

## Microbiology Experiment – Biolog GEN III plates

### Background

Over the past 6 weeks, we have examined many our organism's traits such as Gram stain reaction, carbon metabolism, nitrogen metabolism, the production of exoenzymes, inhibition by antibiotics, temperature, oxygen requirements and now are beginning to use Bergey's Manual of Determinative Bacteriology to identify our unknown organism. While this approach has been useful to learn about our organism and principles of microbiology, it would take far too long if decisions about a patient's diagnosis and medical treatment were dependent on this information. In clinical microbiology, more rapid tests are done to provide an identification as quickly as possible. These tests include API test strips, Enterotubes, Vitek "cards", and finally, Biolog GEN III plates, which we will use here. The principle by which these methods work is that a variety of tests are conducted simultaneously, in a convenient, standardized format (that can be distributed commercially), and the results are compared to a database to identify the organism.

The **Biolog GEN III test plate** contains different nutrients or inhibitory substances dried into the bottom of each well of a 96 well plate (Figure 1). Cells grown on a plate of Biolog Universal Growth medium + 5% sheep's blood (BUG+Blood) are suspended in an inoculating fluid at a specific cell density and added to the wells. The plates are incubated at the desired temperature in the OmniLog instrument. The inoculating fluid contains a redox dye that turns purple if the organism is actively metabolizing in the well. In columns 1-9, the carbon source is varied (A1 is the negative control) so that if the organism is able to utilize the particular compound present, a purple color will result. In columns 10-12, a carbon source is available in all wells, as well as specific potentially inhibitory substances (A10 is the positive control and lacks inhibitory substances). Inhibition of growth will decrease the intensity of purple color that will develop in the well. The response in each well is determined by scanning the plate every 15 minutes, on the 15 minute mark. The pattern of respiration is compared to a database to identify the organism. We will use the "Full Data Logger" option in order to collect data over a 36 hr period.

	1	2	3	4	5	6	7	8	9	10	11	12
A	negative control	Dextrin amylose glu- $\alpha$ 1-4, $\alpha$ 1-6 poly	D-maltose glu- $\alpha$ 1-4-glu	D-trehalose glu- $\alpha$ 1- $\alpha$ 1-glu	D-cellobiose glu- $\beta$ 1-4-glu	gentiobiose glu- $\beta$ 1-6-glu	Sucrose glu- $\alpha$ 1- $\beta$ 2-fru	D-turanose glu- $\alpha$ 1- $\alpha$ 3-fru	Stachyose gal( $\alpha$ 1 $\rightarrow$ 6) gal( $\alpha$ 1 $\rightarrow$ 6) glc( $\alpha$ 1 $\leftrightarrow$ 2 $\beta$ ) fru	positive control	pH 6	pH 5
B	D-raffinose gal- $\alpha$ 1-6-glu- $\alpha$ 1- $\beta$ 2-fru	$\alpha$ -D-lactose gal- $\beta$ 1-4-glu ( $\alpha$ )	D-melibiose gal- $\alpha$ 1-6-glu	$\beta$ -methyl-D-glucoside	D-salicin aspirin- $\beta$ 1-glu	N-acetyl-D-glucosamine	N-acetyl- $\beta$ -D-mannosamine	N-acetyl-D-galactosamine	N-acetylneuraminic acid	1% NaCl	4% NaCl	8% NaCl
C	$\alpha$ -D-glucose	D-mannose	D-fructose	D-galactose	3-methyl glucose	D-fucose	L-fucose	L-rhamnose	inosine	1% Na-lactate	fusidic acid	D-serine
D	D-sorbitol	D-mannitol	D-arabitol	myo-inositol	glycerol	D-glucose-6-PO <sub>4</sub>	D-fructose-6-PO <sub>4</sub>	D-aspartic acid	D-serine	Troleandomycin	rifamycinSV	minocycline
E	gelatin	glycyl-L-proline	L-alanine	L-arginine	L-aspartic acid	L-glutamic acid	L-histidine	L-pyrogutamic acid	L-serine	lincomycin	guanidine HCl	niaproof 4
F	pectin	D-galacturonic acid	L-galacturonic acid lactone	D-gluconic acid	D-gluconic acid	Glucuronamide	mucic acid	quinic acid	D-saccharic acid	vancomycin	tetrazolium violet	tetrazolium blue
G	p-hydroxyphenyl-acetic acid	methyl pyruvate	D-lactic acid methyl ester	L-lactic acid	citric acid	$\alpha$ -keto-glutaric acid	D-malic acid	L-malic acid	bromo-succinic acid	nalidixic acid	LiCl	K-tellurite
H	tween-40	$\gamma$ -amino-butyric acid	$\alpha$ -hydroxy-butyric acid	$\beta$ -hydroxy-D,L-butyric acid	$\alpha$ -keto-butyric acid	acetoacetic acid	propionic acid	acetic acid	formic acid	aztreonam	Na-butyrate	Na bromate

## Procedure

**Day 1** - Obtain a Biolog Universal Growth + Blood (BUG+B) plate. Divide and label the plate for you and your lab partner, then inoculate your unknown organisms onto half the plate, streaking for single colonies. Place the plates onto the front bench and they will be stored at 4C, then placed in the incubator on the day before the GEN III plates are to be set up. Sign up on the front bench for a time to come with with your partner to set up the Biolog plate.

**Day 2** - At your scheduled time, retrieve your BUG+B streak plate from the incubator and proceed to the labeling station.

**A. Labeling Station** - Carefully unwrap a GEN III plate from the packaging. Be sure not to touch the bottom of the plate below the wells. Use a dark, extra-fine point Sharpie to label the GEN III plate on the short side of the plate, opposite the Biolog Logo (label the plate, not the lid). Label the plate with the designation UK-XXX for the unknown. Proceed to the inoculation station!

### B. Inoculation Station

- 1. Zero the Turbidimeter** - Wipe the sides of an inoculating fluid (IF-A) tube with a Kimwipe and place it into the turbidimeter. Use the adjustment dial to set the % transmittance to 100%.
- 2. Inoculate the Tube of IF-A** - Estimate the colony size on the BUG+B culture. Use a sterile "Inoculatorz" swab (does not release cotton fibers) to pick up a single colony if they are large, several medium size colonies or a small amount of confluent growth if colonies are extremely small. Remove the IF-A tube from the turbidimeter and vigorously inoculate the IF-A, being sure that the bottom of the swab contacts the bottom of the IF-A tube to dislodge the bacteria.
- 3. Check the Turbidity** - Place the inoculated IF-A tube back in the Turbidimeter and wait for the % transmittance to stabilize between 90 and 98%T. If the % transmittance is above 98%, reinoculate the tube to add more bacteria. If the % transmittance is below 90%, inoculate a fresh tube of IF-A, using a smaller inoculum.
- 4. Fill the Pipettor** - Pour the IF-A cell suspension into a sterile plastic reservoir. Turn on the multi-channel pipettor by pressing the center button - the display should show "Multi - 100uL". Push the pipettor tip holders onto the pipette tips until it clicks. Hold the pipettor so that the tips can draw from the bottom of the reservoir, then click the top button to draw up a sufficient amount of sample for the entire GEN III plate.
- 5. Fill the GEN III Plate** - Lift the lid from the GEN III plate, align the tips to the 8 rows of column 1 such that the tips are contacting the far wall of the well (this will prevent the formation of bubbles). Press the dispense button to dispense 100 uL from each tip, then move the pipettor to align the tips with column 2 and dispense. After dispensing into column 12, the pipettor should beep twice to indicate that the plate is finished. Place the tips over the reservoir and press the dispense button again to "purge" the

tips. Then press the eject button to eject the tips into the autoclave bag. *If you missed a well or two when pipetting, use a standard single channel pipettor to inoculate the missed wells with 100 ul of the IF-A cell suspension.* Replace the lid on the plate. Dispose of the reservoir and swab in the autoclave bag. Then proceed to the data entry station!

### C. Data entry station using the OmniLog Data Collection Software

1. Choose the lowest stack # and position available (not locked). Enter the data requested for each field in the right-side panel

Strain Designation = XXX (your initials)  
 Presumptive species = unknown  
 Growth medium = BUG+Blood  
 Researcher Name = your name  
 Date = today's date (e.g. 2013-02-16)  
 Type strain = NT  
 Course or research = Bio321  
 Institution = Lycoming College  
 Comment 1 = UK-XXX  
 Comment 2 = 25C  
 Click "Save and Next"

2. Place the plate onto a tray with your lab partner, place the tray into the appropriate slot in the OmniLog.

### D. Analysis of Biolog Results

1. Download the pdf files corresponding to the "print screen" (UK-XXX PS.pdf) and report (UK-XXX report.pdf) options on the OmniLog software.

The screenshot displays the OmniLog software interface. On the left, a video window shows a 96-well plate. The main area is divided into three columns: 'Data Value', 'Positive Value', and 'ID'. The 'Data Value' column shows a grid of colored circles representing well colors. The 'Positive Value' column shows a grid of colored circles representing well colors. The 'ID' column shows a table of results.

	PROB	SIM	DIST	Organism T <sub>1</sub>	Species
==>1	0.718	0.548	3.549	GN-NENT	Pseudomonas mephitica
2	0.099	0.065	5.455	GN-NENT	Sphingomonas paucimobilis B
3	0.095	0.062	5.493	GN-NENT	Janthinobacterium lividum (25 C)
4	0.088	0.055	5.562	GN-FAS	Capnocytophaga gingivalis

Below the table, there are fields for 'Plate Status' (Plate Done, Current Status, Plate Done), 'Incubation Hours' (Current Incubation Hours, New), and buttons for 'Mark Plate As Done', 'Restore Plate', 'View Database', and 'View DB on ID Row Click'. At the bottom, there are buttons for 'Done', 'Print Screen', 'Print Report', and 'Print Preview'.

2. Use the Print screen document to address the following questions regarding the **IDENTIFICATION** in your lab report.
- Was a positive identification made?
  - What was the best match?
  - How does this compare to the FAME and 16S-based identifications?
  - Are any of the other Biolog matches the same as your 16S sequence?
  - Examine your 16S rRNA EZtaxon.org results to determine how similar your sequence was to the Biolog best-match organism.
  - Examine the [Biolog Database list](#) to determine if the 16S rRNA best match organism is in the Biolog GEN III database.
3. Go to the class website and open the “Class Biolog Data” excel file. This file contains the exported data normalized to a range of 1-100. Copy the data from the column corresponding to your unknown organism to the appropriate location on the known and unknown microbe data sheet (see next page). For our purposes, a value below 25 is considered negative (-), 25-50 is weak positive (w), while a value above 50 is positive (+). Address the following questions regarding the **METABOLIC PROFILE** in your lab report.
- Did the negative control (A1) give you a negative result? If not, what does this mean? What is a possible explanation? How does this affect your interpretation of the remaining results for columns 1-9?
  - Did the positive control (A10) give you a positive result? If not, what does this mean? What is a possible explanation? How does this affect your interpretation of the remaining results for columns 10-12?
  - Which wells correspond to other tests we’ve done (e.g. phenol red fermentation, Kirby-Bauer, exoenzymes)? Are the results consistent? How do wells that do correspond to other tests differ... i.e. what is being measured in each?
  - How do the results compare to those in Bergey’s Manual or the [IJSEM](#) paper(s) corresponding to the species identified by 16S rRNA sequencing?
  - How do the results compare to gene content of the most closely related genome in [DOE-JGI-IMG](#) or [RAST](#).

Strain	ABG	AED	AHK	AKS	ANG	ARC	BMS
A01	20	9	78	84	15	10	13
A02	99	98	97	98	97	14	95
A03	98	98	96	98	98	6	97
A04	98	98	94	97	97	20	97
A05	98	98	95	93	98	7	98
A06	97	98	92	95	99	4	98
A07	10	83	90	91	98	6	98
A08	9	99	80	81	98	5	98
A09	10	68	83	72	7	7	17
A10	97	59	82	84	97	91	95
A11	96	29	85	82	95	92	94
A12	12	1	67	77	82	95	81
B01	14	83	98	97	7	7	10
B02	13	99	70	84	25	5	95
B03	14	99	92	93	38	3	92
B04	10	97	95	95	78	6	95
B05	9	62	86	86	97	3	95
B06	96	99	89	86	89	10	96
B07	9	29	43	74	9	5	69
B08	98	29	35	56	89	3	90
B09	7	99	0	37	2	5	4
B10	55	7	82	89	95	91	93
B11	9	6	83	77	58	21	92
B12	20	6	87	79	18	6	62
C01	99	96	94	89	97	79	97
C02	99	98	82	83	94	70	93
C03	11	98	74	88	83	22	92
C04	99	99	96	92	95	84	93
C05	10	15	31	74	43	3	49
C06	11	12	76	70	97	8	31
C07	17	25	43	68	95	6	31
C08	10	99	15	51	95	95	33
C09	7	23	1	51	42	48	81
C10	87	4	77	88	91	95	91
C11	9	13	4	4	5	92	4
C12	10	5	4	4	5	70	4
D01	11	17	31	74	7	45	38
D02	11	20	90	78	91	38	92
D03	6	19	19	68	8	30	25
D04	8	17	67	83	5	62	94
D05	8	18	76	63	89	42	92
D06	28	46	40	65	25	4	92
D07	36	35	50	61	68	5	92
D08	5	9	53	39	13	4	21
D09	5	5	3	0	2	60	1
D10	9	9	4	4	5	89	4
D11	93	11	4	4	5	90	4
D12	12	17	4	4	6	60	5
E01	97	35	93	88	30	10	21
E02	95	94	63	49	45	7	28
E03	32	20	50	63	16	60	77
E04	80	97	76	76	13	80	48
E05	96	38	85	81	44	90	82
E06	98	99	86	84	55	97	87
E07	41	29	70	70	3	98	12
E08	14	22	67	63	32	82	22
E09	92	10	45	41	13	96	79
E10	91	15	74	71	5	89	4
E11	10	11	4	14	67	83	79
E12	15	3	4	4	5	94	4
F01	23	46	93	89	77	12	95
F02	98	32	80	65	64	96	27
F03	11	13	1	44	2	7	2
F04	17	32	80	81	96	88	95
F05	72	99	95	72	44	98	35
F06	24	30	60	56	41	14	17
F07	15	33	65	49	21	97	15
F08	19	23	67	54	20	100	23
F09	14	30	33	24	2	95	7
F10	95	18	4	4	5	87	4
F11	99	76	4	4	22	98	18
F12	99	49	4	4	19	99	20
G01	12	9	11	63	95	12	3
G02	15	18	85	72	3	12	1
G03	19	24	78	87	11	7	13
G04	10	25	80	86	76	77	9
G05	31	8	83	84	2	99	97
G06	19	33	76	81	4	36	47
G07	19	24	65	70	5	7	34
G08	19	55	85	78	88	94	96
G09	6	9	45	54	2	14	91
G10	13	15	4	4	93	29	86
G11	9	4	80	76	93	4	94
G12	20	9	87	89	95	97	95
H01	89	6	92	92	61	20	95
H02	18	17	94	84	8	88	2
H03	15	9	93	87	83	12	4
H04	16	11	91	91	10	53	5
H05	11	9	74	88	93	15	13
H06	89	12	92	88	95	12	94
H07	9	9	96	86	16	16	55
H08	98	10	86	87	69	78	91
H09	10	8	96	86	4	14	3
H10	96	37	6	4	96	86	93
H11	14	12	92	92	85	6	88
H12	15	1	21	21	70	12	64

Microsoft Excel interface showing a spreadsheet with columns A through I. The spreadsheet contains a list of strains and their corresponding values. The interface includes the ribbon (File, Home, Insert, Page Layout, Formulas, Data, Review, View) and the status bar (Ready).

	A	B	C	D	E	F	G	H	I
1			abbrev	K-XXX	K-pub IJSEM	K-genome	UK-XXX	ID-pub IJSEM	ID-genome
127	Genll@36	A01	neg control				20		
128	Genll@36	A02	dextrin				99		
129	Genll@36	A03	D-maltose				98		
130	Genll@36	A04	D-trehalose				98		
131	Genll@36	A05	D-cellobiose				98		
132	Genll@36	A06	gentiobiose				97		
133	Genll@36	A07	sucrose				10		
134	Genll@36	A08	D-turanose				9		
135	Genll@36	A09	stachyose				10		
136	Genll@36	A10	pos control				97		
137	Genll@36	A11	pH 6				96		
138	Genll@36	A12	pH 5				12		
139	Genll@36	B01	D-raffinose				14		
140	Genll@36	B02	α-D-lactose				13		
141	Genll@36	B03	D-melibiose				14		
142	Genll@36	B04	β-methyl-D-glucoside				10		
143	Genll@36	B05	D-salicin				9		
144	Genll@36	B06	N-acetyl-D-glucosamine				96		
145	Genll@36	B07	N-acetyl-β-D-mannosamine				9		
146	Genll@36	B08	N-acetyl-D-galactosamine				98		
147	Genll@36	B09	N-acetylneuraminic acid				7		
148	Genll@36	B10	1% NaCl				55		
149	Genll@36	B11	4% NaCl				9		
150	Genll@36	B12	8% NaCl				20		
151	Genll@36	C01	α-D-glucose				99		
152	Genll@36	C02	D-mannose				99		
153	Genll@36	C03	D-fructose				11		
154	Genll@36	C04	D-galactose				99		
155	Genll@36	C05	3-methyl glucose				10		
156	Genll@36	C06	D-fucose				11		
157	Genll@36	C07	L-fucose				17		
158	Genll@36	C08	L-rhamnose				10		
159	Genll@36	C09	inosine				7		
160	Genll@36	C10	1% Na-lactate				87		