Genomic Deactivation Patterns & Pathogenic Microbes

Part One

Genomic Frequency Introduction:

This report will reveal to you some very powerful frequencies for use in your quest for ultimate vitality by empowering your body to heal itself. If you are new to the ideas of Royal Rife and the use of harmless, electromagnetic frequencies for killing pathogenic microbes you may want to review my "ElectroTherapy Pioneers" Rife Report on Facebook. It includes some basic introductions to the concepts as well as some important updates about practical methods for using this technology. Just "Like" the facebook page and you'll be given the download link.

So what is a "Genomic Frequency"?

When it comes to pathogenic microbes, which is our topic here, this simply refers to a frequency that matches the resonant signature of the microbe. Every microbe vibrates at a specific frequency – and it's this resonant frequency that can be matched harmonically in order to "deactivate" the microbe. These particular frequencies were derived based on the DNA or genomic structure of the microbe.

My friend Craig Ledwell has been researching this topic for 17 years and with his formula has derived a huge array of "Deactivation Patterns" for pathogenic microbes. The patterns involve a harmonic group of frequencies that are designed to be run simultaneously. You can think of this like instead of playing a single note on the piano, you are playing an entire chord, or group of notes. In this case each note is harmonically contributing to the deactivation of the specific pathogenic microbe – so they must be run together to get the best results!

I'm so grateful to Craig for letting me share this info with you. Because he is quite busy using these frequencies and helping people he doesn't have the time to share it with the world so I will be sharing and helping explain how best to use these patterns with frequency generators. This is "Part One" of these "**Genomic Deactivation Patterns**".

Now let me explain how these frequency sets are laid out in this report so you know how to use them…

Followed by each organism (and in some cases some notes about that particular pathogen) you'll see a vertical list of 7-8 frequencies. These make up the harmonic "Deactivation Pattern" and all of these frequencies should be running at the same time. Only some generators have this capability. If you are using my favorite Generator (you know it if you have it) you have this capability – if not contact me at www.FutureTechSupport.com or 1-541-434-0318 and ask for more info on the generator. Also, if you are using that generator then you can use the corresponding "Program" number after either entering all these programs as custom programs or using the special custom program file that I provide in my new private club. Each "Program" number includes all the frequencies below that program number until the next program number is mentioned! These are arranged in groups, each vertical set of frequencies is in a group so they run at the same time.

The new Private Club is at http://www.RifeClub.com/upgrade. Inside the club you'll get access to my ongoing training on how best to use these Genomic Frequencies especially with my favorite generator. If you are using a different generator it might not be perfect for you, but who knows… We'll be doing training calls and I will have special videos and audios just for club members. Hope to see you on the inside!

I wish you the best in health and best of results from these Genomic Frequencies,

Joshua Parker

BTW – The info about my RifeClub private membership where I'll be sharing all the intricate details of how I use these "deactivation patterns" is here at RifeClub.com/upgrade

Acne (bacterial based) - This is a wonderful pattern for a young person with bacterial based acne.
Program: 1500 - Propionibacterium acnes

SK137
1.8
464.3
928.7
1857.3
3714.6
7429.3
14858.6
29717.2

KPA171202
1.8
452.6
905.1
1810.2
3620.4
7240.9
14481.8
28963.5

J165
1.8
463.4
926.9
1853.8
3707.6
7415.2
14830.4
29660.7

SK187
1.8
461.4
922.9
1845.8
3691.6
7383.1
14766.3
29532.5

J139
1.8
466.8
933.7
1867.3
3734.7
7469.3
14938.6
29877.3

These are Genomic Harmonic Frequency Patterns. They are not meant to be run with converge or sweep. All eight frequencies of each Genome should be run together with our 3.1 MHz carrier wave.
I usually run each Genome for 10 minute each and hope I get some hits. I then run the ones they reacted to for one hour each to rid them of the problem. Very few people with Acne react to these Genome, but, for the ones that do, this is their little miracle.

Hello Joshua;
I wanted to write you and tell you how pleased I am with the XXXX, XX4000 and booster. The instruments are superb! I have been doing research for years with other equipment and have never attained the results that I am achieving since I have switched over to these instruments.

My work is based on DNA calculations, it is exact, there are no sweeps or converges used. This work is reproducible and accurate. What amazes me is that I have been using the same frequencies with other instruments for years and never came close to deactivation of pathogens. The sessions would help but there was no big finish. The minute I switched to the XX4000 and Amp that all changed! I have been waiting for the XXXX in order to confirm my results before I contacted you. I would like to start sending patterns to you that you can pass on to other practitioners. I am too busy with my own clinic to keep up with the Rife Groups and all the Internet info out there.

These are my basic settings:

Plasma Tube	No Plasma Tube (direct contact)
Gate Rate to 20, duty cycle 25%	Gate Rate to 20, duty cycle 75%
Square Wave Duty Cycle 90%	Square Wave Duty Cycle 90%

Body Louse or Clothing Louse carry the following diseases: Epidemic Typhus, Trench fever and Relapsing Fever. These can definitely be deadly so I would like to cover these Genomes, even though they are rare!

Epidemic Typhus is caused by Rickettsia prowazekii

Program: 1501 - Rickettsia prowazekii str. Madrid E
4.1
521.2
1042.4
2084.8
4169.6
8339.3
16678.5
33357.0

Trench fever is caused by Bartonella Quintana
Bartonella quintana str. Toulouse
2.9
366.3
732.7
1465.4
2930.7
5861.5
11723.0
23446.0

This is the Genomic Frequency pattern for Candida Albicans. This pattern is used with CAUTION!

Program: 1502 - Candida albicans

Genomic DNA	Mitochondria SC5314
4.8	112.0
610.1	223.9
1220.1	447.9
2440.2	895.8
4880.5	1791.6
9761.0	7166.4
19522.0	14332.8
39043.9	28665.5

These are two groups of Genomic Harmonic Frequency Patterns. They should be run one after the other with no converge or sweeps. This particular microbe cannot be deactivated with just the Genomic DNA, you must also split the Mitochondrial DNA in order for it to be effective!

I use this pattern on all people with chronic diseases, and of course the ones with yeast, WITH CAUTION!
I have made many people deathly ill with this pattern, putting some in the bed for days. If you want to run a patient off or scare one to show them just how sick they are, this one will do it. This pattern is unique in its ability to have a delayed reaction. It is very common for a patient to have a session in the afternoon and have a moderate itching reaction only to wake up at 2am with it tearing them up. Sometimes they tell me they wanted to tear their skin off! This is of course in the extreme and very rare, but, as soon as you get used to using this pattern and start running longer and longer times you will hit on a patient that this pattern will absolutely tear up.

I usually start off with a 10min. Run of each pattern the first session. Give them the night to judge the reaction. If not too bad I proceed to 20min., for each pattern, then 30 min. If they have very little reaction to the 10min., I proceed directly to 30min., for each pattern.

Try not to wait too many days in-between sessions, Yeast is notorious for feeding on its dead brethren and it will bloom if given a chance.

Carrier wave of 3.1 is very effective.
Craig Ledwell OMD 7/16/2011

This is the Genomic Frequency pattern for Chlamydophila pneumonia.

Program: 1503 (all 4 groups) - Chlamydophila pneumonia

TW-183	J138	AR39	CWL029
3.7	3.7	3.7	3.7
471.1	470.9	472.3	472.6
942.1	941.8	944.6	945.1
1884.2	1883.6	1889.3	1890.2
3768.5	3767.3	3778.6	3780.5
7536.9	7534.6	7557.1	7561.0
15073.8	15069.2	15114.2	15122.0
30147.6	30138.4	30228.4	30244.0

This atypical bacterium commonly causes pharyngitis, bronchitis and atypical pneumonia mainly in elderly and debilitated people but in healthy adults also. There are also links to many chronic diseases that may be caused by this pathogen. I use this pattern on all chronic diseases where the root cause is not fully understood. I have found it particularly useful for Arthritic people.
I start with a 10 minute run of each Genomic pattern for a total of 40 minutes. If they react to a particular pattern and I suspect pneumonia, I will run that pattern for an additional 20 minutes which will usually take care of the pneumonia. If I do not suspect pneumonia and they still react, and they have a chronic disease such as progressive arthritis. I will stop at the 40 min session for that day. Give them a day to recover then start a course of therapy for approximately one hour every other day, if tolerated, until there are no more symptoms of the original condition.
You will find the Pneumonia will react to 'One' of the Genome patterns, and it will be deactivated very quickly. All other chronic diseases will take more sessions for deactivation. If this pattern causes reactions such as itching and aching with flu-like symptoms in chronic arthritis you will have a wonderful outcome if the patient will stay with the therapy.
Again, this is a Genomic Harmonic set of Frequency Patterns. It is not meant to be run with converge or sweeps. If you do not dwell on the full pattern running all 8 frequencies at the same time with your 3.1mHz carrier wave you will not have a successful outcome.

Craig Ledwell OMD 7/19/2011

Clostridium difficile is the most serious cause of antibiotic-associated diarrhea (AAD) and can lead to pseudomembranous colitis, a severe infection of the colon, often resulting from eradication of the normal gut flora by antibiotics.

In a very small percentage of the adult population, C. difficile bacteria naturally reside in the gut. Other people accidentally ingest spores of the bacteria while they are patients in a hospital, nursing home, or similar facility. When the bacteria are in a colon in which the normal gut flora has been destroyed (usually after a broad spectrum antibiotic such as Clindamycin has been used) the gut becomes overrun with C. difficile. This overpopulation is harmful because the bacteria release toxins that can cause bloating and diarrhea with abdominal pain, which may become severe. C. difficile infections are the most common cause of pseudomembranous colitis, and in rare cases this can progress to toxic megacolon, which can be life-threatening.
Latent symptoms of C. difficile infection often mimic some flu-like symptoms and can mimic disease flare in people with inflammatory bowel disease-associated colitis.

Program: 1504 - Clostridium difficile
Strain 630
1.1
540.1
1080.3
2160.5
4321.1
8642.2
17284.4
34568.7

CD196
1.1
563.7
1127.5
2255.0
4510.0
9020.0
18040.0
36079.9

R20291
1.1
552.9
1105.8
2211.5
4423.1
8846.1
17692.3
35384.5

These are Genomic Harmonic Frequency Groups for three strains of Clostridium difficile. They are not meant to be run with converge or sweep. All 8 frequencies should be run at the same time, for each strain, with our 3.1 MHz carrier wave.
I will use this pattern on any person with an ongoing colitis, uncontrolled diarrhea, or post-antibiotic difficulty. Run times can be 20 minutes per Genome for a one hour total session. One session is usually enough.
Craig Ledwell OMD 7/28/2011

Escherichia coli

Program: 1505 - Escherichia coli E24377A
(Escherichia coli E24377A is an enterotoxigenic E. coli (ETEC) isolate, ETEC being the leading cause of traveler's diarrhea, characterized by a large volume of watery diarrhea. It belongs to phylogroup B1. ETEC primarily colonizes the small intestine.)
1.8
465.4
930.7
1861.4
3722.9
7445.8
14891.6
29783.1

Escherichia coli O127:H6 str. E2348/69
(Strain E2348/69, a phylogroup B2 strain, was isolated in Taunton, England in 1969 and is widely used as a model for EPEC (enteropathogenic E. coli) strains. It is the first EPEC strain to be fully sequenced. EPEC strains are a leading cause of infantile diarrhea in developing countries.)
1.8
466.7
933.4
1866.7
3733.4
7466.9
14933.7
29867.5

Escherichia coli 55989
(Strain 55989 is an enteroaggregative strain (EAEC) originally isolated from the diarrheagenic stools of an HIV-positive adult suffering from persistent watery diarrhea in the Central African Republic in 2002. It belongs to phylogenetic group B1. EAEC strains form aggregates as their name suggests, and are an emerging cause of gastroenteritis.)
1.8
449.5
899.1
1798.2
3596.3
7192.7
14385.3
28770.6

Escherichia coli O55:H7 str. CB9615
(Isolated from an infant with diarrhea in Germany in 2003.)
1.7
430.2
860.4
1720.9
3441.8
6883.5
13767.1
27534.1

Escherichia coli O26:H11 str. 11368
(Enterohemorrhagic E. coli (EHEC) strains cause diarrhea, hemorrhagic colitis, and life-threatening hemolytic uremic syndrome. O26:H11 strain 11368 was isolated in Japan in 2001 from a patient with diarrhea during a diffuse outbreak.)
1.6
406.7
813.5
1627.0
3254.0
6507.9
13015.8
26031.6

Escherichia coli O157:H7 str. Sakai
(E. coli O157:H7 is a Enterohemorrhagic (EHEC) strain producing large quantities of one or more related, potent toxins that cause severe damage to the lining of intestine. These toxins are closely related to the toxin produced by Shigella dysenteriae. The acute disease caused by the bacterium is called hemorrhagic colitis and is characterized by severe cramping and diarrhea. Undercooked or raw hamburger has been implicated in nearly all documented outbreaks and in other sporadic cases.)
1.6
421.4
842.9
1685.8
3371.6
6743.2
13486.4
26972.8

Program: 1506 - Escherichia coli O157:H7 str. EC4115
(E. coli O157:H7 is a Enterohemorrhagic (EHEC) strain producing large quantities of one or more related, potent toxins that cause severe damage to the lining of intestine. These toxins are closely related to the toxin produced by Shigella dysenteriae. The acute disease caused by the bacterium is called hemorrhagic colitis and is characterized by severe cramping and diarrhea. Undercooked or raw hamburger has been implicated in nearly all documented outbreaks and in other sporadic cases.)
1.6
415.9
831.8
1663.5
3327.0
6654.1
13308.2
26616.4

Escherichia coli O157:H7 str. EDL933
(E. coli O157:H7 is a Enterohemorrhagic (EHEC) strain producing large quantities of one or more related, potent toxins that cause severe damage to the lining of intestine. These toxins are closely related to the toxin produced by Shigella dysenteriae. The acute disease caused by the bacterium is called hemorrhagic colitis and is characterized by severe cramping and diarrhea. Undercooked or raw hamburger has been implicated in nearly all documented outbreaks and in other sporadic cases.)
1.6
419.2
838.9
1676.7
3353.3
6706.6
13413.2
26826.4

Escherichia coli O157:H7 str. TW14359
(E. coli O157:H7 is a Enterohemorrhagic (EHEC) strain producing large quantities of one or more related, potent toxins that cause severe damage to the lining of intestine. These toxins are closely related to the toxin produced by Shigella dysenteriae. The acute disease caused by the bacterium is called hemorrhagic colitis and is characterized by severe cramping and diarrhea. Undercooked or raw hamburger has been implicated in nearly all documented outbreaks and in other sporadic cases.)
1.6
419.2
838.4
1676.7
3353.5
6707.0
13414.0
26827.9

Escherichia coli O103:H2 str. 12009
(Enterohemorrhagic E. coli (EHEC) strains cause diarrhea, hemorrhagic colitis, and life-threatening hemolytic uremic syndrome.)
1.7
425.2
850.5
1701.0
3402.0
6804.0
13608.0
27216.0

Escherichia coli O111:H- str. 11128
(Escherichia coli O157:H7 is a major food-borne infectious pathogen that causes diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome.)
1.7
431.4
862.9
1725.8
3451.6
6903.1
13806.2
27612.4

Escherichia coli CFT073
(Uropathogenic Escherichia coli (UPEC) strains lead to 70-90% of the estimated annual 150 million community-acquired urinary tract infections.)
1.7
443.0
885.9
1771.8
3545.7
7087.4
14174.8
28349.5

Program: 1507 - Escherichia coli 536
(Uropathogenic Escherichia coli (UPEC) strain 536 (O6:K15:H31) is one of the model organisms of extraintestinal pathogenic E. coli.)
1.8
469.2
938.4
1876.8
3753.6
7507.1
15014.3
30028.5

Escherichia coli IAI39
(Strain IAI39 is an extraintestinal pathogenic E. coli strain (ExPEC) isolated from the urine of a patient with urinary tract infection in France in the 1980s.)
1.8
451.5
903.1
1806.1
3612.3
7224.6
14449.2
28898.4

Escherichia coli UMN026
(Strain UMN026 is an extraintestinal pathogenic E. coli strain (ExPEC) isolated from an acute cystitis patient in the USA in 1999. It belongs to phylogenetic group D and is serotype O17:K52:H18. It is a representative of a recently emerged E. coli clonal group ("clonal group A") that is now a widely disseminated cause of drug-resistant urinary tract infections and other extraintestinal infections.)
1.7
445.5
890.9
1781.8
3563.7
7127.4
14254.7
28509.4

Escherichia coli UTI89
(UTI89 is a Uropathogenic E. coli (UPEC) belonging to phylogroup B2, and was recovered from a patient with an acute bladder infection. UPEC strains must adapt to life in several microbial communities in the human body, and have a complex life cycle in the bladder where they cause acute or recurrent urinary tract infection.)
1.8
457.4
914.9
1829.8
3659.6
7319.2
14638.4
29276.8

Escherichia coli S88
(Strain S88 is an extraintestinal pathogenic E. coli strain (ExPEC) isolated from the cerebrospinal fluid of a late onset neonatal meningitis case in France in 1999.)
1.8
460.5
921.0
1842.0
3683.9
7367.9
14735.8
29471.5

Escherichia coli SMS-3-5
(E. coli strain SECEC SMS-3-5 was isolated from Shipyard Creek, USA, an industrial, toxic metal-contaminated coastal environment. It is resistant to a record-number of antibiotics, in many cases at record-high concentrations. This is the first case of resistance to ciprofloxacin and moxifloxacin, two front-line fluoroquinolones, in an environmental strain. It is not known if this strain is a human pathogen yet. I include it for future reference.)
1.8
457.2
914.4
1828.8
3657.7
7315.4
14630.7
29261.5

Program: 1508 - Escherichia fergusonii ATCC 35469
(Escherichia fergusonii is the bacteria that is most closely related to E. coli. The type strain is not virulent in a mouse model, however E. fergusonii has been isolated from human blood, urine and an arm wound. It is not known if this strain is a human pathogen yet. I include it for future reference.)
2.0
505.0
1010.0
2020.0
4040.0
8080.1
16160.1
32320.3

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

Another large group of bacteria that are becoming drug-resistant. You can break these up into four groups. Simple diarrhea, hemorrhagic colitis with severe diarrhea, hemorrhagic colitis with hemolytic uremia and diarrhea, and urinary tract infection.

The simple diarrhea and UTI can usually be deactivated with one half hour session of the correct genome. The others will usually take many days of successive sessions.

Craig Ledwell OMD 8/24/2011

Giardia

Giardia lives inside the intestines of infected humans or other animals. Individuals become infected through ingesting or coming into contact with contaminated food, soil, or water. The Giardia parasite originates from contaminated items and surfaces that have been tainted by the feces of an infected animal. The symptoms of Giardia, which may begin to appear 1–2 weeks after infection, include Diarrhea, excess gas, stomach or abdominal cramps, upset stomach, and nausea. Resulting dehydration and nutritional loss may need immediate attention. The typical infection within an individual can be slight, resolve without conflict, and last between 2–6 weeks.

Program: 1509 - Giardia lamblia ATCC 50803
1.6
414.1
828.2
1656.4
3312.8
6625.5
13251.0
26502.1

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

Run this pattern for 30 min. to deactivate the pathogen.

Program: 1510 - Hepatitis C

Genotype	#1	#2	#3	#4	#5	#6
	469.2	466.1	478.6	483.8	484.4	470.1
	938.4	932.1	957.3	967.6	968.9	940.2
	1876.8	1864.3	1914.6	1935.2	1937.7	1880.4
	3753.7	3728.6	3829.1	3870.5	3875.4	3760.7
	7507.4	7457.1	7658.2	7740.9	7750.9	7521.4
	15014.8	14914.3	15316.5	15481.8	15501.7	15042.8
	30029.6	29828.6	30632.9	30963.7	31003.4	30085.7

These of course are in Frequency Groups, you will need all seven harmonic frequencies per genome to deactivate the virus. You cannot do sweeps or converges if you want success with this virus, one must dwell harmonically on the correct frequency long enough to achieve success.

For my people with a high viral load I start with 5min. per genome for a 30min. 'Total Session'. I will repeat this three times a week as patient response dictates. Some people will experience such a strong 'kill off' that it would not be wise to push too hard. As soon as the people are ready I then increase time limit to 10min. Per Genome for a total of a one hour session. I do not request a viral load count until the patient has no more symptom 'kill off', from past experience the viral load will increase during the 'kill off' phase and then drop dramatically as deactivation ensues. Also, I always do the entire pattern and never split off the individual genome sequences since the people never have had genomic studies done to isolate the correct strain. This pattern has been extremely successful and I hope whomever receives this information will realize the importance of not jumping the gun and overdoing the session. The 'Kill Off' can be huge with genomic based frequency work. These are not guessed at Rife Frequencies, these are calculated from scientific data, they have been clinically researched by myself for years. I release this information in order to begin the transition of 'Rifing' into mainstream medicine.
Craig Ledwell OMD 7/14/2011

Here are the Genomic Frequency patterns for the Herpes Group.

Program: 1511 - HHV 1
Oral and/or Genital, sometimes Ocular (predominately orofacial).
29.7
475.6
951.2
1902.4
3804.8
7609.7
15219.4
30438.8

Program: 1512 - HHV 2
Oral and/or Genital (predominately genital).
29.2
468.0
935.9
1871.9
3743.7
7487.5
14975.0
29950.0

Program: 1513 - HHV 3
Chickenpox and Shingles, sometimes Ocular.
36.2
579.9
1159.7
2319.5
4638.9
9277.9
18555.8
37111.6

Program: 1514 - HHV 4
Epstein-Barr virus (EBV), lymphocryptovirus, infectious mononucleosis, Burkitt's lymphoma, CNS lymphoma in AIDS people, post-transplant (PTLD)
26.2
419.2
838.3
1676.7
3353.3
6706.6
13413.2
26826.4

Program: 1515 - HHV 4 type 1
26.3
421.5
842.9
1685.8
3371.7
6743.3
13486.7
26973.3

Program: 1516 - HHV 5
Cytomegalovirus (CMV), infectious mononucleosis like syndrome, retinitis, and others.
19.2
614.6
1229.2
2458.5
4917.0
9833.9
19667.8
39335.6

Program: 1517 - HHV 6
Roseolovirus, Herpes lymphotropis virus, Sixth disease
28.4
454.5
909.1
1818.1
3636.2
7272.4
14544.9
29089.8

Program: 1518 - HHV 6A
14.1
450.6
901.2
1802.3
3604.6
7209.3
14418.5
28837.1

Program: 1519 - HHV 6B
Current research points to possible MS link.
27.9
446.7
893.4
1786.8
3573.6
7147.2
14294.4
28588.8

Program: 1520 - HHV 7
Roseolovirus, Sixth disease
29.6
473.1
946.1
1892.2
3784.5
7569.0
15138.0
30275.9

Program: 1521 - HHV 8
Kaposi's sarcoma associated herpes, a type of rhadinovirus, primary effusion lymphoma and multicentric Castleman's disease.
32.8
524.9
1049.7
2099.5
4199.0
8398.0
16795.9
33591.9

All of these patterns are Genomic Harmonic Frequency Groups. They are not meant to be run with converge or sweeps. Use all of the frequencies in the group at the same time with your carrier wave. In my own research, 2.4 or 3.1 carrier has worked equally well.
With these particular patterns I usually start at 30min. Then increase up to one hour as 'kill off' symptoms permit. It may take 3 sessions for deactivation of the first three herpes, the others can take more!
My MS people are continuing to get better after 4 months of weekly sessions, but, no big finale yet!
The first three herpes will sometimes break out with herpatic lesions after the sessions, but, these will be dead and they will dry up very quickly.
Craig Ledwell OMD 7/15/2011

Disease	HPV type
Common warts	2, 7
Plantar warts	1, 2, 4, 63
Flat warts	3, 10
Butcher's warts	7
Anogenital warts	6, 11, 42(pending), 44(pending), 16, 18, and 31(pending)
Focal epithelial hyperplasia(oral)	32 and 13 which is pending
Oral and Laryngeal papillomas	6, 7, 11, 16, 32

Disease	HPV Program #
Common warts	1523, 1527
Plantar warts	1522, 1523, 1525, 1533
Flat warts	1524, 1528
Butcher's warts	1527
Anogenital warts	1526, 1529, 42(pending), 44(pending), 1530, 1531, 31(pending)
Focal epithelial hyperplasia(oral)	1532 and 13 (pending)
Oral and Laryngeal papillomas	1526, 1527, 1529, 1530, 1532

Program: 1522 - Human papillomavirus type 1
289.5
579.1
1158.3
2316.6
4633.2
9266.3
18532.6
37065.3

Program: 1523 - Human papillomavirus type 2
287.9
575.8
1151.7
2303.3
4606.6
9213.3
18426.5
36853.1

Program: 1524 - Human papillomavirus type 3
289.4
578.8
1157.5
2315.1
4630.2
9260.4
18520.8
37041.6

Program: 1525 - Human papillomavirus type 4
307.7
615.5
1231.1
2462.1
4924.3
9848.5
19697.1
39394.1

Program: 1526 - Human papillomavirus type 6
286.4
572.8
1145.5
2291.1
4582.1
9164.3
18328.6
36657.2

Program: 1527 - Human papillomavirus type 7
281.9
563.8
1127.7
2255.4
4510.8
9021.6
18043.2
36086.3

Program: 1528 - Human papillomavirus type 10
285.7
571.5
1143.1
2286.2
4572.3
9144.6
18289.2
36578.5

Program: 1529 - Human papillomavirus type 11
285.2
570.5
1141.1
2282.1
4564.2
9128.5
18257.0
36513.9

Program: 1530 - Human papillomavirus type 16
286.3
572.6
1145.1
2290.2
4580.4
9160.8
18321.6
36643.3

Program: 1531 - Human papillomavirus type 18
288.0
576.0
1152.1
2304.2
4608.4
9216.8
18433.6
36867.1

Program: 1532 - Human papillomavirus type 32
284.3
568.5
1137.0
2274.1
4548.2
9096.4
18192.8
36385.5

Program: 1533 - Human papillomavirus type 63
308.0
616.0
1231.9
2463.8
4927.6
9855.2
19710.5
39420.9

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

Here are the Wart patterns, I am sorry but full sequencing has not been finished for some of the Genomes. Don't be discouraged just because a few are missing, I have had success with Genital warts even without the four that are not yet finished.

I usually run 30 min. of each Genome I need to deactivate a wart, and I usually do it two days in a row. Wait a few weeks and see if a repeat is needed.

As for Genital warts, this takes considerably more sessions. If the sessions are working you will definitely notice a reaction within 24 hours; usually this is itching and sometimes burning sensations. I would continue to do the sessions 2 to 3 times a week until the warts fall off. Give it about three weeks to finish the job.

Craig Ledwell OMD 8/26/2011

Flu Virus, Colds, etc. part I

Program: 1534 - Influenza A virus (A/Goose/Guangdong/1/96(H5N1))
166.5
333.0
666.1
1332.2
2664.3
5328.6
10657.3
21314.6

Influenza A virus (A/Hong Kong/1073/99(H9N2))
167.6
335.3
670.6
1341.2
2682.5
5365.0
10729.9
21459.8

Influenza A virus (A/Korea/426/1968(H2N2))
166.8
333.6
672.5
1345.0
2690.1
5380.1
10760.2
21520.4

Influenza A virus (A/New York/392/2004(H3N2))
166.1
332.1
664.3
1328.5
2657.1
5314.2
10628.4
21256.7

Influenza A virus (A/Puerto Rico/8/1934(H1N1))
166.6
333.1
666.2
1332.4
2664.7
5329.4
10658.9
21317.7

Influenza B virus (B/Lee/1/40)
156.6
313.2
626.4
1252.7
2505.4
5010.8
10021.6
20043.3

Program: 1535 - Influenza C virus (C/Ann Arbor/1/50)
180.3
360.5
721.0
1442.0
2884.0
5767.9
11535.8
23071.7

SARS coronavirus
304.3
608.5
1217.0
2434.1
4868.2
9736.1
19472.6
38945.3

Human coronavirus 229E
(Human coronaviruses HCoV-229E in serogroup I and HCoV-OC43 in serogroup II are, after rhinoviruses, the second most important cause of the common cold.)
165.7
331.4
662.7
1325.5
2651.0
5301.9
10603.8
21207.7

Human coronavirus HKU1
(Pneumonia)
302.5
605.0
1209.9
2419.8
4839.7
9679.4
19358.8
38717.5

Human coronavirus NL63
(The virus is found mainly in young children, elderly and immunocompromised individuals with acute respiratory illness during the winter season. Look for Bronchiolitis, Croup.)
164.3
328.5
657.1
1314.1
2628.3
5256.5
10513.0
21026.0

Human coronavirus OC43
(Human coronaviruses HCoV-229E in serogroup I and HCoV-OC43 in serogroup II are, after rhinoviruses, the second most important cause of the common cold.)
294.5
589.0
1178.0
2355.9
4711.8
9423.7
18847.4
37694.7

Program: 1536 - Human enteric coronavirus strain 4408
(A group 2 human coronavirus designated HECV-4408 was isolated from a child with acute diarrhea. Look for a cold or croup with diarrhea.)
292.4
584.9
1169.8
2339.6
4679.1
9358.2
18716.4
37432.9

Human parainfluenza virus 1
(Leading cause of croup in children)
290.1
580.3
1160.5
2321.0
4642.1
9284.1
18568.3
37136.5

Human parainfluenza virus 2
(Less frequently detected cause of croup in children)
289.3
578.6
1157.1
2314.2
4628.4
9256.8
18513.7
37027.4

Human parainfluenza virus 3
(Associated with bronchiolitis and pneumonia)
292.7
585.4
1170.9
2341.7
4683.5
9367.0
18734.0
37468.0

Parainfluenza virus 5 or Simian virus 5
(Croup. Bronchiolitis and pneumonia.
Could be a very important link for Cystic fibrosis, Multiple Sclerosis and Epilepsy.)
296.9
593.7
1187.5
2374.9
4749.9
9499.7
18999.4
37998.8

Human respiratory syncytial virus
((RSV) is a virus that causes respiratory tract infections. It is the major cause of lower respiratory tract infections and hospital visits during infancy and childhood.)
297.3
594.6
1189.1
2378.2
4756.4
9512.8
19025.6
38051.2

Program: 1537 - Human metapneumovirus
(It may be the second most common cause (after the respiratory syncytial virus) of lower respiratory infection in young children.)
169.7
339.4
678.8
1357.6
2715.3
5430.5
10861.1
21722.2

Human rhinovirus C
(The most common viral infective agents in humans and are the predominant cause of the common cold.)
159.4
318.8
637.6
1275.1
2550.2
5100.5
10200.9
20401.8

Human rhinovirus 14
(The most common viral infective agents in humans and are the predominant cause of the common cold.)
156.9
313.8
627.6
1255.1
2510.3
5020.5
10041.1
20082.2

Human rhinovirus 89
(The most common viral infective agents in humans and are the predominant cause of the common cold.)
158.2
316.4
632.8
1265.7
2531.3
5062.7
10125.3
20250.6

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

Look to the CDC for the correct Influenza genome to run, 30 min. of each genome is usually enough.

The SARS coronavirus and the Human coronavirus HKU1 genomes will take a 1 hour run each. The other coronavirus usually can be deactivated with a 30 min. run of each genome.

The Parainfluenza virus family usually takes a one hour run of each genome.
The RSV and Human metapneumovirus genome takes a 30 min. run for deactivation.

The Human rhinovirus genomes usually take a 15 to 30 min. run of each genome for deactivation. I start with 15 min. for each one, if the drip does not dry up by then I run the set of three again.

Craig Ledwell OMD 8/31/2011

Flu Virus, Colds, etc. part II

Human Adenovirus cause the following:

Program 1538 - <u>Conjunctivitis</u>

<u>Human adenovirus D1</u>
(serotype:Human adenovirus 9)
257.9
515.8
1031.6
2063.1
4126.3
8252.6
16505.1
33010.3

<u>Human adenovirus D</u>
258.0
516.0
1032.1
2064.1
4128.3
8256.6
16513.1
33026.3

Human adenovirus 54
(Causes epidemic keratoconjunctivitis (EKC))
259.2
518.4
1036.9
2073.8
4147.6
8295.1
16590.2
33180.4

Program 1539 - Respiratory Illnesses
Respiratory illness caused by adenovirus infection range from the common cold syndrome to pneumonia, croup, and bronchitis. Patients with compromised immune systems are especially susceptible to severe complications of adenovirus infection. Acute respiratory disease (ARD), first recognized among military recruits during World War II, can be caused by adenovirus infections during conditions of crowding and stress.

Human adenovirus type 2
251.9
503.8
1007.5
2015.1
4030.2
8060.4
16120.7
32241.4

Human adenovirus type 5
251.9
503.8
1007.5
2015.0
4030.1
8060.1
16120.3
32240.5

Human adenovirus type 1
251.4
502.9
1005.8
2011.5
4023.0
8046.0
16092.1
32184.1

Human adenovirus E
(serotype:Human adenovirus 4)
251.5
503.0
1005.9
2011.9
4023.8
8047.6
16095.2
32190.4

Human adenovirus C
(serotype:Human adenovirus 2)
251.9
503.8
1007.5
2015.1
4030.2
8060.4
16120.7
32241.4

Human adenovirus B2
260.2
520.3
1040.6
2081.3
4162.6
8325.1
16650.3
33300.6

Program 1540 - Human adenovirus B1
256.1
512.2
1024.5
2049.0
4097.9
8195.8
16391.7
32783.3

Program 1541 - Respiratory Illnesses and Conjuctivitis

Human adenovirus type 35
260.2
520.3
1040.6
2081.3
4162.6
8325.1
16650.3
33300.6

Human adenovirus type 7
254.9
509.8
1019.5
2039.1
4078.2
8156.4
16312.7
32625.4

Human adenovirus B
(serotype:Human adenovirus 11)
258.1
516.2
1032.5
2065.0
4130.0
8260.0
16520.0
33039.9

Gastroenteritis

Human adenovirus A
(serotype:Human adenovirus 12)
265.3
530.5
1061.0
2122.1
4244.2
8488.4
16976.7
33953.4

Human adenovirus F
264.6
529.1
1058.3
2116.6
4233.1
8466.3
16932.5
33865.1

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

I have found a 30 min. run is usually enough to deactivate the virus.

Craig Ledwell OMD 9/1/2011

Lyme Disease

Borrelia burgdorferi is the main cause of Lyme disease in the United States, whereas Borrelia afzelii and Borrelia garinii cause most European cases.

Relapsing Fever

The primary cause of tick-borne relapsing fever in western North America is Borrelia hermsii, recurrent fever agents Borrelia recurrentis and B. duttonii.
Relapsing fever (RF) is a disease caused by several spirochetes of the genus Borrelia. Relapsing fever borrelioses are characterized by recurrent febrile episodes and spirochetemia. There are 2 forms; louse-borne relapsing fever (also known as urban or epidemic RF) is caused by Borrelia recurrentis, and is transmitted by the body louse Pediculus humanus humanus. It is currently known in Ethiopia. Endemic tick-borne relapsing fever (TBRF) is a zoonotic disease transmitted worldwide by softbody ticks of the genus Ornithodoros. It is caused by at least 15 distinct Borrelia species throughout the world, including Borrelia hermsii and Borrelia turicatae (Human pathogen: Probable), carried by the ticks Ornithodoros hermsii and O.turicatae respectively. B.turicatae is pathogenic in dogs and is found in Florida, Texas and Kansas. Strain 91E135 was isolated in 1991 in Texas. Like B.hermsii, B.turicatae evades the mammalian immune system by periodically switching expression among members of two multigene families that encode immunogenic, antigenically distinct outer surface proteins.

Program: 1542 - Borrelia burgdorferi B31

5.0
318.1
636.1
1272.2
2544.2
5089.0
10177.9
20355.9

Borrelia burgdorferi ZS7
5.0
319.5
638.9
1277.9
2555.8
5111.5
10223.0
20446.0

Borrelia duttonii Ly
4.9
621.8
1243.6
2487.3
4974.5
9949.1
19898.1
39796.2

Borrelia garinii Pbi
5.0
320.3
640.7
1281.4
2562.7
5125.4
10250.8
20501.7

Borrelia hermsii DAH
4.9
314.1
628.1
1256.3
2512.5
5025.1
10050.1
20100.2

Borrelia recurrentis A1
4.9
622.3
1244.6
2489.1
4978.2
9956.5
19912.9
39825.9

Program: 1543 - **Borrelia turicatae 91E135**
4.9
315.8
631.5
1263.1
2526.2
5052.3
10104.6
20209.3

These are Genomic Harmonic Frequency Patterns. Each pattern should be run with all eight frequencies, at the same time, to be effective. Converge and Sweep are NOT to be used! Run with our 3.1 MHz carrier wave.

The first two genomes are the main ones for Lyme, but, I would also set up another block with the remaining to see if there is any reaction.

I would start off with 10 min. of each Genome, and judge the reaction. Make up a Block of patterns with the ones that were reacted too (itching, etc.) in the first session for follow-ups. It will take many sessions to deactivate this particular pathogen. Good Luck!

Craig Ledwell OMD 8/4/2011

Here is the Genomic Frequency pattern for Molluscum's. This is the skin tag disease in children and adults.

Program: 1544 - Molluscum
23.8
380.6
761.1
1522.2
3044.5
6089.0
12177.9
24355.8

This is a Genomic Harmonic Frequency Pattern group. It is not meant to be run in converge or sweep mode. All frequencies should be run at the same time with your carrier wave, 3.1 or 2.5.

I have used this pattern many times on children, it is always effective! Run for One Hour, the child or adult will tear themselves up reacting. A hot bath and Benadryl afterward will help. Expect the skin tags to fall off within two weeks. One session is enough!

Craig Ledwell OMD 7/16/2011

This is the Genomic Frequency pattern for Mycoplasmic Pneumonia.

Program: 1545 - Mycoplasma Pneumonia

5.5
354.8
709.6
1419.2
2838.5
5677.0
11353.9
22707.9

This Genomic Harmonic Frequency Pattern is to be run without converge or sweep.
Use all Frequencies at the same time with a 3.1 carrier for One Hour..

Program: 1546 - Relapsing Fever

The primary cause of tick-borne relapsing fever in western North America is Borrelia hermsii, recurrent fever agents Borrelia recurrentis and B. duttonii.

Borrelia duttonii Ly
4.9
621.8
1243.6
2487.3
4974.5
9949.1
19898.1
39796.2

Borrelia garinii Pbi
5.0
320.3
640.7
1281.4
2562.7
5125.4
10250.8
20501.7

Borrelia hermsii DAH
4.9
314.1
628.1
1256.3
2512.5
5025.1
10050.1
20100.2

Borrelia recurrentis A1
4.9
622.3
1244.6
2489.1
4978.2
9956.5
19912.9
39825.9

Borrelia turicatae 91E135
4.9
315.8
631.5
1263.1
2526.2
5052.3
10104.6
20209.3

These are Genomic Harmonic Frequency Patterns. Each pattern should be run with all eight frequencies, at the same time, to be effective. Converge and Sweep are NOT to be used!

I would start off with 10 min. of each Genome, and judge the reaction. Follow-up with 30 min. each.

Craig Ledwell OMD 8/19/2011

Salmonella

Salmonellosis is an infection with bacteria called Salmonella. Salmonella germs have been known to cause illness for over 100 years.

Most persons infected with Salmonella develop diarrhea, fever, and abdominal cramps 12 to 72 hours after infection. The illness usually lasts 4 to 7 days, and most persons recover without issue. However, in some persons, the diarrhea may be so severe that the patient needs to be hospitalized. In these patients, the Salmonella infection may spread from the intestines to the blood stream, and then to other body sites and can cause death unless the person is treated promptly with antibiotics. The elderly, infants, and those with impaired immune systems are more likely to have a severe illness.

Program: 1547 - Salmonella enterica subsp. enterica serovar Typhimurium str. LT2
(This subspecies is a leading cause of human gastroenteritis, the incidence of non-typhoid salmonellosis is increasing worldwide, causing millions of infections and many deaths in the human population each year.)
1.9
477.1
954.1
1908.3
3816.5
7633.1
15266.1
30532.3

Salmonella enterica subsp. arizonae serovar 62:z4,z23:-- str. RSK2980
(This subspecies is usually found associated with reptiles, although contact with infected animals can result in the spread of the organism to humans or animals such as turkeys.
Disease: Gastroenteritis)
2.0
503.7
1007.4
2014.7
4029.4
8058.8
16117.7
32235.4

Salmonella enterica subsp. enterica serovar Agona str. SL483
(S. Agona is a major cause of human foodborne illness in the United States and around the world. Disease: Gastroenteritis)
1.9
482.9
965.8
1931.6
3863.3
7726.6
15453.1
30906.2

Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67
(This subspecies a highly invasive serovar among non-typhoidal Salmonella, usually causes sepsis or extra-intestinal focal infections in humans.
Diseases: Bacteremia, gastroenteritis)
1.9
487.3
974.5
1949.1
3898.2
7796.4
15592.7
31185.4

Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853
(This subspecies a highly invasive serovar among non-typhoidal Salmonella, usually causes sepsis or extra-intestinal focal infections in humans.
Diseases: Bacteremia, gastroenteritis)
1.9
478.5
957.0
1914.0
3828.0
7656.0
15311.9
30623.9

Salmonella enterica subsp. enterica serovar Enteritidis str. P125109
(The nontyphoidal Salmonella are the leading cause of bacterial food borne illness in humans, making these pathogens an immediate biomedical, public health, and biodefense concern.
Disease: Salmonellosis)
1.9
494.5
989.1
1978.1
3956.3
7912.6
15825.2
31650.3

Program: 1548 - Salmonella enterica subsp. enterica serovar Heidelberg str. SL476
(This subspecies a highly invasive serovar among non-typhoidal Salmonella, usually causes sepsis or extra-intestinal focal infections in humans.
Diseases: Bacteremia, gastroenteritis)
1.9
474.0
948.0
1896.0
3792.1
7584.1
15168.3
30336.6

Salmonella enterica subsp. enterica serovar Newport str. SL254
(This subspecies a highly invasive serovar among non-typhoidal Salmonella, usually causes sepsis or extra-intestinal focal infections in humans.
Diseases: Bacteremia, gastroenteritis)
1.9
480.0
960.0
1920.0
3840.1
7680.2
15360.3
30720.7

Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633
(This serovar is the predominant cause of salmonellosis in Southeast Asia, a major source of imported food products to the United States.)
1.9
492.1
984.2
1968.4
3936.8
7873.5
15747.1
31494.2

Salmonella enterica serovars often have a broad host range, and some cause both gastrointestinal and systemic disease. But the serovars Paratyphi A and Typhi are restricted to humans and cause only systemic disease. Salmonella enterica serovar Typhi (S. typhi) is the etiological agent of typhoid fever, a serious invasive bacterial disease of humans with an annual global burden of approximately 16 million cases, leading to 600,000 fatalities.

Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601
1.0
505.8
1011.5
2023.1
4046.1
8092.3
16184.5
32369.1

Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150
1.0
505.4
1010.8
2021.6
4043.1
8086.2
16172.4
32344.8

Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7
1.9
476.9
953.8
1907.7
3815.4
7630.8
15261.6
30523.1

Program: 1549 - Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594
1.9
479.5
958.9
1917.9
3835.8
7671.5
15343.1
30686.1

Salmonella enterica subsp. enterica serovar Typhi str. CT18
1.9
481.9
963.7
1927.5
3854.9
7709.9
15419.8
30839.5

Salmonella enterica subsp. enterica serovar Typhi str. Ty2
1.9
483.6
967.2
1934.3
3868.7
7737.4
15474.7
30949.4

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

There are nine common Genomes which you will be most concerned with, of these, the first one is the most prevalent. I find it very common to get E. Coli or Salmonella at restaurants these days. Symptoms usually present very soon after ingestion with a sharp gut pain followed by diarrhea.

I will run 10 min. of the first pattern (Salmonella enterica subsp. enterica serovar Typhimurium str. LT2), to take care of the symptoms. If this is not effective I then proceed to run 5 min. of the other eight and this usually takes care of the problem.

If you have a patient with confirmed Typhoid Fever, they should be on pharmaceutical therapy and symptomology may be controlled. I will run 5 min. of each of the six patterns and watch for a reaction. If you have a confirmed reaction I would proceed with a one hour run of the correct genome.

PS: Salmonella can hide in the Gallbladder and lab test may be inconclusive. Ask the patient if they are having a malar flush fever at night and if they had diarrhea. If these symptoms are chronic you may want to try the six patterns and watch for reactions.

Craig Ledwell OMD 8/21/2011

Shigella

Shigella species are commonly pathogenic to humans, causing severe gastroenteritis (bacillary dysentery). In healthy adults, dysentery is a self-limiting disease, but it can be fatal to infants and young children, causing over 1 million deaths a year.

Program: 1550 - Shigella boydii CDC 3083-94

(Shigella boydii CDC 3083-94/BS512 was originally isolated from a 12-year-old boy in Arizona, USA.)

2.0
502.0
1004.0
2008.1
4016.2
8032.3
16064.6
32129.2

Shigella boydii Sb227

(Shigella boydii (strain Sb227) was isolated from epidemics in China during the 1950's.)

2.0
512.7
1025.4
2050.8
4101.6
8203.2
16406.5
32812.9

Shigella dysenteriae Sd197

(Shigella dysenteriae (strain Sd197) was isolated from epidemics in China during the 1950's.)

2.1
530.4
1060.7
2121.5
4243.0
8486.0
16971.9
33943.8

Shigella flexneri 2a str. 2457T

2.0
503.8
1007.7
2015.3
4030.7
8061.4
16122.8
32245.5

Shigella flexneri 2a str. 301
2.0
503.0
1006.0
2011.9
4023.8
8047.6
16095.3
32190.6

Shigella flexneri 5 str. 8401
2.0
506.6
1013.2
2026.4
4052.8
8105.6
16211.1
32422.2

Program: 1551 - Shigella sonnei Ss046
1.9
480.2
960.5
1921.0
3842.0
7684.0
15367.9
30735.8

These are Genomic Harmonic Frequency Patterns. They are not meant to be converged or used in sweeps. All eight frequencies of the pattern should be run at the same time with our 3.1mHz carrier wave.

I will run each of these patterns for 5 min. each and watch for a reaction. Then proceed with a 30 min. run of the correct Genome to deactivate the pathogen.

P.S. For infants or very young children, they will usually start to fidget and cry when you hit the correct Genome.

Craig Ledwell OMD 8/24/2011

Hello Joshua,
This is a very important pattern set I am giving you with this letter. It is nothing short of a Miracle, but it can also be dangerous if not run properly. With most people, this pattern set used without converge is completely effective. But, I have found inter-mutation within the genome of some of the strains make it necessary to use a slight converge for complete deactivation. This will be an ongoing issue with this Bacterium, also with Strep, E. Coli and Cancer. We may need to have a seminar, down the road, for some of these 'Mutated Nightmares'.

Program: 1552 - Staphylococcus

COL (MRSA)
1.6
412.4
824.8
1649.7
3299.4
6598.7
26394.8
13197.4

JH1 (MRSA)
1.6
398.6
797.3
1594.6
3189.1
6378.3
12756.6
25513.2

JH9 (VISA-type vancomycin resistance)
1.6
398.6
797.2
1594.5
3188.9
6377.9
12755.7
25511.5

MRSA252
1.6
399.2
798.4
1596.7
3193.4
6386.8
12773.7
25547.4

MSSA476
1.6
413.8
827.7
1655.3
3310.7
6621.4
13242.8
26485.5

MW2 (MRSA)
1.6
410.8
821.6
1643.2
3286.4
6572.9
13145.8
26291.5

Program: 1553 - MU3 (MRSA/hetero-VISA)
1.6
402.3
804.6
1609.2
3218.3
6436.6
12873.3
25746.5

MU50 (VRSA)
1.6
402.5
805.0
1610.1
3220.1
6440.3
12880.6
25761.2

N315 (MRSA)
1.6
411.6
823.3
1646.5
3293.0
6586.1
13172.1
26344.3

NCTC8325 (MRSA)
1.6
410.7
821.3
1642.7
3285.4
6570.8
13141.6
26283.1

USA300 FPR3757
1.6
403.3
806.7
1613.3
3226.6
6453.2
12906.4
25812.8

USA300 TCH1516
1.6
403.3
806.6
1613.2
3226.4
6452.9
12905.8
25811.5

Program: 1554 - Haemolyticus JCSC1435 (Well known for its highly resistant anti-biotic phenotype, this bacteria can cause meningitis, skin or soft tissue infections, prosthetic join infections, or bacteremia.)
1.7
431.6
863.1
1726.1
3452.2
6904.5
13808.9
27617.8

Lugdunensis HKU9-01 (Staphylococcus lugdunensis is a member of the coagulase-negative staphylococci and commonly found as part of the human skin flora. It is a significant cause of catheter-related bacteremia and also causes serious infections like native valve endocarditis in previously healthy individuals.)
1.7
435.9
871.7
1743.4
3486.8
6973.7
13947.3
27894.7

Saprophyticus ATCC 15305 (Can cause acute and recurrent urinary tract infections as well as bloodstream infections.)
1.8
460.4
920.8
1841.6
3683.3
7366.6
14733.2
29466.3

Newman
1.6
402.5
804.9
1609.9
3219.7
6439.5
12878.9
25757.9

Epidermis ATCC 12228
1.8
463.6
927.2
1854.4
3708.8
7417.6
14835.1
29670.3

Epidermis RP62A
1.7
442.8
885.6
1771.3
3542.6
7085.2
14170.3
28340.7

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I have tried to list the Major Staph Pathogens that have been sequenced at this time. This list will grow as more mutations occur. The last two Epidermal Staph are not as important, but, there can be binding and one would do well to include them in sets to run with the others.
I usually start with 5 minute run of each pattern for the first session; this gives you one hour and thirty minutes. I know it is a long time, but, unless you have the particular genome isolated by a lab, you may not be able to differentiate which one it is. Set these up as blocks of six patterns and you may find the last six are not as common as the others which will help you with run times on the second session. I would not push my luck with a sick person on the first session; you may set them up with a very serious kill-off if the Staph is at bone level. Kill-off may take 24hs., be prepared for the long haul and prepare your people. It may take weeks to completely deactivate a deep seated Staph. There's a tendency to want to give up if antibiotics have been used to push the Staph 'Deep'. Assure them to continue with therapy until there is no more reaction or you will leave them at the same level they were at, before you started. The bacteria will re-grow and surface at a later date more virulent than before.

After the first session I increase to 10 minute runs per genome. If there are no adverse side effects after the second session I will increase run time to 20 minutes per genome, which is the limit. By then you should be able to differentiate the correct genome and your sessions will not be as long.

These set of patterns are absolute 'Miracles'! They have saved many lives! Make sure to run them on anyone who is fatigued and they may really help clear the immune system and alleviate their tiredness.

Craig Ledwell OMD 7/25/2011

Streptococcus pneumoniae

Despite the name, the organism causes many types of pneumococcal infections other than pneumonia, including acute sinusitis, otitis media, meningitis, bacteremia, sepsis, osteomyelitis, septic arthritis, endocarditis, peritonitis, pericarditis, cellulitis, and brain abscess.

S. pneumoniae is the most common cause of bacterial meningitis in adults, children, and dogs, and is one of the top two isolates found in ear infection, otitis media. Pneumococcal pneumonia is more common in the very young and the very old.

Program: 1555 - Streptococcus pneumoniae 670-6B
2.0
517.2
1034.5
2069.0
4138.0
8276.0
16552.0
33103.9

Streptococcus pneumoniae 70585
2.1
530.4
1060.7
2121.4
4242.9
8485.7
16971.4
33942.8

Streptococcus pneumoniae AP200
2.1
543.8
1087.6
2175.3
4350.6
8701.2
17402.4
34804.7

Streptococcus pneumoniae ATCC 700669
2.0
521.6
1043.2
2086.4
4172.9
8345.8
16691.5
33383.0

Streptococcus pneumoniae CGSP14
2.0
524.5
1048.9
2097.9
4195.8
8391.5
16783.1
33566.1

Streptococcus pneumoniae D39
2.2
566.3
1132.5
2265.1
4530.2
9060.4
18120.7
36241.5

Program: 1556 - Streptococcus pneumoniae G54
2.2
557.3
1114.7
2229.3
4458.6
8917.3
17834.5
35669.0

Streptococcus pneumoniae Hungary19A-6
2.0
516.0
1031.9
2063.9
4127.7
8255.5
16510.9
33021.8

Streptococcus pneumoniae JJA
2.1
546.5
1093.0
2185.9
4371.8
8743.6
17487.3
34974.6

Streptococcus pneumoniae P1031
2.1
548.6
1097.3
2194.6
4389.1
8778.2
17556.4
35112.9

Streptococcus pneumoniae R6
2.2
568.4
1136.7
2273.4
4546.9
9093.7
18187.4
36374.8
Streptococcus pneumoniae TCH8431/19A
2.2
554.7
1109.4
2218.8
4437.7
8875.3
17750.7
35501.4

Program: 1557 - Streptococcus pneumoniae TIGR4
2.1
536.2
1072.4
2144.8
4289.7
8579.3
17158.6
34317.3

Streptococcus pneumoniae Taiwan19F-14
2.1
548.6
1097.1
2194.3
4388.6
8777.1
17554.2
35108.5

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As you can see we have many genome's for this bacteria, there will be more as time goes on. When I suspect Pneumonia, I run the Mycoplasma Pneumonia pattern first. If this one is not effective I then proceed with these Strep patterns. There is no particular genome that is more prevalent then the next, sorry, you may have to run them all for 20 minutes each if you really have a Strep pneumonia case. Sometimes you can get a clue from the CDC website as to the current strain that is infecting your area.

As for acute sinusitis, otitis media, bacteremia, sepsis, osteomyelitis, septic arthritis. I will run each Genome for 5 minutes and watch for reactions, and then proceed with a 20 minute run of each reactive pattern.
Sepsis, osteo and septic arthritis should be run no more than 20 minutes a day to prevent over kill, even safer bet with sepsis is to run every other day if you have a sick person. Always watch the whites of the eyes on any sick person. I have found it is an accurate measurement of Liver Toxicity; those eyes will glaze over and sometimes turn yellow. Stop the session and give them a day to recoup!

I have had one case of confirmed bacterial meningitis since I have perfected the Genomic Patterning. It took two 40 min. sessions spaced one day apart in order to deactivate the pathogen. It also takes two 40 min. sessions to deactivate cellulites.
Craig Ledwell OMD 8/9/2011

Streptococcus pyogenes is considered responsible for a wider variety of human disease than any other bacterial species.

This pathogen is responsible for a vast number of human infections that range from uncomplicated conditions to clinically severe invasive diseases. Some of the diseases are: pharyngitis (most common), tonsillitis (commonly referred to as Strep throat), sinusitis, otitis, pneumonia, impetigo, erysipelas, cellulitis, joint or bone infections, necrotizing fasciitis, myositis, meningitis, endocarditis, scarlet fever.

S. pyogenes can also cause disease in the form of post infectious "nonpyogenic" (not associated with local bacterial multiplication and pus formation) syndromes. These autoimmune-mediated complications follow a small percentage of infections and include rheumatic fever and acute post infectious glomerulonephritis. Both conditions appear several weeks following the initial streptococcal infection. Rheumatic fever is characterized by inflammation of the joints and/or heart following an episode of streptococcal pharyngitis. Acute glomerulonephritis, inflammation of the renal glomerulus, can follow streptococcal pharyngitis or skin infection.

Program: 1558 - Streptococcus pyogenes M1 GAS
2.4
312.7
625.5
1251.0
2501.9
5003.8
10007.6
20015.3

Streptococcus pyogenes MGAS10270
2.3
600.9
1201.8
2403.5
4807.1
9614.2
19228.4
38456.7

Streptococcus pyogenes MGAS10394
2.4
609.9
1219.7
2439.4
4878.9
9757.8
19515.5
39031.1

Streptococcus pyogenes MGAS10750
2.3
598.1
1196.3
2392.6
4785.1
9570.2
19140.4
38280.8

Streptococcus pyogenes MGAS2096
2.4
622.8
1245.6
2491.3
4982.5
9965.1
19930.1
39860.3

Streptococcus pyogenes MGAS315
2.4
609.7
1219.3
2438.6
4877.2
9754.5
19508.9
39017.9

Program: 1559 - Streptococcus pyogenes MGAS5005
2.5
315.1
630.2
1260.4
2520.8
5041.6
10083.2
20166.5

Streptococcus pyogenes MGAS6180
2.4
610.6
1221.2
2442.4
4881.8
9769.6
19539.2
39078.5
Streptococcus pyogenes MGAS8232
2.4
611.4
1222.8
2445.7
4891.4
9782.8
19565.6
39131.2

Streptococcus pyogenes MGAS9429
2.5
315.5
630.9
1261.8
2523.7
5047.3
10094.7
20189.4

Streptococcus pyogenes NZ131
2.5
319.1
638.1
1276.2
2552.4
5104.8
10209.7
20419.3

Streptococcus pyogenes SSI-1
2.4
611.7
1223.3
2446.7
4893.3
9786.6
19573.3
39146.5

Program: 1560 - Streptococcus pyogenes str. Manfredo
2.5
314.6
629.3
1258.5
2517.1
5034.2
10068.4
20136.7
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As you can see we have many genome's for this bacteria, there will be more as time goes on. When I suspect Pneumonia, I run the Mycoplasma Pneumonia pattern first. If this one is not effective I then proceed with these Strep patterns. There is no particular genome that is more prevalent then the next, sorry, you may have to run them all for 20 minutes each if you really have a Strep pneumonia case. Sometimes you can get a clue from the CDC website as to the current strain that is infecting your area.

Strep Throat is very easy to kill, usually a 5 minute run of each Genome will deactivate it in one session, sometimes it will take two. It is an absolute miracle to watch a child with Strep Throat lose all symptoms of the disease while they are on the table. When you observe this for yourself, you will understand the importance of the Genomic Patterning and also the inherent danger. I can't stress enough the danger of overkill when you work at this level! If you have a very serious case, and you run these patterns too long per Genome, you will make your patient so toxic that they will not survive!

I mention this in order to give you a clinical lesson on how to treat cellulites that has progressed to the level of Necrotizing fasciitis. By the time you see them the cellulites will be in the acute stage, they will probably be on heavy doses of antibiotics (which they should be on). Running the usual 5 min. testing procedure to isolate the correct Genome will not be effective because the antibiotics have affected the usual immune response, itching etc. Do not be tempted to increase run time on the first session. Give

them till the next day, then increase run time to 10 min. per Genome. Continue this for another day, if they need it!

Once you get them over the critical stage, then let the antibiotics do their work, you will usually have a very positive outcome.

You need to understand this technique of using Antibiotics with Genomic Patterning is very effective as a combined therapy. In the long run this marriage of Chemistry with frequency patterning will be the key to Medicine! I will explain this more thoroughly when we discuss Cancer and the use of Chemo.

P.S. Always take your time when you are clinically evaluating your patient with any of the diseases listed in this group. Always inquire if they remember having a sore throat before they became ill. I find it is extremely common that the patient had a slight sore throat up to two weeks before any clinical manifestation of their disease!

Craig Ledwell OMD 8/9/2011

Program: 1561 – **Rhinotracheitis** (for cats!) Feline viral rhinotracheitis (FVR) is an upper respiratory infection of cats caused by feline herpesvirus 1, of the family Herpesviridae.
Feline herpesvirus 1
266.6
533.3
1066.5
2133.1
4266.1
8532.3
17064.6
34129.2

Bonus Bartonella Deactivation Sets:

These were requested due to their common association with Lyme infections and have thus been added after the other programs had been alphabetized so it is a bit out of order – but quite important.

Bartonella

Bartonella bacilliformis
Bartonella bacilliformis is the etiologic agent of Carrion´s disease or Oroya fever(acute phase of infection) and Verruga peruanaor Peruvian wart(chronic phase of infection). The acute phase of the disease is a life
threatening disease characterized by massive invasion of bartonella to human red blood cells and consequently an acute hemolysis and fever. If the infection is not treated the case fatality rate is 40 to 85% Patients
in this phase of the infection can be complicated by overwhelming infections primarily by enterobacterias (Salmonella spp) and parasites (Toxoplasma gondii, Pneumocystis jirovecci). The chronic phase is
characterized by benign eruptive lesions that are pruritic and bleeding, and other symptoms like malaise and osteoarticular pain. Bartonella can be isolated from blood cultures and secretion of the lesions in
people from endemic areas.

Program 1562 - Bartonella bacilliformis KC583
3.1
400.9
801.8
1603.7
3207.3
6414.6
12829.3
25658.5

Bartonella clarridgeiae
Cat scratch disease (CSD) (also known as "Cat scratch fever", "Inoculation lymphoreticulosis", and "Subacute regional lymphadenitis") is a usually benign infectious disease caused by the intracellular bacterium Bartonella
clarridgeiae.

Bartonella clarridgeiae 73
3.0
380.5
760.9
1521.8
3043.6
6087.2
12174.5

24348.9

Bartonella grahamii
One of the causes of Endocarditisand Neuroretinitis.

Bartonella grahamii as4aup
1.9
494.9
989.7
1979.5
3959.0
7918.0
15835.9
31671.9

Bartonella henselae
Bartonella henselae, formerly Rochalimæa, is a proteobacterium that can cause bacteremia, endocarditis, bacillary angiomatosis, and peliosis hepatis. It is also the causative agent of cat-scratch disease(Bartonellosis)
which, as the name suggests, occurs after a cat bite or scratch. The disease is characterized by lymphadenopathy (swelling of the lymph nodes) and fever.

Peliosis hepatis caused by B. henselae can occur alone or develop with cutaneous bacillary angiomatosisor bacteremia. Patients with peliosis hepatitis present with gastrointestinal symptoms, fever, chills, and an enlarged
liver and spleen containing blood-filled cavities. This systemic disease is mostly seen in patients infected with HIV and other immune-compromised individuals.

Bartonella henselae str. Houston-1
2.3
600.0
1200.0
2400.1
4800.1
9600.3
19200.5
38401.1
Bartonella quintana
Bartonella quintana, originally known as Rochalimaea quintana, and "Rickettsia quintana", is a microorganism that is transmitted by the human body louse. This microorganism is the causative agent of trench fever. This bacteria resulted in over 1 million soldiers in Europe during
World War I being infected with Trench Fever.

Bartonella quintana str. Toulouse
2.9
366.3

732.7
1465.4
2930.7
5861.5
11723.0
23446.0

Bartonella tribocorum
A new cause of Endocarditis.

Bartonella tribocorum CIP 105476
1.7
442.4
884.8
1769.6
3539.2
7078.3
14156.6
28313.3

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Craig Ledwell OMD