

Lesson 14

Mechanisms of control of mRNA processing & degradation in neural cells: P-bodies and stress granules

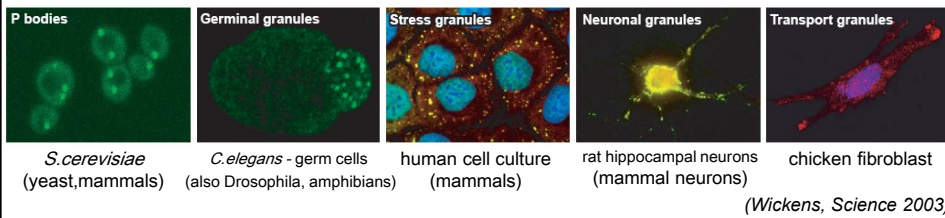
The different mRNA granules

Polysomes - translating mRNA

Stress Granules - mRNA stopped in translation initiation
(= “lost in translation”)

P-bodies – mRNA for degradation + translation repression
(= “a place to die, a place to sleep”)

mRNP granules (byproducts of mRNA metabolism)



RNA granules could be ancient

RNA granules may provide an early form of epigenetic regulation

**Sequester mRNAs until they reached a certain cytoplasmic region.
(transport, neuronal granules)**

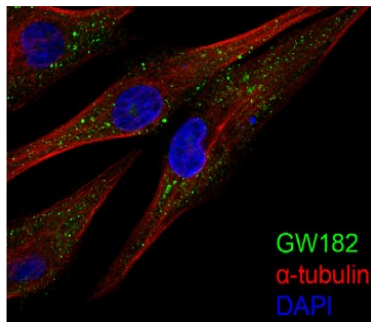
Control which mRNAs are expressed under severe stress (SG)

Cytoplasmic heredity in germ cells (germinal granules)



What are P-bodies?

human autoimmune serum produced a unique cytoplasmic discrete speckled staining pattern on human HeLa cells (Eystathiou et al., 2002)



- mammalian processing (P) bodies
also known as:
- GW bodies (glycine- and tryptophan-rich cytoplasmic bodies;
- or Dcp-containing bodies

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Autoantibodies against PB correlated with autoimmune diseases

GW182/TNRC6A,
GW2/TNRC6B,
GW3/TNRC6C,
Ge-1/Hedls/RCD8,
LSm1-7,
Ago2/EIF2C2,
RAP55/LSm14A,
diacyl-phosphatidylethanolamine

Idiopathic ataxia,
Motor and sensory neuropathy,
Sjögren Syndrome,
Sistemic Lupus Erythematosus,
Rheumatoid arthritis
Primary biliary cirrhosis

What are P-bodies?

cytoplasmic foci: aggregates of translationally repressed **mRNPs**

Translation repression & RNA interference (RNAi) or RNA silencing pathways,
non-sense 5'→3' degradation, mRNA transport and stabilization

conserved core proteins:

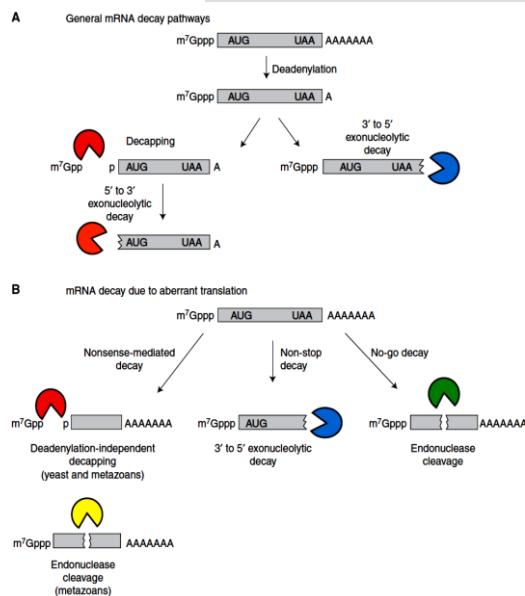
- mRNA decapping machinery
 - deadenylase complex
- } general repression / decay machinery

additional proteins:

- species/condition specific:
- mi/siRNA repression factors (RISC)
 - RNA binding prot-s + translation repressors
 - nonsense-mediated decay (NMD) proteins
= degradation of improperly processed mRNA
(premature stop-codons)

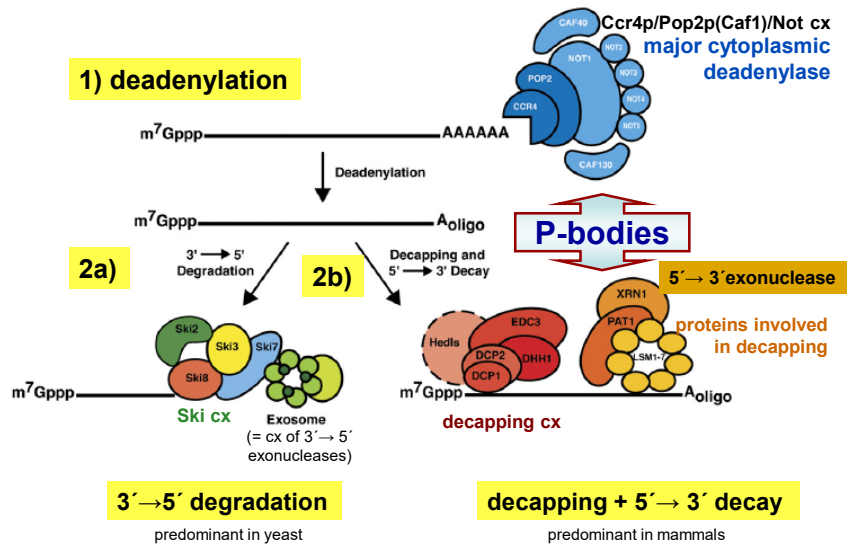
C.J. Decker and R. Parker

DEGRADATION OF EUKARYOTIC mRNA



DEGRADATION OF EUKARYOTIC mRNA

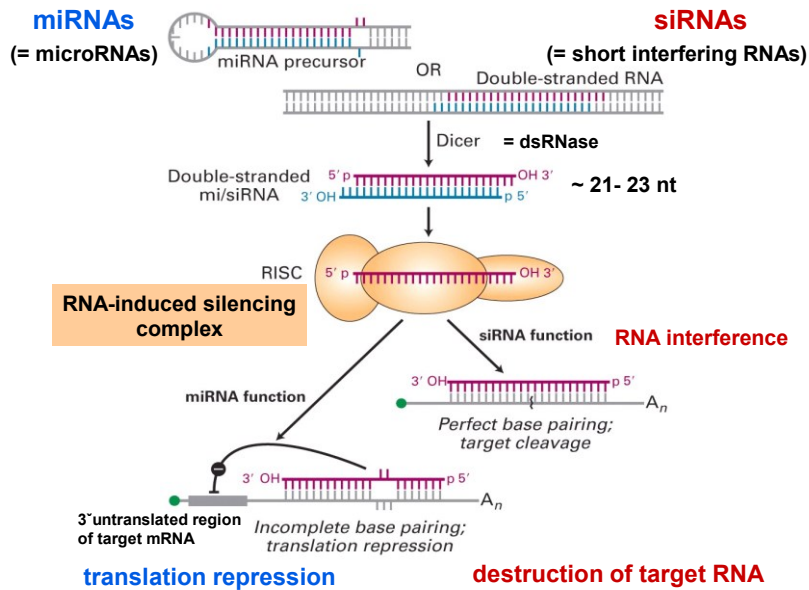
deadenylation-dependent pathways



<http://www.ibiology.org/ibioseminars/genetics-gene-regulation/roy-parker-part-1.html>

(adapted from Parker & Sheth, MolCell 2007)

GENE SILENCING



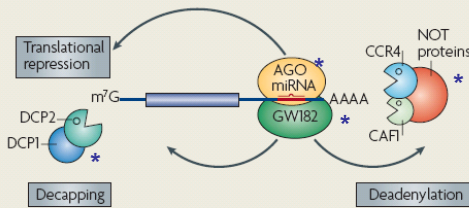
(Lodish et al., 5th ed., adapted from Hutvagner & Zamore 2002)

GENE SILENCING & P-bodies

miRNAs

may target mRNAs into P-bodies

b miRNA-mediated gene silencing in animals

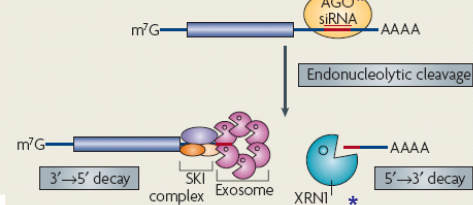


translation repression
mRNA decay (mainly in plants)

siRNAs

mRNA decay

a siRNA-mediated gene silencing



* = P-body components

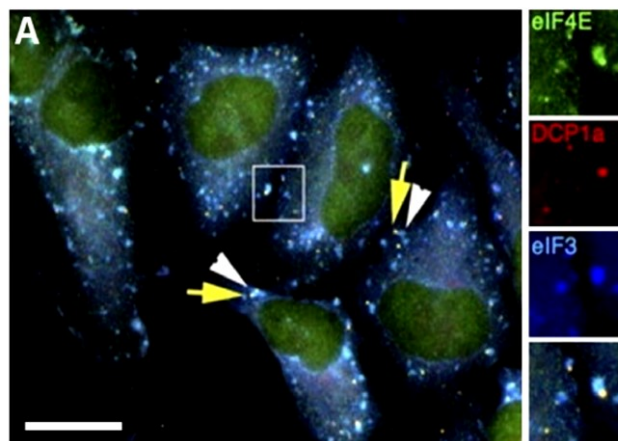
AGO = Argonaute proteins – essential components of **RISC**

characteristic domains: PAZ & PIWI (similar to RNase-H domain)

(Eulalia, Nat Rev Mol Cell Biol 2007)

What is a Stress Granule?

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Stress Granules are non-membranous mRNPs (Found in Yeast, Protozoa, Metazoa, Plants)

Range in size from 0.1 to 2.0 μm (Virus= 100 nm, Bacteria=1.5 μm , Eucaryotic Cell 15-60 μm)

Stress Granule

100–2000 nm non-membranous transient cytoplasmic bodies induced upon environmental stress

>**response to arrest of translation initiation** induced by treatment with drugs (sodium arsenite, cycloheximide), heat shock, osmotic shock, oxygen deprivation, glucose deprivation, UV irradiation or viral infection

contain aggregates of mRNA + translation initiation factors

48S preinitiation cx: eIF4 subunits, 40S ribosomal subunits, poly(A)binding protein 1 (PABP-1)

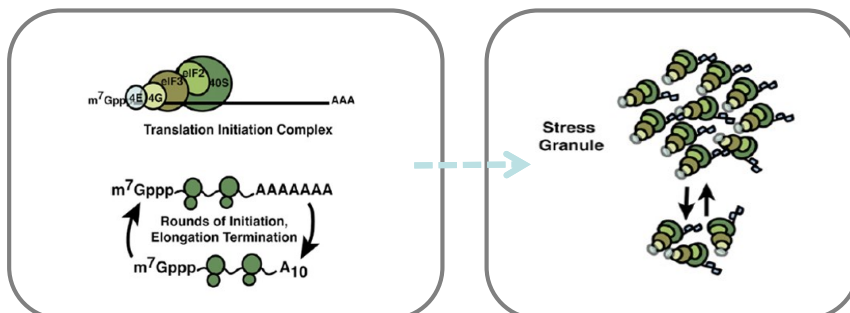
RNA binding proteins with self-interaction domains
(TIA proteins)

often associated with P-bodies

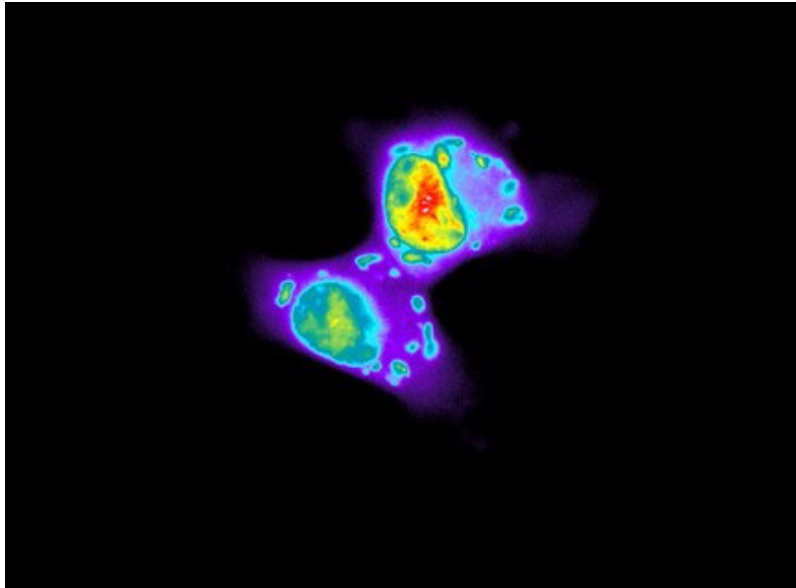
? mRNA moving between the compartments

Stress Granule Formation

- eIF2alpha phosphorylation induces the formation of Stress Granules
- There are many eIF2alpha kinases that can phosphorylate in response to various stresses



Stress Granule Formation



Kedersha et al. 2000 JCB

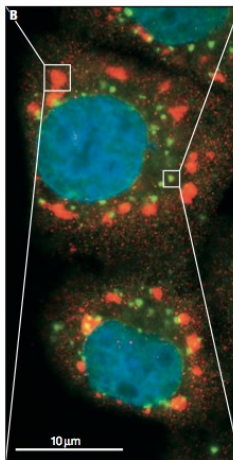
Distinguishing between SG and PB

•Composition. There are lots of shared components but many are unique to either the Stress Granule or the P-body.

•SG markers include PABP, eIF3, 4A, and 4G whereas PB markers include DCP2, XRN4 etc.

A Stress granules

polyA-mRNA	
40S	
eIF4E	Translation initiation
eIF4G	
eIF3	
eIF2	
TIA-1	Translation control
TIAR	
Fragile-X	
CPEB	
PABP	mRNA decay
HuR	
Dhh1	
Staufen	
G3BP	
TTP	
BRF1	
BRF2	
SMN	snRNP assembly
Rpp20	RNA processing
TRAF2	Signalling
Roquin	Ubiquitin ligase
FAST	Scaffold



C P-bodies

mRNA	
Xrn1	5'-3' Exonuclease
Ccr4	Deadenylation
Caf1	
Not1-4	
Lsm1-7	
Dcp1-2	Decapping
Edc3	
Hedls	
Pat1	
Dhh1	Translation control
CPEB	
eIF4E	
eIF4E-T	
Smg5,7	NMD
Upf1	
TTP	AMD
BRF1	
BRF2	
miRNA	miRNA pathway
Ago1-4	
GW182	
FAST	
FAST	Scaffold

CYCLING OF EUKARYOTIC mRNA

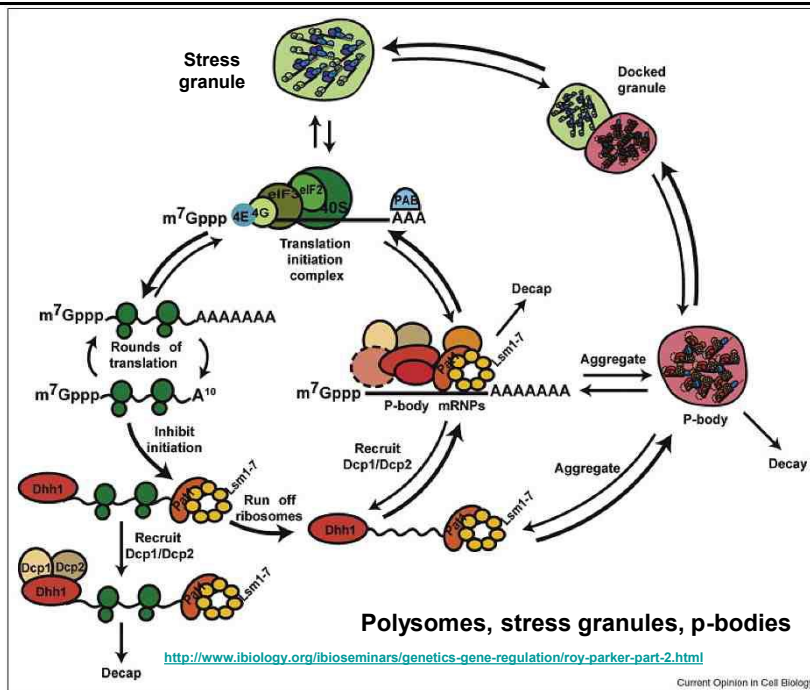
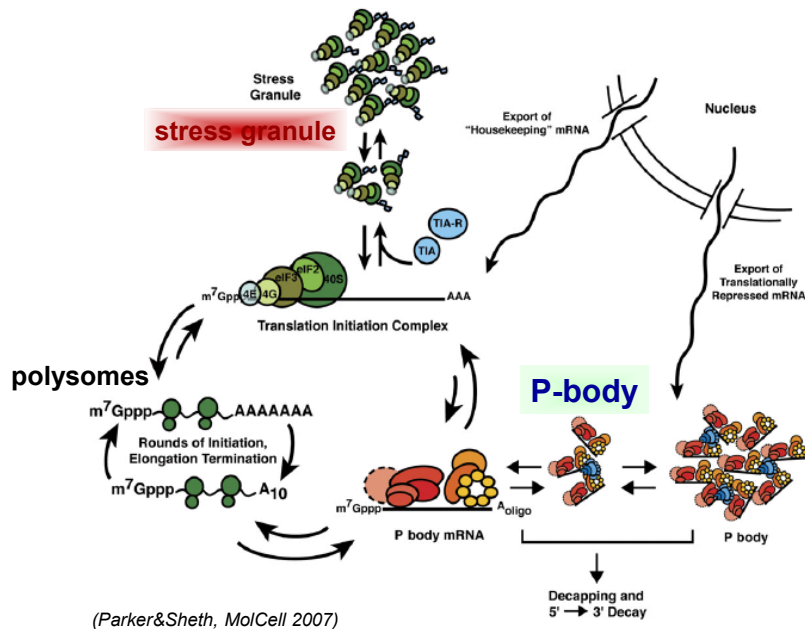
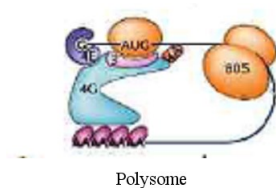




Figure 1. A Continuum of mRNP Granules
Select examples of mRNP granules with compositional similarities to both stress granules and P-bodies: *C. elegans* blastomere germ granules (Gallo et al., 2008), *C. elegans* arrested oocyte foci (Jad et al., 2008), *Drosophila* neuronal transport granules (Barlow et al., 2008), dendritic P-body (Cough et al., 2008). Components observed solely in stress granules are highlighted in red, those solely in P-bodies in green, and those seen in both foci in yellow. Lists are not exhaustive, and with specific experimental manipulation, some P-body/stress granule "distinct" components have been observed in both structures.

1. Stalled initiation complexes

mRNA transcripts
eIF3
eIF4F (eIF4E, eIF4A and eIF4G)
eIF4B
small ribosomal subunits
PABP-1



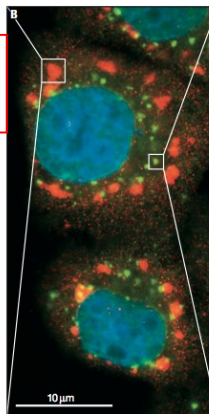
A Stress granules

polyA-mRNA
40S
eIF4E
eIF4G
eIF3
eIF2

TIA-1
TIAR
Fragile-X
CPEB
PABP
HuR
Dhh1
Staufen
G3BP
TTP
BRF1
BRF2

SMN
Rpp20
TRAF2
Roquin
FAST

Translation initiation
Translation control
mRNA decay
snRNP assembly
RNA processing
Signalling
Ubiquitin ligase
Scaffold



C P-bodies

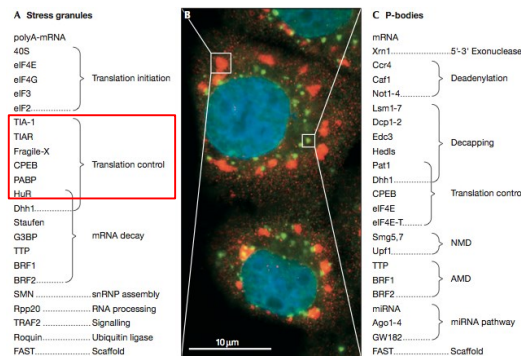
mRNA
Xrn1
Ccr4
Caf1
Not1-4
Lsm1-7
Dcp1-2
Edc3
Hds
Pat1
Dhh1
CPEB
eIF4E
eIF4E-T
Smg5,7
Upf1
TTP
BRF1
BRF2
Ago1-4
GW182
FAST

5'-3' Exonuclease
Deadenylation
Decapping
Translation control
NMD
AMD
miRNA pathway
Scaffold

2. mRNA binding proteins linked to translational silencing (mRNA stability)

A. Translational silencing members; TIA-1, TIAR, FMRP, FAST, Argonaute, CPEB (cytoplasmic polyadenylation element binding protein), FXR1, Lsm14

TIA-1-(T cell internal antigen 1) -binds 3' UTR (ARE) of COX-2 (Cyclooxygenase-2)
conversion of free arachidonic acid to prostaglandins
-Translational silencer(Dixon et al., 2003)
-Nucleates SGs
-Interacts with other proteins (FAST, SRC3, PMR1,FBP)



Stress granules

polyA-mRNA

40S

eIF4E

eIF4G

eIF3

eIF2

TIA-1

TIAR

Fragile-X

CPEB

PABP

HuR

Dhh1

Staufen

G3BH

TTP

BRF1

BRF2

SMN

Rpp20

TRAF2

Roquin

FAST

Translation initiation

Translation control

mRNA decay

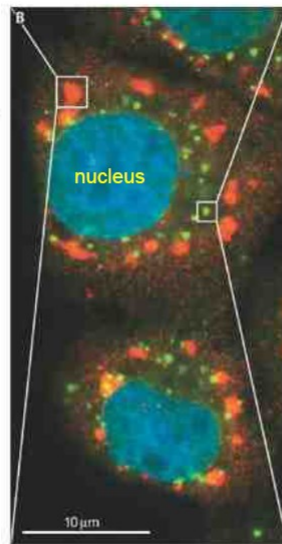
snRNP assembly

RNA processing

Signaling

Ubiquitin ligase

Scaffold



P-bodies

mRNA

Xrn1

Ccr4

Caf1

Not1-4

Lsm1-7

Dcp1-2

Edc3

Hedls

Pat1

Dhh1

CPEB

eIF4E

eIF4E-T

Smg5,7

Upf1

TTP

BRF1

BRF2

miRNA

Ago1-4

GW182

FAST

5'-3' Exonuclease

Deadenylation

Decapping

Translational control

Nonsense mediated Decay (NMD)

ARE mediated Decay (AMD)

miRNA pathway

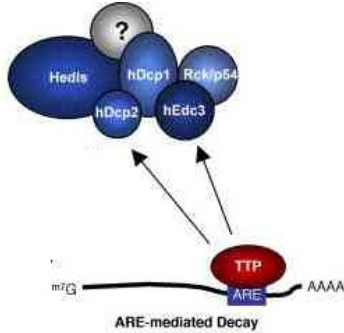
Scaffold

EMBO reports 7:143

B. RNA decay-associated SG components;

–Argonaute proteins, TTP, BRF1, PMR1, RNA helicase RCK

TTP- Tris-tetraprolin



Some of them in polysomes;
FXRP1, RCK, PMR1, Argonaute

TIA-1 and TIAR- constitutively
active translational silencers

Present in both SG and PB

3. RNA binding proteins that regulate aspects of RNA metabolism

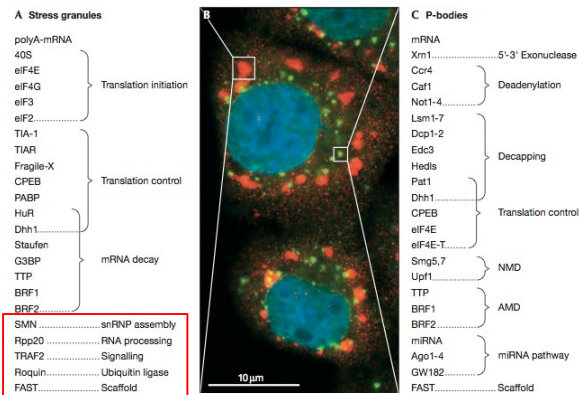
(splicing, RNA editing and RNA localization)

SMN, FAST, transposon ORF1, Rpp20, LINE1, IP5K

SMN – assembly of snRNPs

-Survival of Motor Neurons protein (product of the spinal muscular atrophy-determining gene

-Part of a large protein complex that functions in the assembly of spliceosomal snRNPs (ATP dependent) (Pellizzoni et al., 2002).



FAST – fas-activated serine-threonine phosphoprotein

- Survival protein that is tethered – mitochondrial membrane
- Environmental conditions – FAST moves to SG
- A regulator of alternative splicing
 - eg. Promotes the inclusion of FGFR2 (Fibroblast growth factor receptor -2) exon IIIb (recruited by IAS1- a U-rich intronic splicing enhancer) (Simarro et al., 2007)
- Acts as scaffolding protein – bind to TIA-1 and nucleates both SG and PBs (associated with both SG & PB)

Rpp20- RNA processing

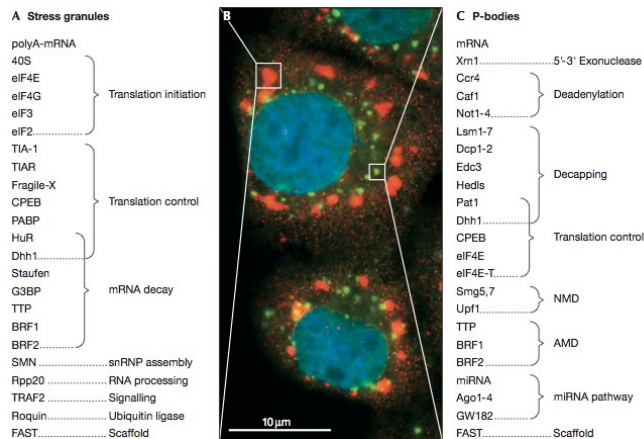
- Subunit of t-RNA processing enzyme ribonuclease P (RNaseP)
- Ribonuclease P required for the processing of 5' of precursor t-RNA (Jarrous et al., 1999).

4. Newly discovered SG components;

recruited to SG by interacting with core SG components
 (“piggyback” interactions)
 eg. FAST, FBP/KSRP, PMR1 all bind to TIA-1

5. ‘Orphan’ class of SG associated proteins

eg. TRAF binds to eIF4G; DIS1 binds to eIF3



Their mRNA composition - selective

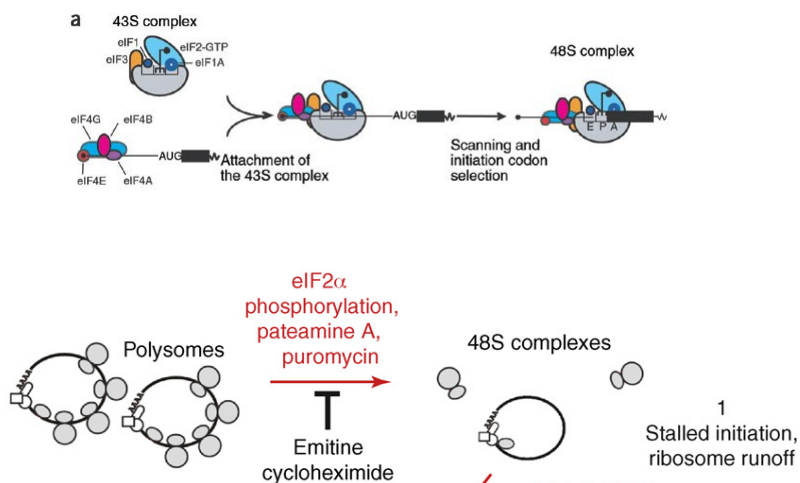
- contain transcripts encoding housekeeping genes
- Endogenous cellular mRNAs encoding glyceraldehyde-3-phosphate dehydrogenase (GAPDH), β -actin, IGF2 (Insuline-like growth factor II)
- exclude those encoding stress-induced genes
 - Heat shock protein 70 and 90 (*HSP70*, *HSP90*) (Kedersha and Anderson, 2009)

SGs are selective and turnover quickly

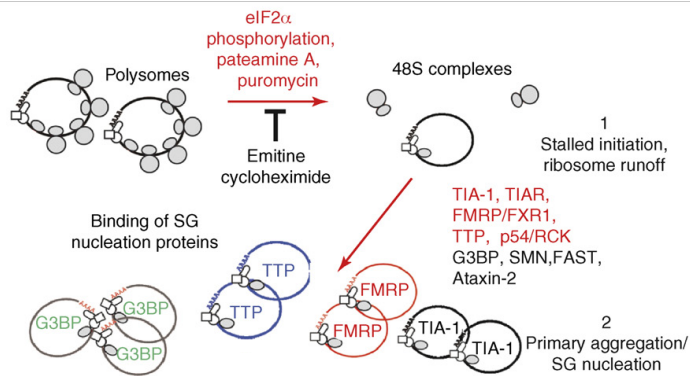
- Under stress only some mRNAs are found in SGs.
- Only ~25% of transcripts can be found in SGs
- Of note, under heat stress, the transcripts for HSPs are excluded from SG assembly.
- SG markers vary. Some are always with the SG, others under only some conditions.
- SG components have a short half life. Seconds to Minutes. (mRNA Triage and sorting?)

Stages of SG assembly

Stage 1: Stalled initiation and ribosome runoff

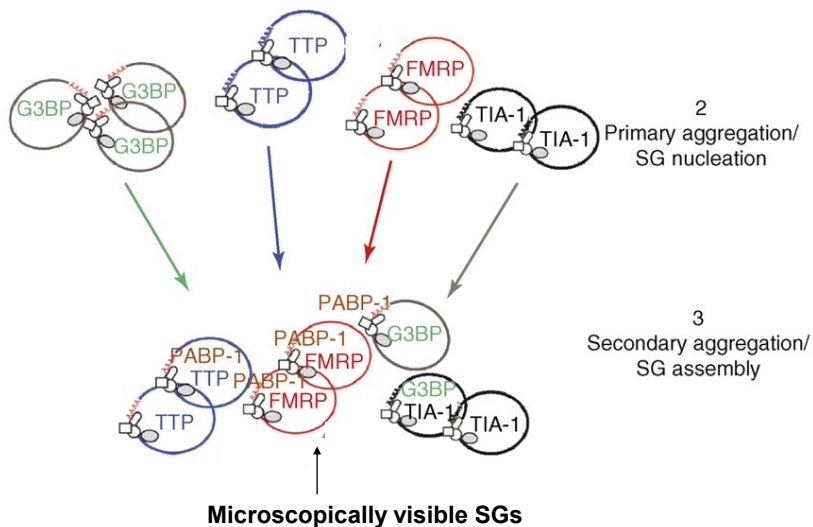


Stage 2: Primary aggregation/SG nucleation

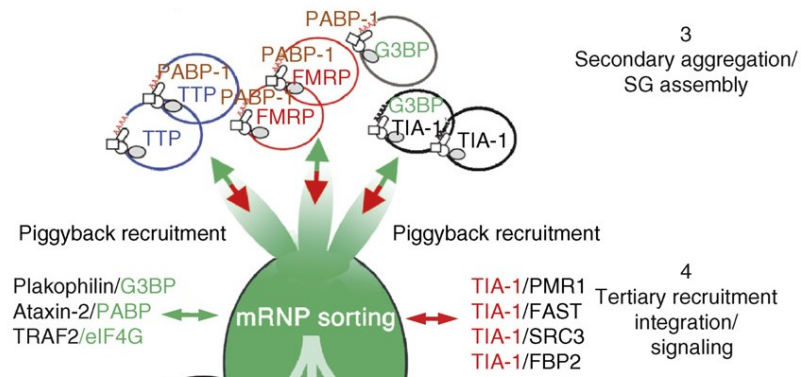


Stress granule nucleators: they induce SGs when over-expressed;
they become part of the SGs they nucleate;
their ability to induce SGs requires nonpolysomal 48S mRNPs

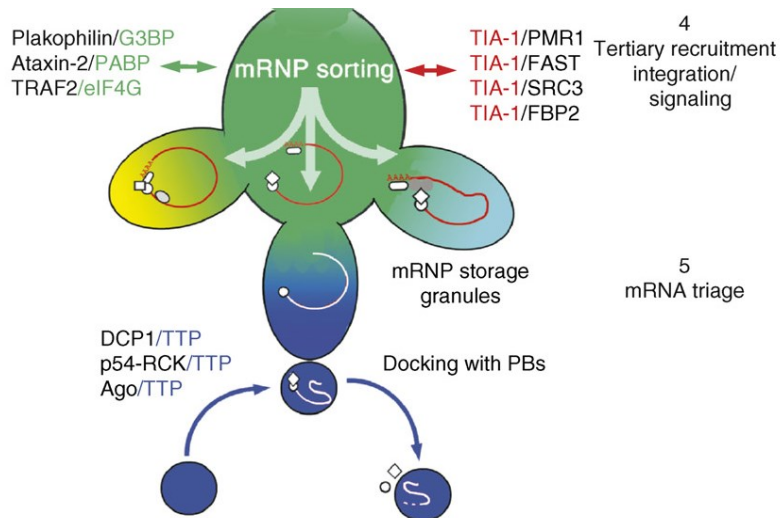
Stage 3: Secondary aggregation



Stage 4: Integration and signaling

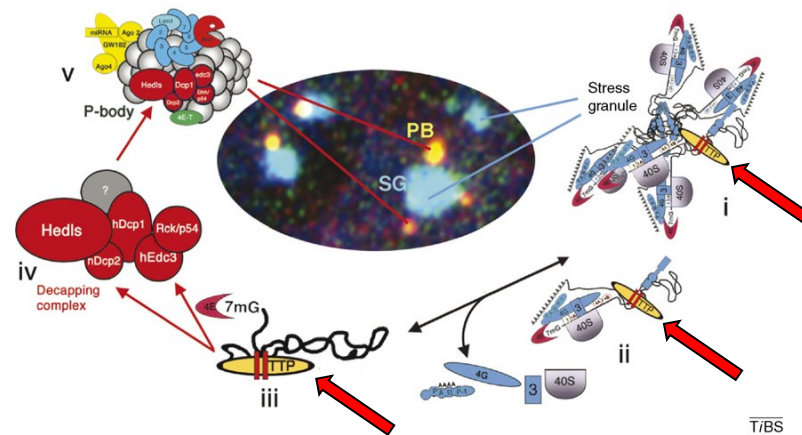


Stage 5: mRNA triage

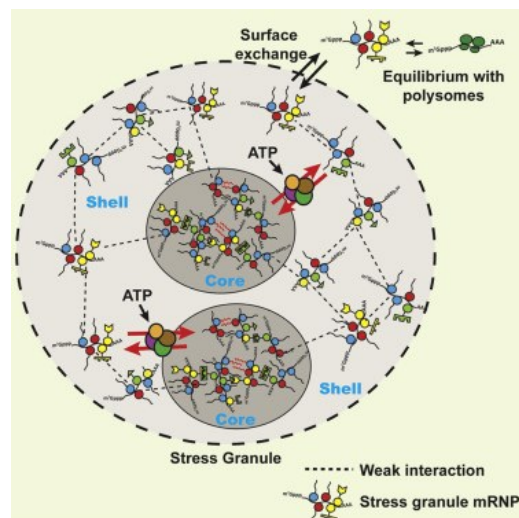


T/BS

TTP dynamically links SGs with PBs during mRNA triage

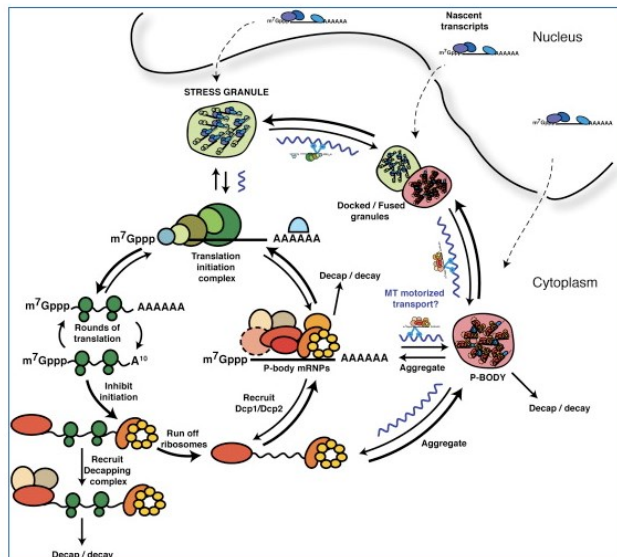


ATP modulates structure and protein content of Stress Granules and its equilibrium with polysomes



Jain et al., Cell 2016

Cellular transport of SG and PB



Buchon & Parker (2010) Mol Cell

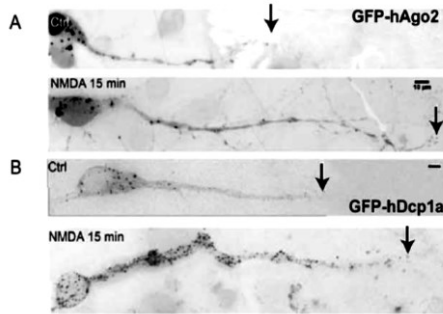
P-bodies move dynamically in a number of ways

- Passively within a confined cytoplasmic region where interactions with mRNA transcripts may be based on random encounters rather than on an active or directed mechanism;
- Bidirectionally along microtubules to facilitate interactions with mRNA transcripts;
- Actively along the nuclear periphery where interactions could occur with the nuclear pore complex and exported mRNAs
- In channel-like regions between mitochondria
- GW182 and miRNA-loaded Ago2 bound to silenced mRNA can move into extracellular exosomes and may be exported to other cells

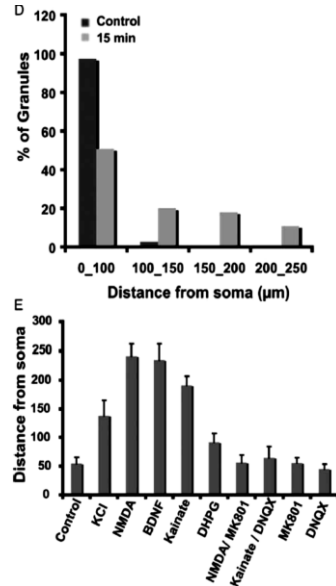
The International Journal of Biochemistry & Cell Biology 42 (2010) 828–843

P-bodies move dynamically in stimulated neurons

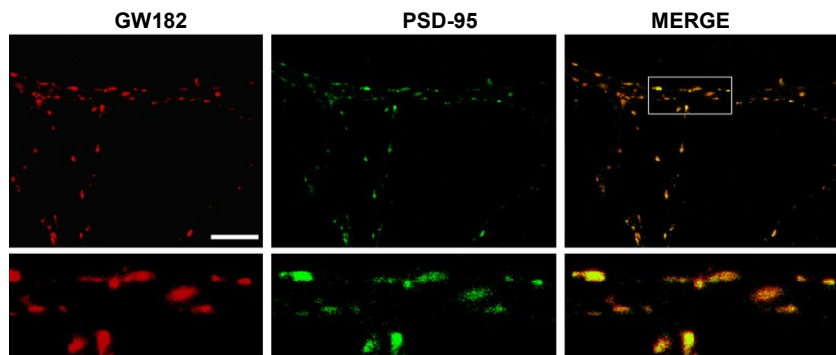
Cougot et al. • P-Body-Like Structures in Rat Neurons



J. Neurosci., December 17, 2008 • 28(51):13793–13804



P-bodies are located within Post-Synaptic densities



The International Journal of Biochemistry & Cell Biology 42 (2010) 828–843

High stability of neuronal P-bodies suggest that unlike P-bodies in other cell types, they represent stable structures, consistent with the idea that they are involved in mRNP storage rather than degradation

SG component exchange (PB and SG docking)

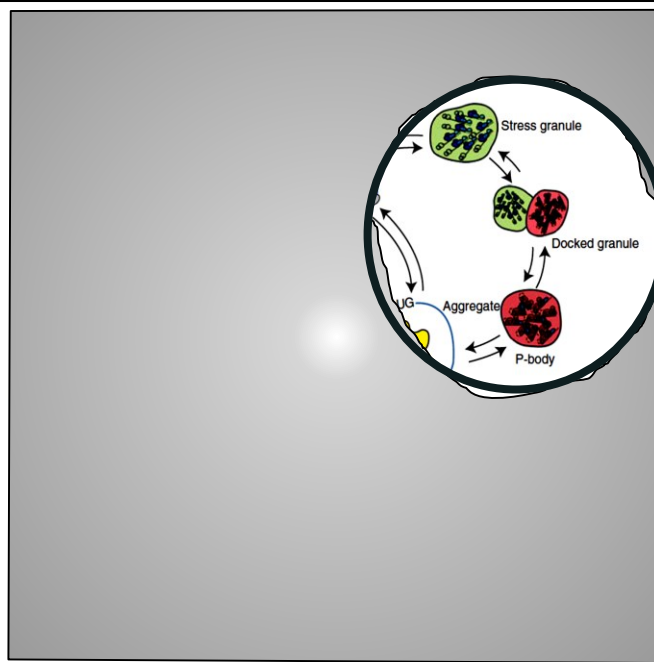
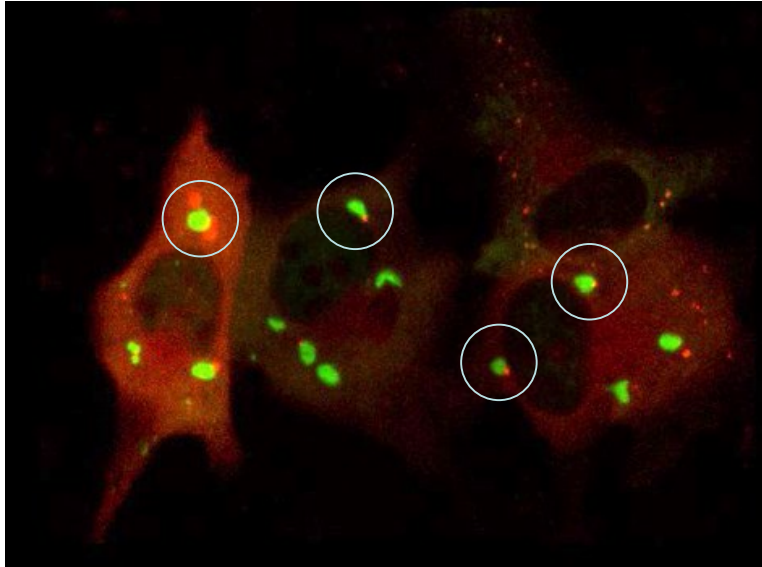


Figure 3. Model of the "mRNA cycle." Showing the dynamic movement of mRNA between polysomes, P-bodies, and stress granules, and the possible mRNP transitions between the different states of the mRNA.

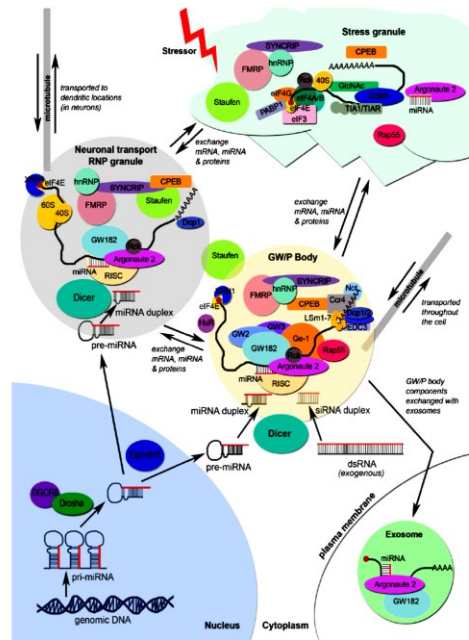
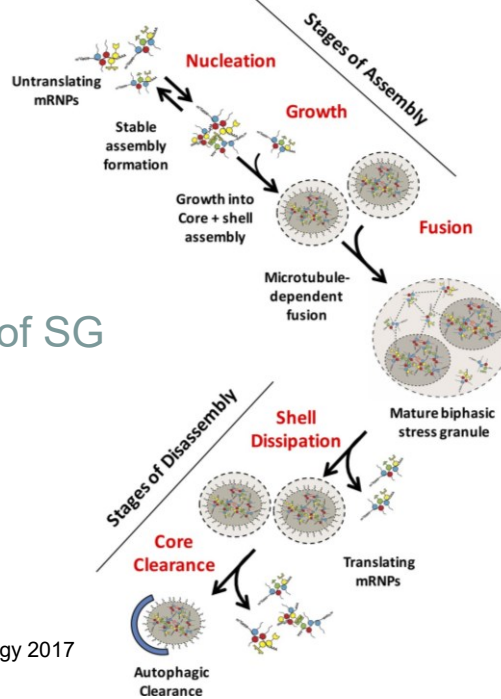
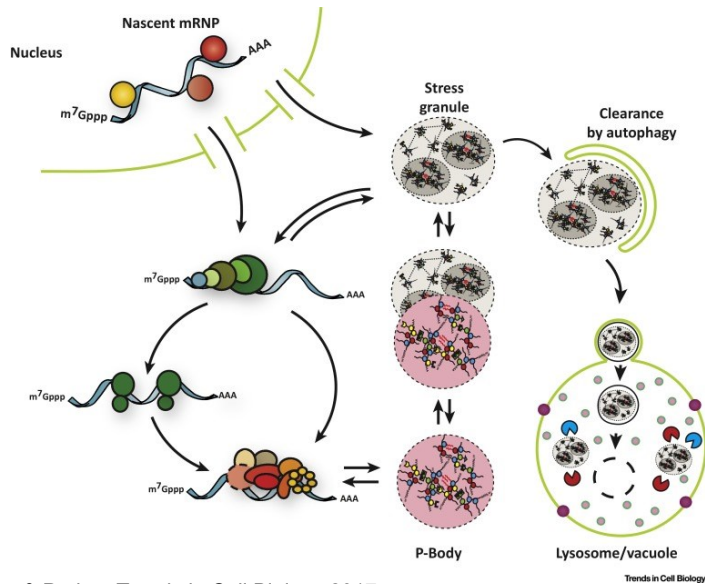


Fig. 9. Conceptual model of a generalized mammalian cell showing the relationships between GWIP bodies, stress granules and neuronal transport RNP granules and their various proteins and RNA components. GWIP body components GW182 and several amounts of Ago2, miRNA and miRNA have recently been shown to be recruited from living cells into extracellular exosomes.

Final destiny of SG



Protter & Parker. Trends in Cell Biology 2017



Sequestration of TRAF2 into stress granules interrupts tumor necrosis factor signaling under stress conditions (Mol. Cel. Biol. 2005, 2450-2462)

