5/SMG7-mediated degradation
 - b) Isolation and degradation in P-bodies

