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TITLE:

Using Microtiter Dish Radiolabeling for Multiple In Vivo Measurements Of *Escherichia coli* (p)ppGpp Followed by Thin Layer Chromatography

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SUMMARY:

The growth of radiolabeled bacterial cultures in microtiter dishes facilitates high throughput sampling that allows multiple technical and biological replicate assays of nucleotide pool abundance, including that of (p)ppGpp. The effects of growth transitions provoked by sources of physiological stress as well as recovery from stress can be monitored.

ABSTRACT:

The (p)ppGpp nucleotide functions as a global regulator in bacteria in response to a variety of physical and nutritional stress. It has a rapid onset, in seconds, which leads to accumulation of levels that approach or exceed those of GTP pools. Stress reversal occasions a rapid disappearance of (p)ppGpp, often with a half-life of less than a minute. The presence of (p)ppGpp results in alterations of cellular gene expression and metabolism that counter the damaging effects of stress. Gram-negative and Gram-positive bacteria have different response mechanisms, but both depend on (p)ppGpp concentration. In any event, there is a need to simultaneously monitor many radiolabeled bacterial cultures at time intervals that may vary from 10 seconds to hours during critical stress transition periods. This protocol addresses this technical challenge. The method takes advantage of temperature- and shaker-controlled microtiter dish incubators that allow parallel monitoring of growth (absorbance) and rapid sampling of uniformly phosphate-radiolabeled cultures to resolve and quantitate nucleotide pools by thin-layer chromatography on PEI-cellulose. Small amounts of sample are needed for multiple technical and biological replicates of analyses. Complex growth transitions, such as diauxic growth and rapid (p)ppGpp turnover rates can be quantitatively assessed by this method.

INTRODUCTION:

The (p)ppGpp second messenger is a global regulator that modulates the expression of a large number of genes, including genes for synthesizing ribosomes and amino acids^{1,2}. Although initially discovered in *Escherichia coli*³, (p)ppGpp can be found in both Gram positive and Gram negative bacteria as well as in plant chloroplasts^{4,5}. For *E. coli* and other Gram-negative bacteria, (p)ppGpp interacts directly with RNA polymerase at two different sites⁶⁻⁸. In Gram positives, (p)ppGpp inhibits GTP abundance, which is sensed by CodY, a GTP-binding protein with gene-specific DNA recognition motifs that lead to regulation^{9,10}. (p)ppGpp accumulates in response to starvation for different nutrients and stress conditions, resulting in slow growth and adjustments of gene expression to allow adaptation to stress^{11,12}.

The net amount of ppGpp accumulated reflects a balance between synthetase and hydrolase activities. In *E. coli* RelA is a strong synthetase and SpoT is bifunctional, with a strong hydrolase and a weak synthetase, each of which might be regulated differently in a stress dependent manner. The strong RelA synthetase is activated when the availability of codon-specified charged tRNA bound to the ribosomal A site when it fails to keep up with the demands of protein synthesis¹³⁻¹⁵. The weak SpoT (p)ppGpp synthetase is activated while the strong (p)ppGpp hydrolase is inhibited in response to other stress conditions and through other mechanisms. Under some conditions, proteins such as ACP or Rsd can bind to SpoT, which also change the balance between hydrolysis and synthesis^{16,17}. In Gram positives, synthesis and hydrolysis reflect a more complex balance between a single RelA SpoT homolog (RSH) protein with strong synthesis and hydrolysis activities as well as smaller hydrolases and/or synthetases¹².

The (p)ppGpp nucleotides were first discovered as unusual ³²P labeled spots that appeared on autoradiograms of thin-layer chromatograms (TLC) during a stringent response induced by amino acid starvation³. More detailed labeling protocols have been reviewed¹⁸. The protocol described here (**Figure 1**) is a modification of these protocols that allows monitoring growth of multiple samples on microtiter plates. This facilitates multiple biological and technical estimates of (p)ppGpp abundance changes and was initially developed for studies of diauxic shifts¹⁹. Labelling of (p)ppGpp with ³²P and detection by TLC also allows measurements of (p)ppGpp degradation rates. Alternative methods have been developed to determine (p)ppGpp levels such as mass spectrometry, HPLC²⁰, fluorescent chemosensors^{21,22}, and GFP gene fusions to promoters affected by ppGpp^{23,24}. Fluorescent chemosensors currently have a limited use due small spectral shifts after binding ppGpp as well as problems distinguishing between ppGpp and pppGpp²¹. This method is efficient to detect (p)ppGpp in vitro, but not in cellular extracts. Methods involving HPLC have been improved²⁰ but require expensive equipment and are not well adapted to high through-put. Finally, GFP fusions can give an estimate of ppGpp dependent activation or inhibition, but do not measure ppGpp itself. While each of these alternative methods are valuable, they require expensive equipment or substantial hands-on time, or they are otherwise not amenable to multiple kinetic sampling and subsequent processing. With the method described here, 96 samples can be applied to six TLC plates in about 20 minutes (18 samples per plate), resolved by TLC development in less than a couple of hours, with quantitative data obtained after several hours or overnight, depending on labeling intensity.

89 **PROTOCOL:**

91 **1. Media preparation**

93 1.1. For MOPS (3-(N-morpholino)propanesulfonic acid) media²⁵, use 1/10 volume of 10x MOPS
94 salts, 1/100 volume of 100x micronutrients solution, 3 mM sodium phosphate for overnight
95 cultures or 0.2 mM sodium phosphate for uniform labeling with ³²P, 0.2% glucose and 1 µg/mL
96 thiamin (vitamin B1). Add amino acids at 40 µg/mL if required.

98 1.1.1. For MOPS salts, use 400 mM MOPS, 40 mM Tricine, 0.1 mM FeSO₄, 95 mM NH₄Cl, 2.6 mM
99 K₂SO₄, 5 µM CaCl₂, 10.56 mM MgCl₂, and 500 mM NaCl. Add the different components in the
100 order written to avoid precipitation. Adjust to pH 7.4 with KOH and sterilize by filtration.

102 1.1.2. For 100x micronutrients solution, use 3 µM (NH₄)₆(MO₇)₂₄, 0.4 mM H₃BO₄, 30 µM CoCl₂, 10
103 µM CuSO₄, 80 µM MnCl₂, and 10 µM ZnSO₄. Sterilize by autoclaving.

105 1.1.3. For glucose (20%) and sodium phosphate (300 mM) solutions, sterilize as separate 100x
106 stocks by autoclaving. Sterilize 100x stocks of thiamine and amino acid mixtures by filtration.
107 Prepare fresh media from sterile stock solutions for each experiment.

109 **2. Labelling with ³²P**

111 2.1. Grow overnight cultures in MOPS media with 3 mM sodium phosphate.

113 2.2. In a 24 well plate, add 550 µL of MOPS media containing 0.2 mM sodium phosphate carrier
114 and 30 µL of each bacterial inoculum (dilution 1/20). This will produce an initial inoculum of
115 OD_{600nm} 0.1. Use one well with fresh media as a sterility control.

117 2.3. Place the plate on a shaking incubator at 37 °C shaking at 900 rpm for 30 min. Cultures are
118 heated from below and shaking provides aeration. Attach the plate firmly with tape to avoid
119 tilting or spills. Growth can be monitored with a replicate plate in parallel in media lacking ³²P
120 using a plate reader and incubating under the same conditions.

122 2.4. Add 100 µCi to each well of ³²P orthophosphate (20 µL from a 5 mCi/mL stock).

124 NOTE: The amount of radioactivity can also be adjusted to meet experimental needs. For low
125 basal levels 100 µCi with 0.2 mM carrier phosphate works well, but for measuring (p)ppGpp levels
126 that are expected to become equivalent to GTP pools, label can be dropped to 25 or 50 µCi.
127 Lowering carrier phosphate below 0.2 mM is not recommended to avoid phosphate levels
128 becoming limiting for growth.

130 **CAUTION:** ³²P is a β emitting isotope so use proper shielding specified for safety. All radioactive
131 material must be properly disposed taking all the possible precautions.

2.5. Grow in shaking incubator for 1 to 2 doublings (an hour or more) to allow external label to largely equilibrate with intracellular nucleotide pools before inducing stress.

3. Induction of stress or starvation

3.1. Induce stress using a method of your choosing, depending on the sort of stress studied, e.g. adding metabolic pathway inhibitors, changing temperature, exhausting required nutrients, shifting osmolarity shifts, inducing oxidative stress, adding toxins, etc.

3.1.1. For example, add 100 µg/mL L-valine to induce isoleucine starvation in *E. coli* K-12 strains. Increased levels of ppGpp will be observed after 5 minutes of induction.

4. Sampling and ppGpp extraction

4.1. Add 20 µL of each labelled cell sample to a 0.2 mL PCR tube containing 20 µL of ice cold 6 M Formic acid.

4.2. Immediately place the samples in dry ice.

4.3. Enhance cellular extraction efficiency by 3 cycles of freezing and thawing.

4.4. Just before spotting PEI cellulose thin layer chromatograms, centrifuge samples for 1 min at maximum speed to pellet cell debris to avoid spotting it on chromatograms.

5. Thin-layer chromatography

5.1. With a soft pencil, mark an origin line 1 cm from the edge of the 20 cm x 20 cm PEI-Cellulose TLC plate that has had 5 cm removed from the top with scissors. Apply 5 µL as a droplet in the PEI surface for each sample. Begin ascending development without allowing this spot to dry, which improve resolution by minimizing streaking.

5.2. Do ascending development in a tank with a layer of 1.5 M KH₂PO₄ (pH 3.4) solution shallow enough so that liquid does not touch the origin sample spot. Cover the tank with an air-tight seal and allow liquid ascent to the top of the trimmed sheet, 15 cm. To achieve pH 3.4 for a 1.5 M KH₂PO₄ solution, it is necessary adjust the pH by addition of H₃PO₄.

5.3. Remove the fully developed chromatogram and air dry at room temperature.

5.4. Cut and discard the top (pH front) portion of the chromatogram containing the free ³²P into radioactive waste. This portion is represented in yellow color in **Figure 2** and easily visualized under UV light. If measuring only (p)ppGpp nucleotides that migrate slower than GTP, it is recommended to run a UV-visible GTP standard and then cut and discard a larger upper portion (anything above GTP, as shown in **Figure 2**).

177 5.5. Expose autoradiographic films overnight with a phosphor screen.

178
179 5.6. Develop the film. Capture and quantitate the phosphor screen signal with a phosphorimager.

180 181 **6. Quantitation of (p)ppGpp**

182
183 6.1. Quantitate radioactive spots with Image J^{26,27}.

184
185 NOTE: The amount of (p)ppGpp can be normalized to total amount of G nucleotides observed in
186 each sample (**Figure 2**). If the amount of background is homogeneous, a single blank (box 4 from
187 **Figure 2**) can be subtracted to correct for background. Total G is the sum of GTP + ppGpp +
188 pppGpp detected. This normalization assumes that GMP and GDP levels are negligible, which is
189 true for *E. coli*. The ratio of a given nucleotide to total G provides an important way to correct for
190 variations of applied sample volume.

191 192 **7. Measurement of the rate of ppGpp decay**

193
194 NOTE: A modification of this protocol allows measurements of ppGpp decay rates.

195
196 7.1. After provoking stress or starvation for a time sufficient to allow ppGpp accumulation (step
197 3), reverse the stress in order to block continued ppGpp synthesis, which allows detection of
198 hydrolytic rates. The procedure for reversal will depend on the stress. For example, add 200
199 µg/mL of chloramphenicol to reverse any amino acid starvation.

200
201 7.2. Decay rates are usually rapid but may vary, so take samples every 20-30 seconds up to 2
202 minutes. Process samples as in step 4.

203
204 7.3. Once the TLC is developed (as in step 5) and the levels of ppGpp obtained during the time
205 course, plot residual ppGpp content on a semi-logarithmic plot vs time to allow visualization of
206 zero order rates of decay, as a straight line, and estimation of the ppGpp half-life.

207 208 **REPRESENTATIVE RESULTS:**

209
210 In *E. coli* K-12 strains, the addition of valine provokes an endogenous starvation of isoleucine,
211 which results an increase of ppGpp levels after 5 minutes³. Cells grown in MOPS containing all
212 amino acids except for ILV were labeled with ³²P as indicated in **Figure 1**. Once labelled, 6 µL of
213 10 mg/mL L-valine (100 µg/mL final concentration) was added to produce isoleucine starvation.
214 Samples were taken 0 and 5 minutes after the addition of valine. After 5 minutes (**Figure 3A**), a
215 2 and 2.5-fold increase in the levels of ppGpp and pppGpp occurred. As a negative control, a cell-
216 free labelled sample was used to detect possible compounds that were not orthophosphate in
217 the ³²P source. Also, including a ppGpp deficient strain (*ΔrelA ΔspoT*) as a negative control could
218 help a better identification of the spots.

219
220 Reversal of isoleucine starvation can be achieved by chloramphenicol, an inhibitor of protein

synthesis, which reduces consumption of charged ile-tRNA and in turn, restores high ratios of charged to uncharged tRNA. Activation of the strong RelA-mediated ppGpp synthetase is abolished, which allows a measure of ppGpp degradation unperturbed by residual synthesis. Therefore, 200 µg/mL of chloramphenicol was added to the starved cultures and samples were taken at 20 second intervals thereafter. In this case, ppGpp decayed with a half-life of about 64 seconds (**Figure 3B**).

FIGURE AND TABLE LEGENDS:

Figure 1: Measurement of ppGpp by TLC workflow. Schematic representation of the protocol to extract ppGpp from bacterial cultures and its posterior detection by TLC.

Figure 2: Representative TLC analysis. Schematic representation of the results obtained after autoradiography and phosphor screen overnight with the TLC. The spots to be measured are shown in red. The formula to calculate the fractional amount of ppGpp is also shown. Total G refers to the total amount of GTP + ppGpp + pppGpp detected in the sample. The yellow band represent the pH front visible under UV light. Scissors indicate where we recommend cutting the chromatogram for discarding most of the radioactivity. The arrow indicates the direction of the flow during ascending development with 1.5 M phosphate buffer.

Figure 3: measurement of synthesis and decay of ppGpp. (A) Detection of ppGpp by TLC for samples 0 and 5 minutes after addition of valine. Spots corresponding to GTP, ppGpp and pppGpp are marked. A cell-free culture was included as negative control (C-). (B) Decay of ppGpp after addition of chloramphenicol to reverse amino acid starvation. The ppGpp half-life is determined from the exponential decay rate represented by dotted lines. Error bars reflect SD from duplicates. Y-axis is represented in a semilogarithmic (\log_2) scale.

DISCUSSION:

Achieving near uniform labeling of the cells is a critical step for this protocol. Therefore, the use of defined media, such as MOPS or Tris media, is crucial to allow variation of carrier phosphate concentrations and specific activity. Phosphate buffered media, such as M9 or media A, cannot be used. Most undefined media contain variable amounts of phosphate, such as LB, tryptone and casamino acids. The phosphate isotope ^{33}P is a weaker emitter that can be substituted for ^{32}P . Advantages of the substitution are that it is safer and has a half-life of 25 days instead of 14 days for ^{32}P . However, the more energetic emissions of ^{32}P considerably enhance detection sensitivity. It is important to stress the dangers of working with isotopes and the importance of using proper shielding protections and disposal. The recent discovery of a riboswitch able to detect specifically ppGpp²⁸ may someday lead to a safer way to detect ppGpp in vitro and in vivo. As mentioned in the introduction, other methods exist, although the use of phosphate labelling remains a sensitive, direct and rapid approach for through-put measurements of bacterial (p)ppGpp as well as other phosphate labeled compounds, such as ribo- or deoxyribo-NTP pools, PRPP, PPi or sugar phosphates.

Another critical step is to ensure that the growth of the parallel cultures (shaking incubator and plate reader) is similar. When studying nutrient exhaustion, such as diauxic shift¹⁹, the synchrony between cultures is crucial. The comparability of growth on labeled and unlabeled plates can be assessed by OD₆₀₀ measurements of an unlabeled well on the otherwise radioactive plate. To increase the number of samples tested, a 96 well plate can be used instead¹⁹, but the amount of media required to minimize evaporation will reduce culture aeration. Basal levels of (p)ppGpp will be slightly higher during growth in a 96 well plate compared to a 24 well plate due to the reduced aeration. Therefore, for measuring basal levels, a 24 well plate growth is recommended. To measure variations of more strongly induced (p)ppGpp levels, a 96 well plate is preferred. The choice between 24 and 96 well microtiter plates depends on the experimental goal.

Variations of this protocol have many potential applications for different conditions of stress. Recently we have applied it to measure accumulation and decay of ppGpp during classical diauxic shifts from glucose to lactose and to other alternative sugars. These studies revealed involvement of both glucose starvation and amino acid starvation¹⁹. Here we describe amino acid starvation induced by valine in *E. coli* K12 strains as a simpler and well-studied stress condition³. This example might be used as a control before performing more complicated starvation situations. Amino acid starvation can be provoked by adding limited amounts of a required amino acid that is exhausted during growth; adding an inhibitor of tRNA aminoacylation or synthesis (serine hydroxamate, mupirocin, or 3-aminotriazole) or for *E. coli* K12 adding valine in the absence of isoleucine). Serine hydroxamate is often used to inhibit tRNA^{Ser} aminoacylation but requires high concentrations, which may cause problems due to the hydroxamate reactivity with other compounds. Reversal of serine hydroxamate effects by adding a large amounts of serine can have non-desired effects¹. Although SHX has been proven to be effective as a diagnostic of ppGpp production, we do not recommend its use for physiological studies to produce amino acid starvation, because normal (p)ppGpp feedback mechanisms are abolished, such as physiological consequences of lowering superfluous activities but allowing activation of stress survival regulatory circuits.

Modifications of the TLC procedures described here are necessary in order to properly separate noncanonical regulatory nucleotides, such as (p)ppApp²⁹, from mixed samples with (p)ppGpp. It has been shown that pppApp has an antagonistic role to ppGpp in vitro^{30,31}; therefore, better separation of both compounds is required for future studies.

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DISCLOSURES:

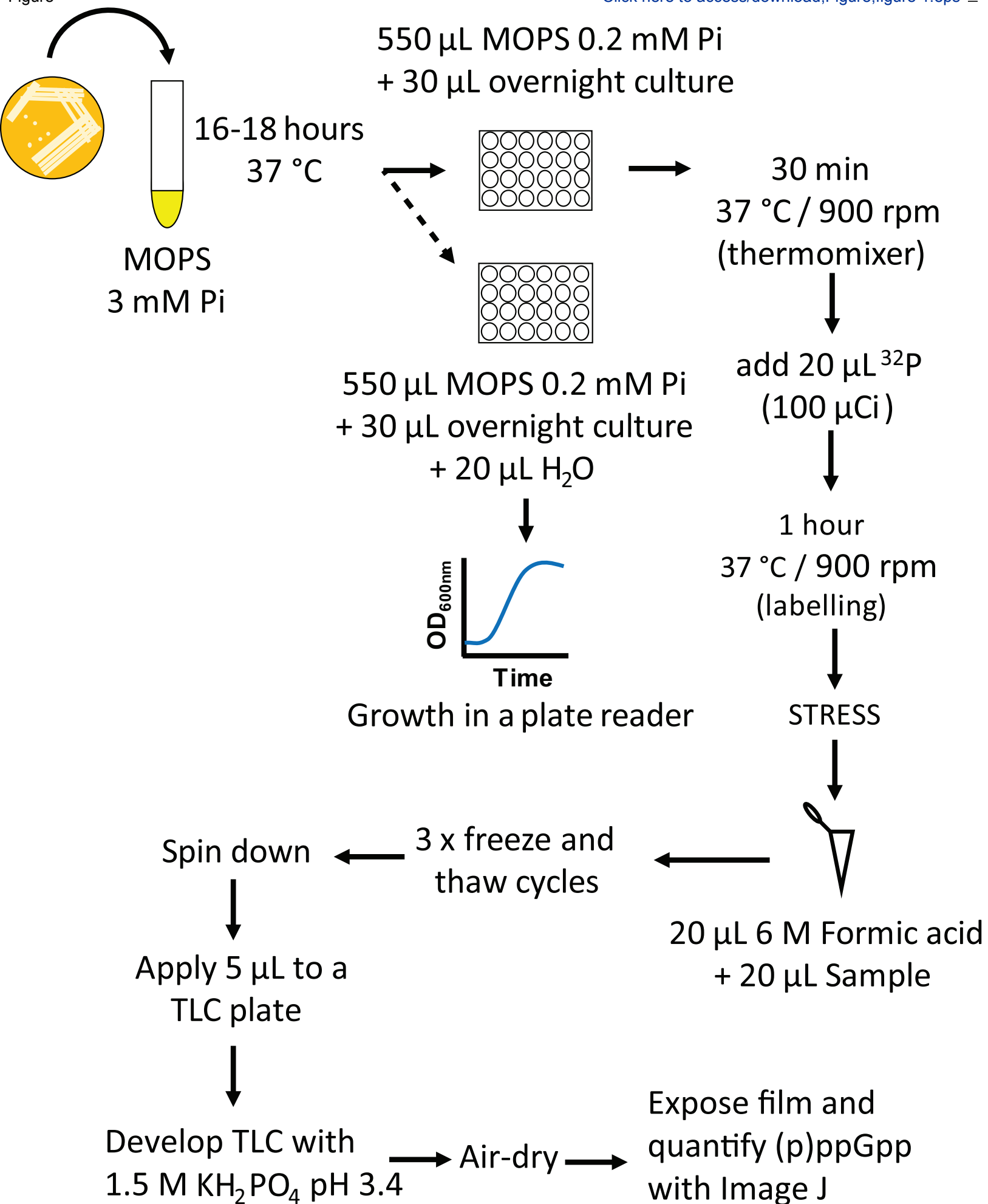
The authors have nothing to disclose.

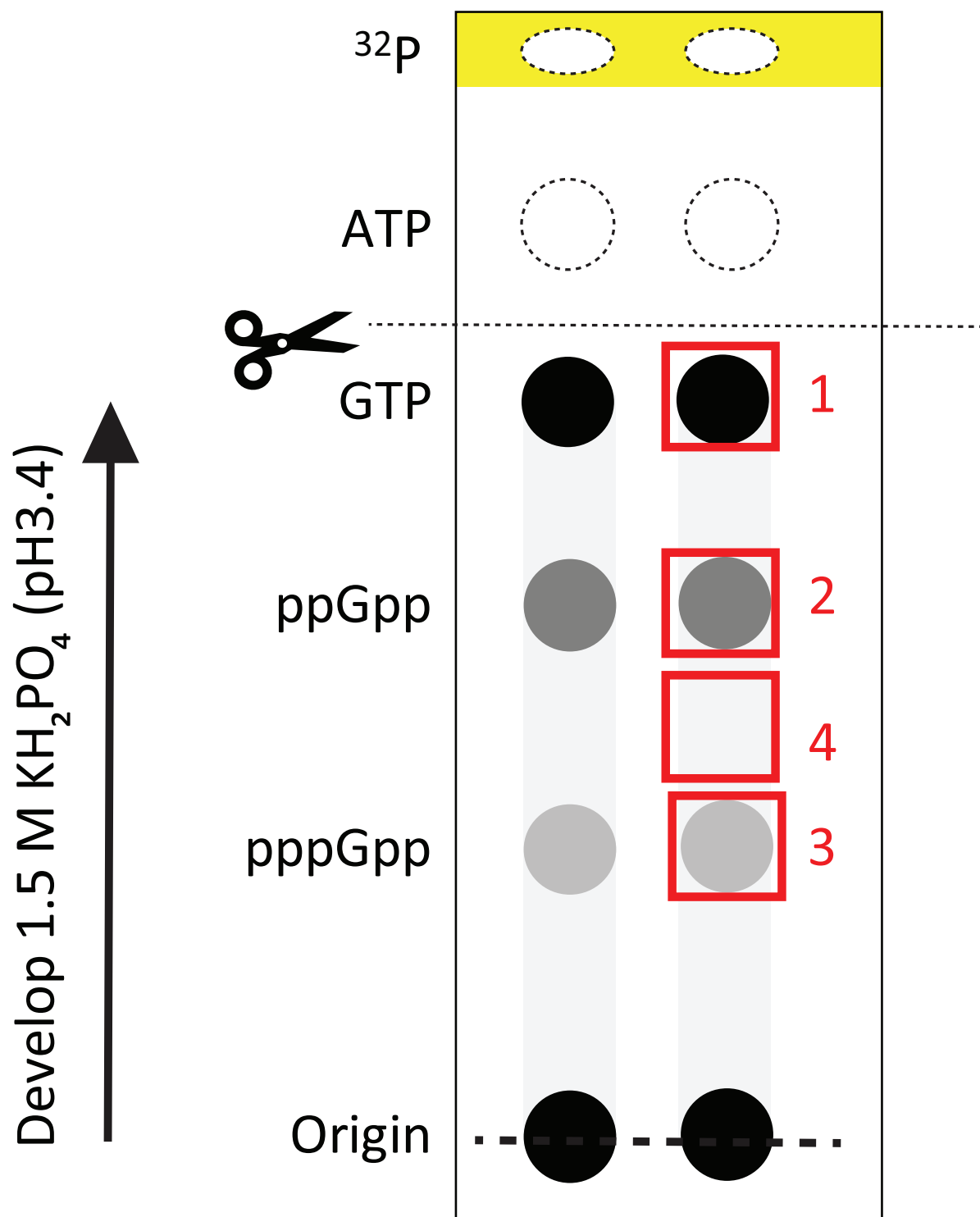
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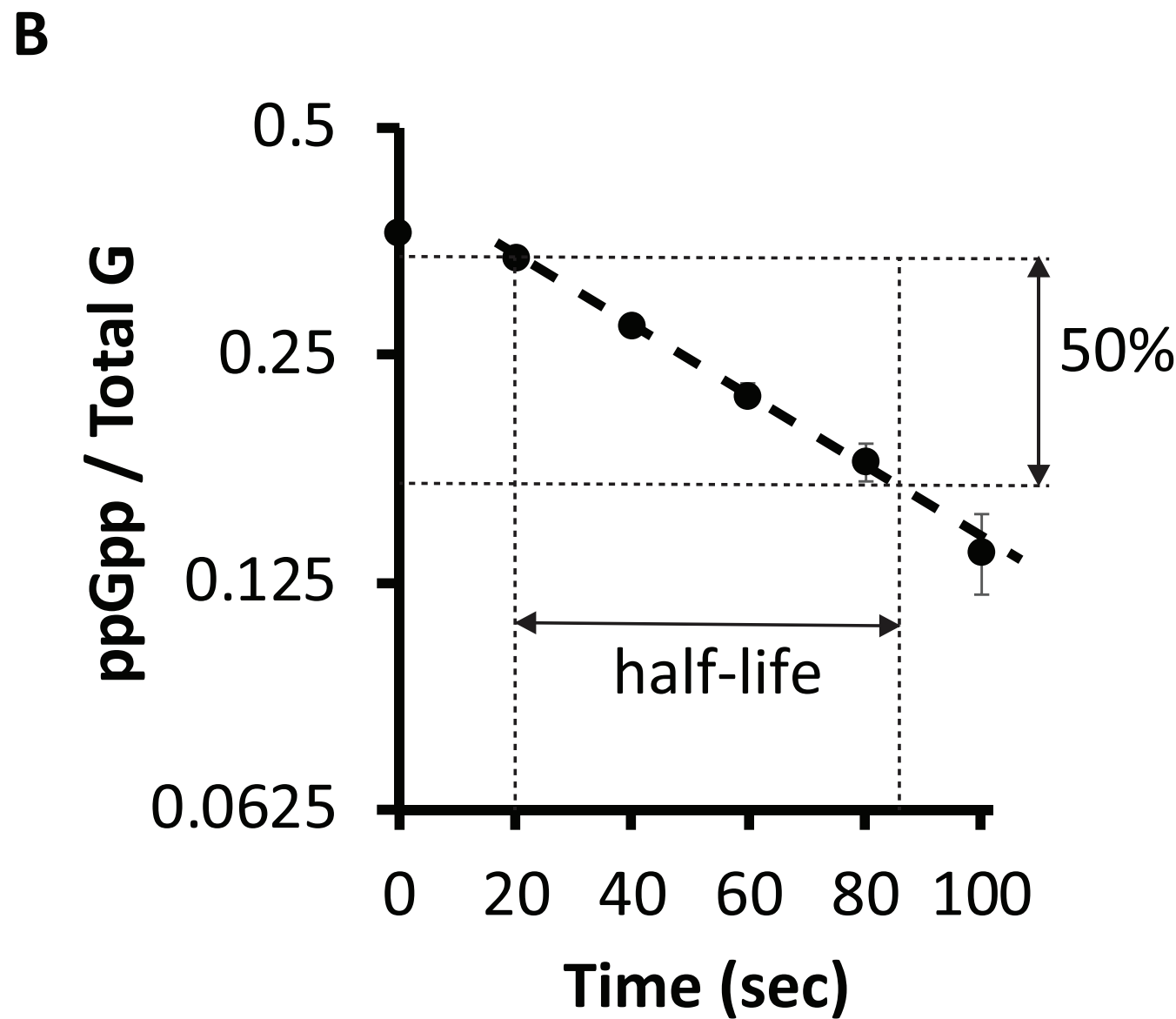
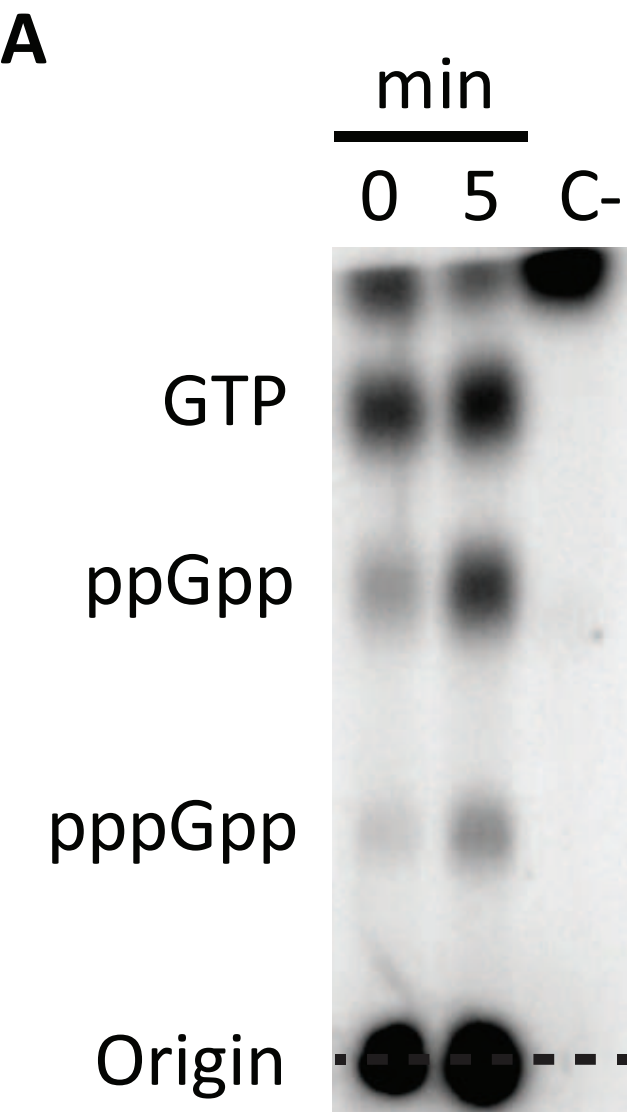
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Fractional amount of ppGpp =
$$\frac{\text{ppGpp (2)} - \text{blank (4)}}{\text{Total G ((1-4) + (2-4) + (3-4))}}$$



Name of Material/ Equipment	Company	Catalog Number	Comments/Description
$(\text{NH}_4)_6(\text{MO}_7)_{24}$	Fisher Scientifics	A-674	
Autoradiography film	Denville scientific inc.	E3218	
CaCl_2	J.T.Baker	1-1309	
Chloramphenicol	RPI	C61000-25.0	
CoCl_2	Fisher Scientifics	C-371	
CuSO_4	J.T.Baker	1843	
FeSO_4	Fisher Scientifics	I-146	
Formic acid	Fisher Biotech	BP1215-500	
Glucose	Macron	4912-12	
H_3BO_4	Macron	2549-04	
H_3PO_4	J.T.Baker	0260-02	
K_2SO_4	Sigma	P9458-250G	
KH_2PO_4	Fisher Biotech	BP362-500	
L-Valine	Sigma	V-6504	
MgCl_2	Fisher Scientifics	FL-06-0303	
Microplate reader Synergy HT	Biotek	Synergy HT	
MnCl_2	Sigma	M-9522	
MOPS	Sigma	M1254-1KG	
Na_2HPO_4	Mallinckrodt	7892	
NaCl	J.T.Baker	3624-01	
NaH_2PO_4	Mallinckrodt	7917	
NH_4Cl	Sigma	A0171-500G	
P-32 radionuclide, orthophosphoric acid in 1 mL water (5 mCi)	Perkin Elmer	NEX053005MC	
Storage phosphor screen	Kodak	So230	
Thermomixer	Eppendorf	5382000015	
Thiamine	Sigma	T-4625	
TLC PEI Cellulose F	Merk-Millipore	1.05579.0001	
Tricine	RPI	T2400-500.0	

Typhoon 9400 imager
ZnSO₄

GE Healthcare
Fisher Scientifics Z-68

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Title of Article:	USE OF MICROTITER DISH RADIOLABELING FOR MULTIPLE IN VIVO MEASUREMENTS OF ESCHERICHIA COLI (T)PPGPP FOLLOWED BY TLC
Author(s):	LLORENÇ FERNÁNDEZ-COLL AND MICHAEL CASHEL

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We believe that all the required changes were made in the manuscript in a traceable way, so it can be easily spotted by the editor and the reviewers. We agree in all the reviewer's comments and we think that they improve substantially our manuscript.

Editorial comments: all the format changed were performed as suggested.

Reviewer 1: all the suggested changes were addressed. We discussed with further detail the advantages of TLC method over other methods as suggested. A better description of the preparation of MOPS was provided. About comparing growth in thermomixer vs plate reader, in our case is quite similar, but we agree that it is a crucial step, so we included a comment on the discussion.

Reviewer 2: all the suggested changes were addressed. We actually use 100 μCi /well. We consider that for low basal levels 100 μCi with 0.2 mM carrier phosphate works well, but for measuring (p)ppGpp levels that are expected to become equivalent to GTP pools, we consider that it can be dropped to 25 or 50 μCi /well. Although it may seem too much, most of the signal will be discarded before exposing the film by removing the pH front that contains free ^{32}P (and even more if we remove any nucleotides on top of GTP). This has been addressed in the text.

We hope that this will satisfy all the comments and concerns.

Yours faithfully,

Llorenç Fernández-Coll and Michael Cashel