

## **Culture Growth**

1. Grow an overnight 5.0 ml LB culture of the strains to be evaluated.
2. Inoculate the overnights to 30 ml LB and do a short growth curve to get the cells at mid log-phase ( $OD_{600} = 0.5$ ).
3. Pellet cells at 5k, 5 min., 4°C. All steps and solutions from here forward are to be on ice.
4. Re-suspend pellet in 300µl cold Sodium Acetate (0.3M, pH 4.5), 10 mM EDTA.
5. Cells added to 0.3 g of glass beads and snap froze in etoH and dry ice bath then transferred to -20 degrees C. hold samples here until all cultures are at this point

## **tRNA Extraction**

6. Add 300µl phenol:chloroform (pH 4.7) to the samples.
7. Vortex eppy 4-5 times for 30 second bursts with incubation on ice in between.
8. Centrifuge samples for 15 minutes, 4°C, max speed.
9. Transfer top layer (aqueous phase) to new tubes and repeat the phenol extraction by adding 300ul phenol:chloroform (pH 4.7), spinning for 15 minutes, 4°C, max speed & removing the aqueous phase to a fresh eppy.
10. The RNA is etoH precipitated by adding 3 volumes of cold 100% etoH and spinning at max speed for 25 minutes, 4°C.
11. RNA pellet is re-suspended in 60 ul cold sodium acetate (0.3 M, pH 4.5).
12. Precipitate the RNA by adding 400 ul 100% etoH and spinning at max speed for 25 min., 4°C. decant.. spin again 1 min. and remove traces of etoH w/ pipette..
13. air dry the pellet while on ice..
14. re-suspend the pellet in 50 ul cold sodium acetate (10 mM, pH4.5).
15. quantitate RNA by spectrophotometry ( $A_{260}$ ) and analyze the integrity of the RNA by running a 2.0% agarose gel.

## **Gel Electrophoresis**

16. Mix the RNA sample with 2X loading buffer. (recipe step #18)

17. Run the 14% denaturing acid gel at 50 volts, 4°C for 24 hours ..

Using BioRad miniprotein II gel rigs (1.0 mm).... make ea. gel as follows..

3.5 ml - 40% polyacrylamide (19:1)

4.2 g - urea

3.0 ml – sodium acetate 1.0 M (pH 5.0)..... final concentration is 0.3M

melt this urea by heating in 70 degree C H<sub>2</sub>O bath

pH adjust the melted acrylamide/urea gel to pH 5.0 by adding acetic acid as needed (spotting onto pH paper) de-gass gel solution and polymerize w / 34 ul TEMED & 124 ul 10% ammonium persulfate.

18. Make the 2X loading dye..

4.2 g - urea

3.0 ml – sodium acetate 1.0 M (pH 5.0)..... final concentration is 0.3M

melt the urea by heating in 70 degree C H<sub>2</sub>O bath, Qs volume to 10.0 ml w/ H<sub>2</sub>O

pH adjust the melted solution to pH 5.0 by adding acetic acid as needed

add 5 ug xylene cyanol and 5 ug bromophenol blue

19. tRNA de-acylation: add an equal volume of (100 mM Tris-HCl, 100 mM NaCl pH 9.5) to RNA samples and incubate 70 degree C, 30 min.

20. electrophoresis buffer: 0.3 M sodium acetate pH5.0

### **IMPORTANT NOTE:**

The pH of the buffer will drift during the electrophoresis run... the inside will become very basic and this will cause the de-acylation of samples... 0.3 M sodium acetate pH 5.0 will be stable for 7-8 hours of electrophoresis.. the buffer must be routinely removed from the unit and mixed, then returned to continue the run. for the entire 24 hour run, 50V, 4°C.

The tRNAs should have migrated to about  $\frac{3}{4}$  down the gel. The 0.3 M sodium acetate electrophoresis buffer must be pH adjusted using acetic acid and not HCl.

## **Transfer**

20. Electroblot the RNA to nylon membranes using the biorad western blotting sandwich cassettes... transfer buffer:

final concentration

1 liter

Tris-Oac pH 7.8 (10 mM)-----10 ml 1.0 M Tris-Oac pH 7.8

Sodium Acetate (5 mM)-----0.41 g Sodium Acetate

EDTA (0.5 mM)----- 1.0 ml EDTA (0.5 M pH 8.0)

Transfer conditions: 40v, 2 hours, 4 degree C.

21. UV crosslink RNA to membrane using optimal setting on UV crosslinker. After crosslinking any blocking/hybridization/detection method of your choice can be applied to the blot (see note at end of protocol about detection).

### **Hybridization & Detection**

22. DIG tailed probe prepared per manufacturer's protocol.

23. Prehybridize membrane 2 hours 42 degrees C in hyb bottles w/ 25 ml prehyb.

#### 50 ml prehyb buffer

500 ul -- 10% N- lauroylsarcosine

12.5 ml ---20 x SSC

5 ml -----10 X blocking reagent (Roche cat # 1096176)

50 ul -----20% SDS

300 ul ----salmon sperm DNA (3.7 mg/ml). QS to final volume of 50 ml w/ ddH<sub>2</sub>O

24. Hybridize w/ 1.5 pmol DIG tailed probe / ml hyb solution Overnight 42 degrees C

#### 50 ml hyb buffer

500 ul -- 10% N- lauroylsarcosine

12.5 ml ---20 x SSC

5 ml -----10 X blocking reagent (Roche cat # 1096176 diluted in maleic acid buffer)

50 ul -----20% SDS

QS to final volume of 50 ml w/ ddH<sub>2</sub>O

25. Post-hybridization washes

1 wash for 15 min, 42 degrees C, (6XSSC, 0.1%SDS)

2 washes for 15 min. ea., 42 degrees C, (4XSSC, 0.1%SDS)

1 wash for 15 min, room temp, (2XSSC, 0.1%SDS)

26. Dig detection:

- equilibrate filter for 2 min. in detection buffer (100 mM Tris-HCl, 100 mM NaCl pH 9.5)

- block filter 30 min. in 1X blocking reagent (the 10 X blocking reagent diluted in maleic acid buffer) room temperature.

- hybridize anti-DIG AP FAB fragments (1:10,000) in 1X blocking reagent for 30 min room temp.

- wash filters 2 X in washing buffer (maleic acid buffer w/ 0.3% Tween)

- dropwise add substrate (CSPD ready to use) onto filters.. seal in bag.

- incubate filters in the bag at 37 degree C for 15 min..

then expose filters to film for a duration of time to give a good exposure, picture.

### **Several things to consider about detection!**

This protocol outlines the use of DIG-tailed oligos. From experience... I have found that the addition of the DIG-UTPs to the end of the oligo can cause hybridization problems in some circumstances. For hybridization/detection I have had much more reproducible results when I switched to using biotinylated oligos and the Phototope®-Star Detection Kit from NEB. Obviously, using radioactive probes would also cause no hybridization interference and works quite well.

Best of luck!

If using this protocol, please cite original publication:

Jester BC, Levengood JD, Roy H, Ibba M, Devine KM. Nonorthologous replacement of lysyl-tRNA synthetase prevents addition of lysine analogues to the genetic code. *Proc Natl Acad Sci U S A*. 2003 Nov 25;100(24):14351-6