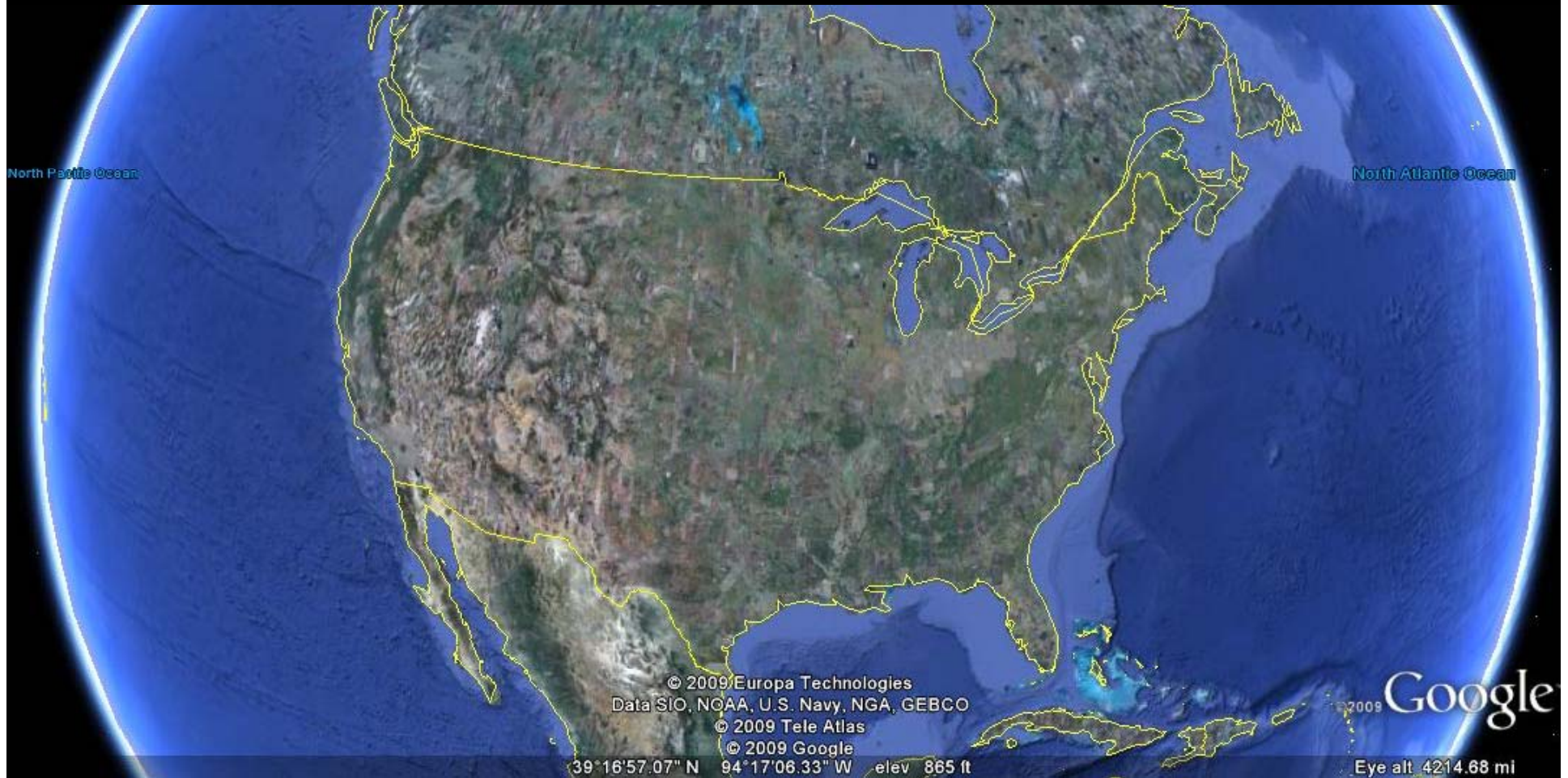


PATHOGENIC BACTERIA IN NORTH AMERICAN SOILS: A JOINT USGS-USEPA SURVEY



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Richard Allen, Ph.D. - USEPA

Study Objectives

- Study scale - Continental United States, 1 site per 1600 km², 4,851 samples.
 1. For pilot study data see *Smith et al. 2009. Geochemical Studies of North American Soils: Results from the Pilot Study Phase of the North American Soil Geochemical Landscapes Project. Applied Geochemistry, 24(8):1355-1356.*
- Determine the most sensitive and specific polymerase chain reaction (PCR)-based detection of pathogens from a wide range of soil types.
 1. Determine the presence of specific pathogens in the soil samples.
 2. *Bacillus anthracis* (4,851 samples, standard PCR, presence/absence, with verification by the University of South Florida's Center for Biological Defense, Tampa, Florida).
 3. *Yersinia pestis* (2,133 samples, quantitative-PCR).
 4. *Fransicella tularensis* (2,133 samples, quantitative-PCR).
- Relate pathogen data to geochemistry and climate to aid in -
 1. Outbreak investigations (natural and human induced)
 1. Wildlife
 2. Livestock
 3. Human
 2. Model development.

Soil Microbiology

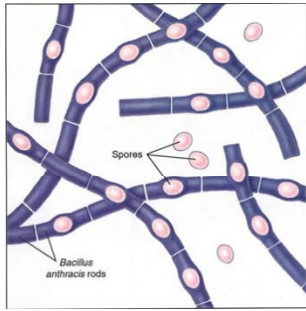
1. Bacteria populations in soils typically range from 10^6 to 10^9 cells/gram as determined via direct count assay.
2. Culturable bacteria numbers may range from 0 to 10^7 colony forming units/gram of soil.
3. The current estimate of culturable bacteria and any sample type is 0.1 to 10% of the total population.
4. Current estimates put the typical number of bacteria genotypes per gram of soil at 10,000.
5. The dominant bacteria genera typically found is *Bacillus*.
6. Virus populations are typically 1 to 2 logs less than the bacteria populations (opposite of aquatic environments).
7. $\sim 10^6$ fungi per gram of soil.
8. $\sim 10^4$ protozoa per gram of soil

Bacillus anthracis

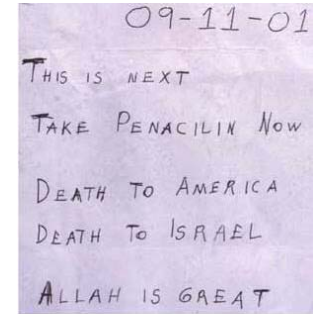
1. Gram positive
2. Non-motile
3. Rod-shaped with square-shaped ends forming chains
4. 1 to 1.2 μ m in width
5. 3 to 5 μ m in length
6. Endospore former (spores 0.1 to 0.5 μ m)
7. Genome – 5,227,293 bp
8. Virulence plasmids – pX01 (189,000 bp, toxin), pX02 (96,000 bp, capsule)
9. Can be grown under aerobic or anaerobic conditions
10. Growth rate – in vitro, typically less than 30 minutes
11. Prevalence in soil survey studies – typically less than 5%
12. First identified as the causative agent of anthrax by Robert Koch

(Koch, R., 1876. Die aetiologie der milzbrand-krankheit, begrundet auf die entwicklungsgeschichte de *Bacillus Anthracis*. *Beitr. Biol. Pflanz.* 2, 277-311)





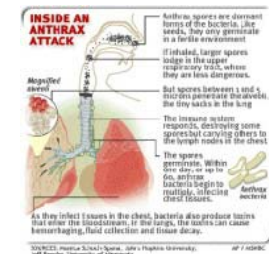
Anthrax



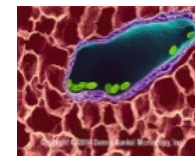
- Cutaneous – primary cause = occupational exposure (cuts/abrasions) to contaminated hides, symptoms/illness = ~2 week incubation, sore development with swelling, possible black crusted pustule with a broad zone of edema, may also develop painful lymph nodes, fever and headache. Fatality rate for untreated cases ~20%



- Gastrointestinal – primary cause = consumption of contaminated meat, symptoms/illness = fever, abdominal pain, vomiting, bloody diarrhea which may progress to toxemia, shock and death. Fatality rates for untreated cases range from 25 – 60%.



- Pulmonary – primary cause = occupational exposure to contaminated dust, hair, hides, symptoms/illness = flu-like, fever, fatigue, headache, muscle aches, shortness of breath that progress to bronchitis, shock and death. Fatality rate for untreated cases, 100%. Can be fatal when treatment started after symptoms appear.



Outbreaks associated with heavy precipitation and flooding

Topographical lows in grazing areas that may allow ponding of water can present higher risk



Bacillus sp./anthracis Detection Protocol

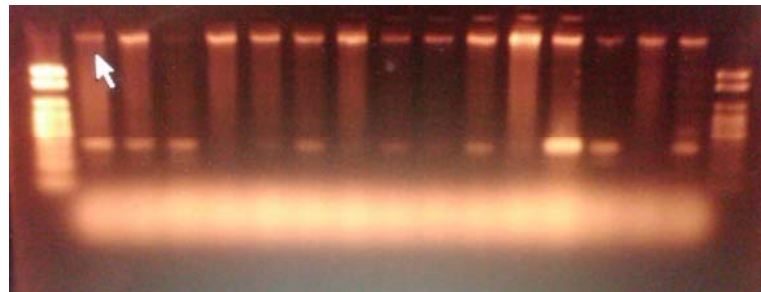
~0.25g of soil



BA-RF = GACGATCATYTWGGAAACCG
BA-RR = GGNGTYTCRATYGGACACAT
= 359-base pair region of *rpoB* gene (encodes the RNA polymerase b-subunit) that is specific for *Bacillus* species at the genus level

Ba-SF = TTCGTCCTGTTATTGCAG
= 208-base pair region of the same gene that is specific for *B. anthracis*

(PCR amplification profile and primer sequences from - Ko et al., 2003.
Identification of *Bacillus anthracis* by *rpoB* Sequence Analysis and Multiplex PCR.
Journal of Clinical Microbiology. 41(7):2908-2914)

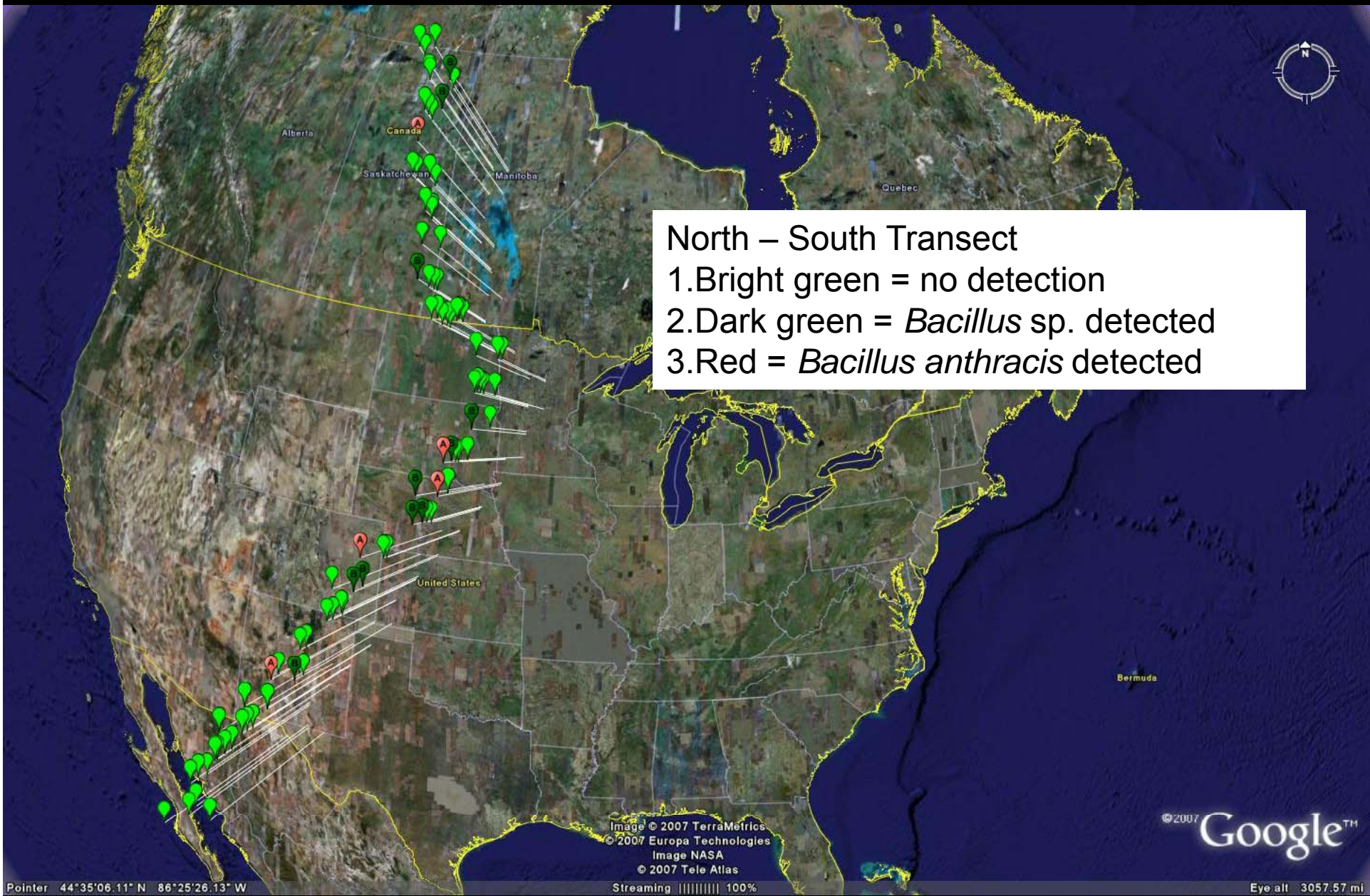


The background of the slide features a microscopic view of Bacillus anthracis spores. The spores are depicted as dark blue, rod-shaped structures with rounded ends, arranged in various orientations. Each spore contains a prominent, bright red, oval-shaped core, representing the endospore. The spores are scattered across the white background, with some appearing in small clusters or chains.

Bacillus anthracis Pilot Study

- 104 samples collected along a North-South transect extending from Manitoba, Canada to El Paso, Texas (2004, sample sites approximately every 40km).
- 19 samples collected in New Orleans following the flood event caused by Hurricane Katrina (2005).
- 32 samples collected along the Gulf Coast and from New Orleans in 2007.

North – South Transect
1. Bright green = no detection
2. Dark green = *Bacillus* sp. detected
3. Red = *Bacillus anthracis* detected



New Orleans post Katrina sites and results, 2005



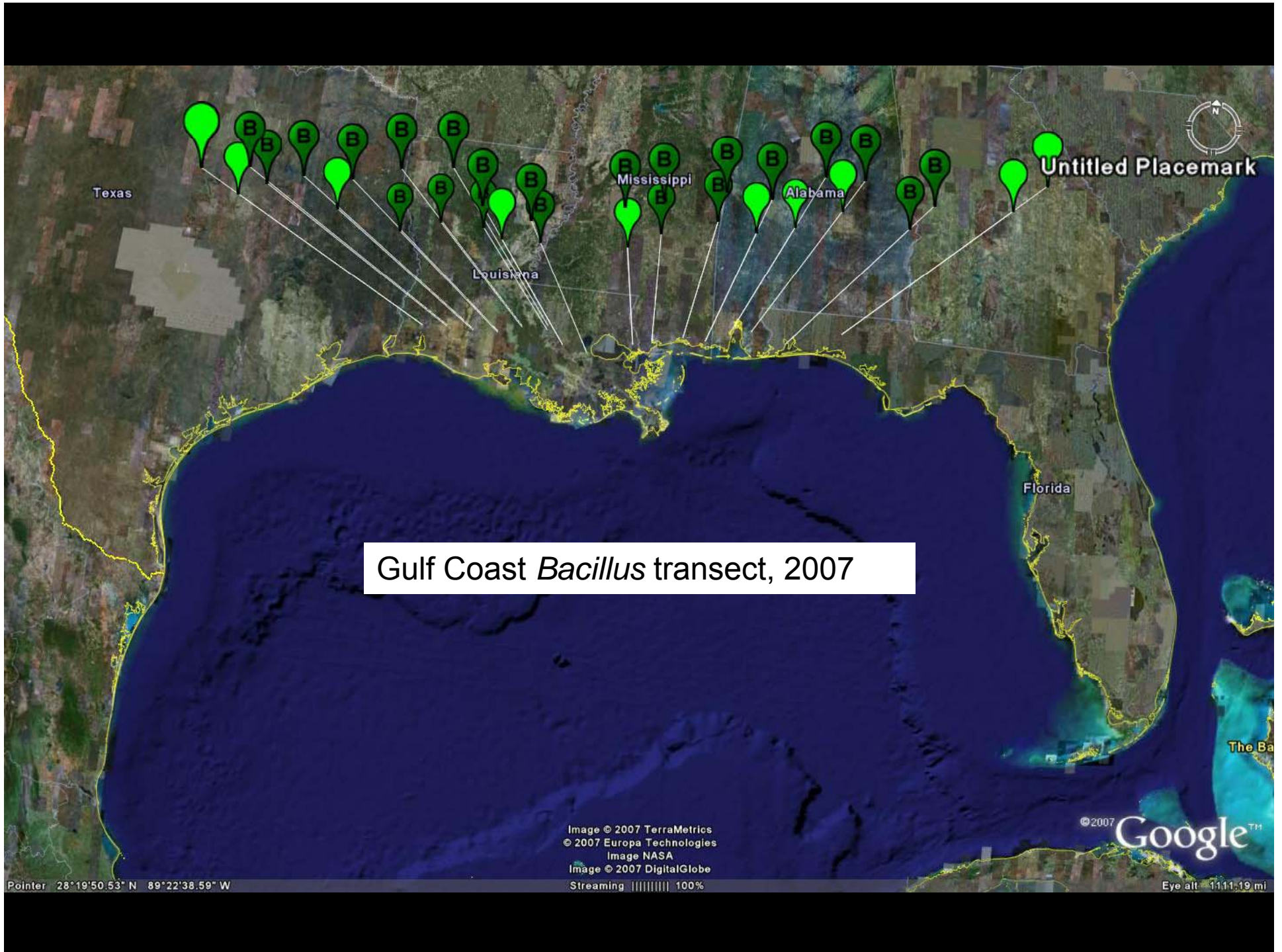
Fig. 2. 2005 Post-Katrina New Orleans and Chalmette, LA, sample sites.

Post-Katrina New Orleans

Katrina passed east of New Orleans 8/29/05
Samples collected 9/15/05 and assayed on 10/4/05

- 5 of 19 samples were PCR positive for *Bacillus sp.* and *Bacillus anthracis* (six sites were positive for human enteroviruses. One site positive for both *B. anthracis* and enteroviruses).
- All positive for pX01 plasmid and one positive for pX01/pX02 per USF's Center for Biological Defense.
- PCR positive sites were sampled and screened again on 8/10/07. No *B. anthracis* positive samples. Two positive for *Bacillus sp.*
- 32 Gulf Coast sites extending from Sulfur, Louisiana, to DeFuniakSprings, Florida - No *B. anthracis* detected, 22 were positive for *Bacillus sp.*

Additionally, motility, Gram stain, hemolysis, and γ -phage sensitivity were determined on isolates obtained from samples



Gulf Coast *Bacillus* transect, 2007

Pointer 28°19'50.53" N 89°22'38.59" W

Image © 2007 TerraMetrics
© 2007 Europa Technologies
Image NASA
Image © 2007 DigitalGlobe
Streaming ||||| 100%

©2007 Google™
Eye alt 1111.19 mi

USGS geochemistry data obtained at each sample site

Table 2. Major and trace element data for soils collected at a depth of 0-5 cm.

Lab No.	Field No.	State	Latitude	Longitude	COUL TITR CRBNT C %	Biolog nrmalized median	CVAA Hg ppm	ICPAES_MS Al %	ICPAES_MS Ca %	ICPAES_MS Fe %	ICPAES_MS K %	ICPAES_MS Mg %	ICPAES_MS Na %	ICPAES_MS S %	ICPAES_MS Ti %	ICPAES_MS Ag ppm	ICPAES_MS As ppm
C-241462	48-4d1-PH	KY	38.0	-85.0	0.02	103	0.00	0.02	0.00	0.00	0.00	0.39	0.42	0.09	0.30	<1	7
C-241563	48-4d2-PH	KY	38.0	-85.0	0.02	105	0.05	6.5	0.42	3.56	2.55	0.59	0.48	0.04	0.36	<1	7
C-241436	48-3-PH	KY	38.0	-84.8	0.16	103	0.05	3.84	1.09	2.52	1.25	0.37	0.28	0.06	0.25	<1	8
C-241461	46-2d1-PH	WV	38.0	-80.5	0.01	106	0.04	3.27	0.06	1.48	0.57	0.14	0.11	0.03	0.26	<1	5

Table 2. Major and trace elem

Lab No.	Field No.	ICPAES_MS Ba ppm	ICPAES_MS Be ppm	ICPAES_MS Bi ppm	ICPAES_MS Cd ppm	ICPAES_MS Ce ppm	ICPAES_MS Co ppm	ICPAES_MS Cr ppm	ICPAES_MS Cs ppm	ICPAES_MS Cu ppm	ICPAES_MS Ga ppm	ICPAES_MS In ppm	ICPAES_MS La ppm	ICPAES_MS Li ppm	ICPAES_MS Mn ppm	ICPAES_MS Mo ppm	ICPAES_MS Nb ppm
C-241462	48-4d1-PH	384	2.3	0.22	0.2	85.9	16.9	60	4.78	21.3	16.3	0.06	42.8	38	1280	0.67	10.4
C-241563	48-4d2-PH	472	1.8	0.23	0.2	84	18.2	48	4.47	14.5	14.2	0.06	40.1	32	1180	0.64	8
C-241436	48-3-PH	412	1.6	0.18	0.2	82.6	14.9	40	2.58	22.4	9.6	0.04	39.5	22	2780	0.89	7.2
C-241461	46-2d1-PH	175	0.7	0.16	<0.1	40.8	3.8	33	2.75	6.8	7.63	0.03	19.5	26	88	1.02	7.9

Table 2. Major and trace elem

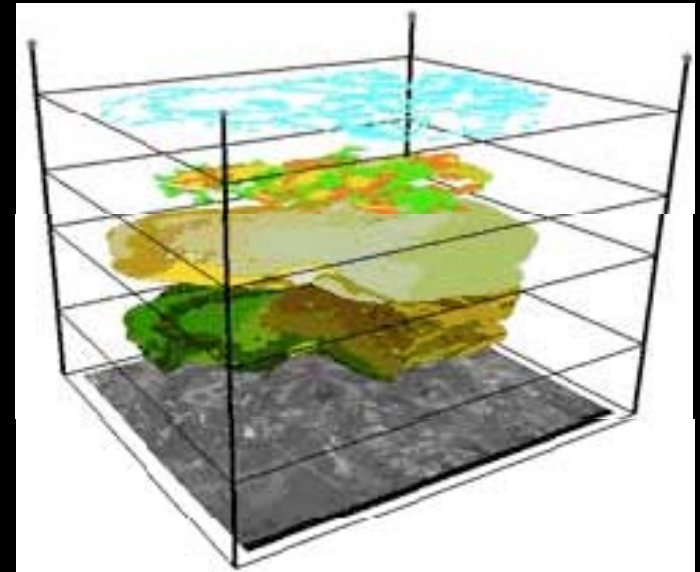
Lab No.	Field No.	ICPAES_MS Ni ppm	ICPAES_MS P ppm	ICPAES_MS Pb ppm	ICPAES_MS Rb ppm	ICPAES_MS Sb ppm	ICPAES_MS Sc ppm	ICPAES_MS Sr ppm	ICPAES_MS Sr ppm	ICPAES_MS Te ppm	ICPAES_MS Th ppm	ICPAES_MS Tl ppm	ICPAES_MS U ppm	ICPAES_MS V ppm	ICPAES_MS W ppm	ICPAES_MS Y ppm	ICPAES_MS Zn ppm
C-241462	48-4d1-PH	27	1190	24.5	93.5	0.52	13.2	2	69.3	<0.1	12	0.6	3.2	81	0.8	27.8	83
C-241563	48-4d2-PH	30.8	1140	24.1	93.1	0.42	12.2	1.9	63	<0.1	12.3	0.6	3.3	80	0.6	26.6	91
C-241436	48-3-PH	17	3580	34.8	59.8	0.42	7.9	1.3	89.9	<0.1	13.5	0.5	3.7	53	0.6	28.5	63
C-241461	46-2d1-PH	10.3	434	18.3	37.3	0.47	4.4	1.2	39.5	<0.1	67	0.3	2.2	46	0.7	8.1	30

Table 2. Major and trace elem

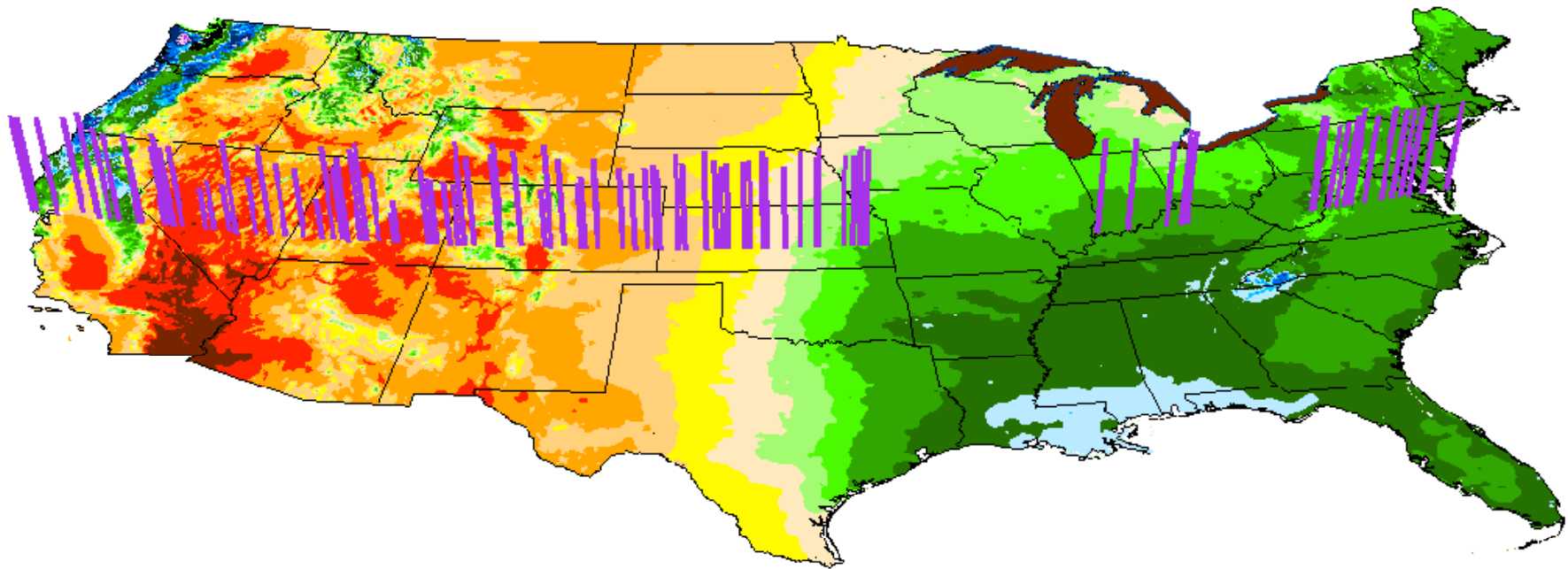
Lab No.	Field No.	Hyd Sb ppm	Hyd Se ppm	Combust. Total C %	Combust. Total S %
C-241462	48-4d1-PH	<0.6	0.5	4.78	<0.05
C-241563	48-4d2-PH	<0.6	0.4	2.96	<0.05
C-241436	48-3-PH	<0.6	0.3	4.03	<0.05
C-241461	46-2d1-PH	<0.6	0.6	3.33	<0.05

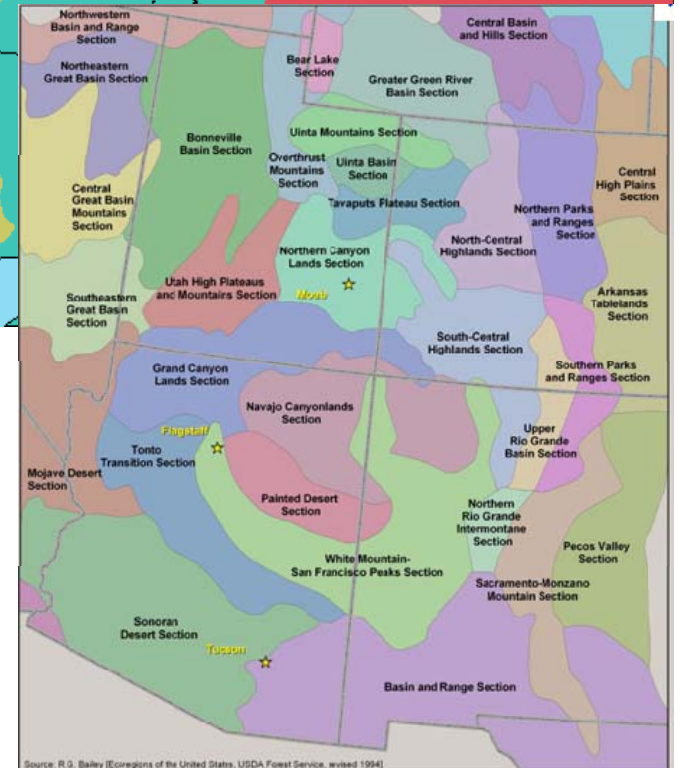
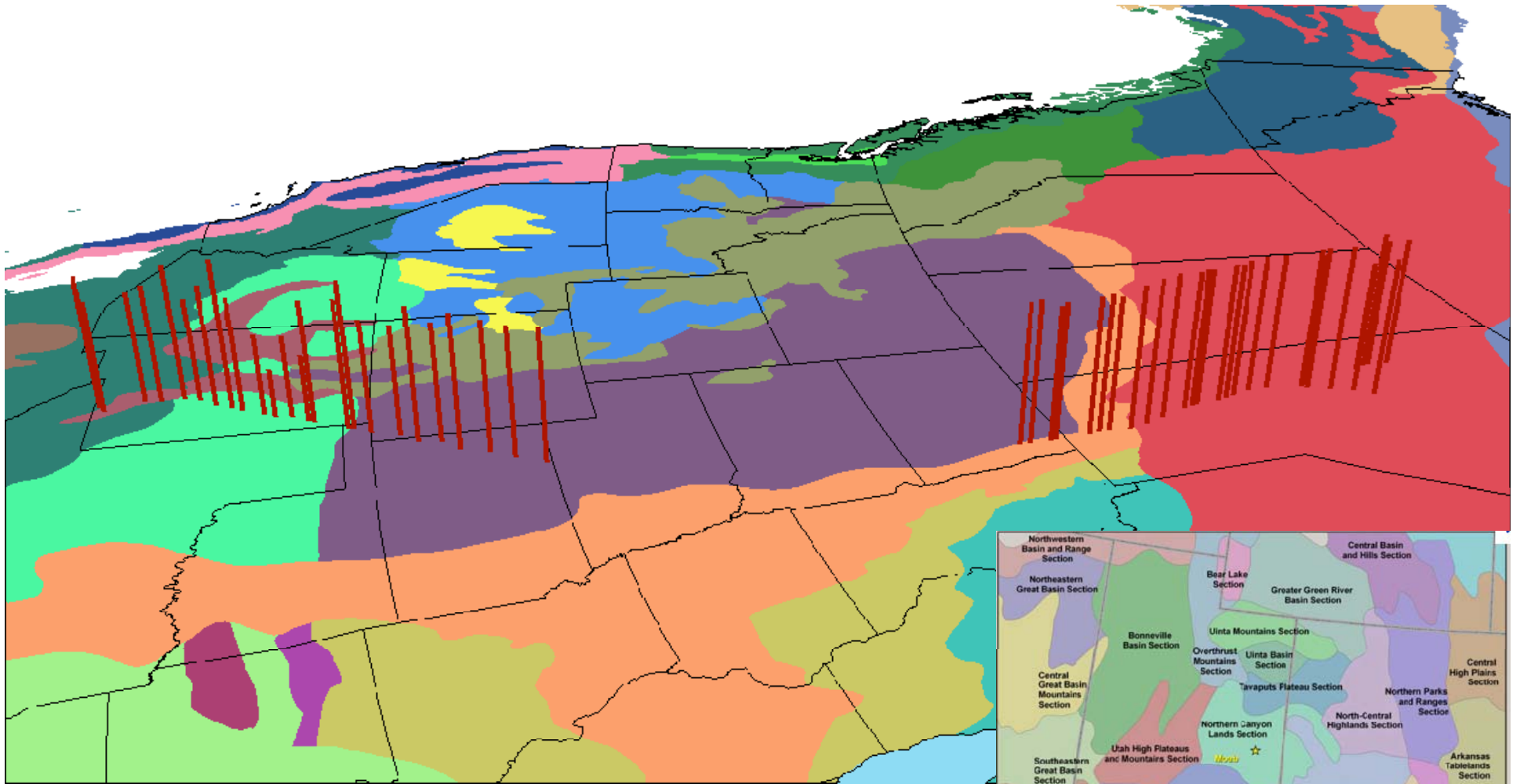


Top soil map, USGS



BioLog EcoPlate versus Precipitation
USGS Geochemical Landscape Project Pilot Study, EW transect





BioLog EcoPlate versus EcoRegions
 USGS Geochemical Landscape Pilot Study, NS transect

Source: R.G. Bailey (Ecoregions of the United States, USDA Forest Service, revised 1994)

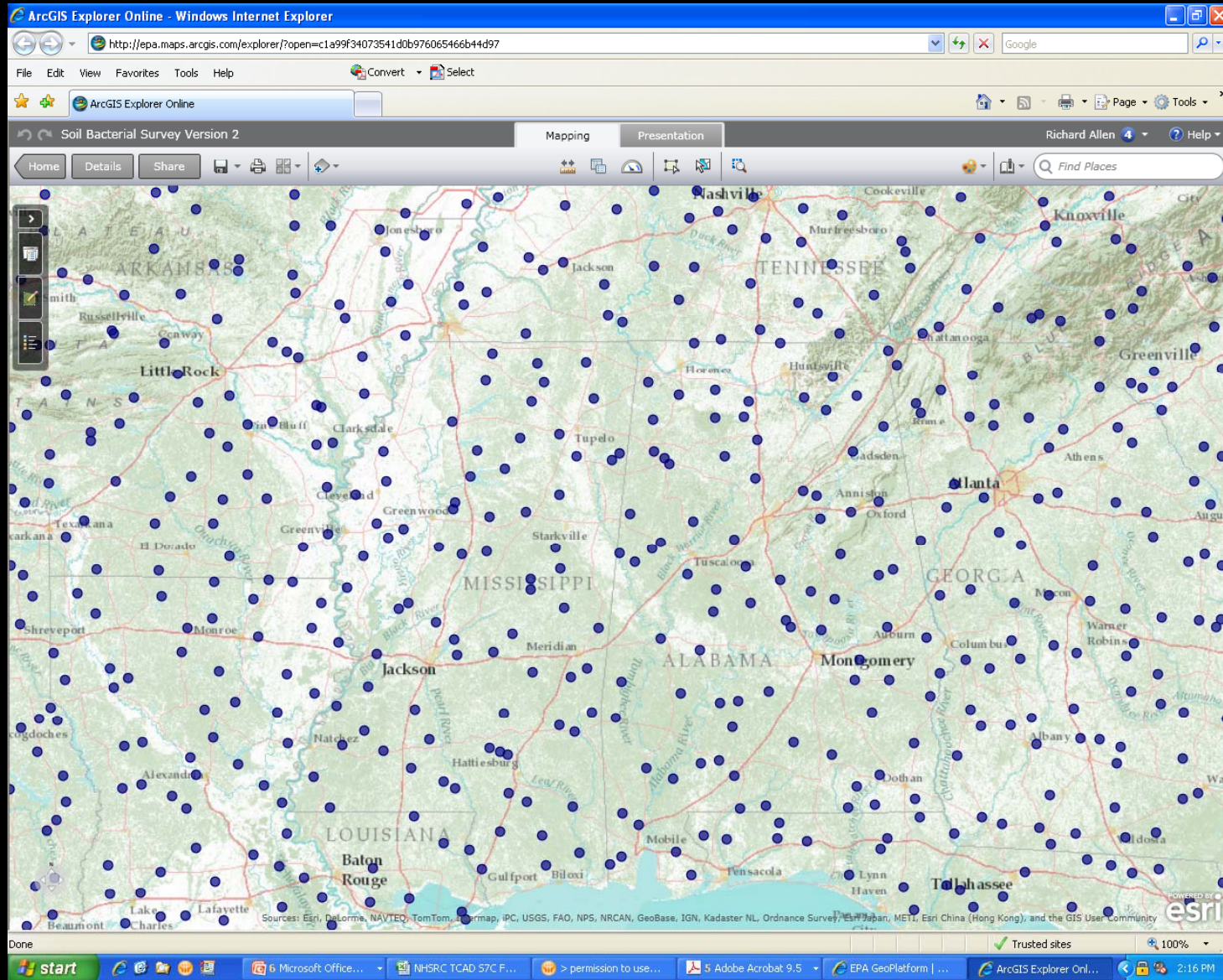
Pilot Study Summary

- The highest *B. anthracis* prevalence was noted following flooding of New Orleans.
- In non-flooded soils *B. anthracis* prevalence was less than 5% for the North-South transect and 0% for the Gulf Coast transect.
- There was a statistically significant relationship between soils with elevated moisture content ($\geq 15.0\%$ weight) and the presence of *Bacillus sp./B. anthracis* in both the North-South and Gulf Coast transects (p -value *Bacillus sp./B. anthracis* = 0.003/0.001).
- In the North-South transect statistically significant relationships were noted between the occurrence of *Bacillus sp.* and the elements Co, Cu, Pb, Sn, Tl, and Zn. These relationships were not observed in the New Orleans samples or along the Gulf Coast.
Elements such as Cu, and Zn are utilized by *Bacillus sp.* to enhance virulence and impart resistance to antibiotics, H₂O₂, and UV stress.

Survey – Continental U.S.

1. 4,851 sites uniformly distributed.
2. MoBio's PowerSoil Kit which utilizes 0.25g for DNA extraction and is more sensitive than their UltraClean Soils Kit which screens 1.0g of soil (4CFU vs 170CFU/g of soil) will be utilized for DNA extraction.
3. Primers for detection of *Bacillus sp.* (*rpoB rif* region 359 bp) and *B. anthracis* (*rpoB* 208bp).
4. Qiagen's HotStart Master Mix Plus Kit and gel/amplicon visualization with SYBRGold will be utilized to determine presence/absence.
5. Confirmation of PCR positives by the USF's Center for Biological Defense and Northern Arizona University.

USGS-USEPA sample site layer



USGS-USEPA sample site layer – Site specific information

The screenshot displays the ArcGIS Explorer Online interface within a Windows Internet Explorer browser. The browser's address bar shows the URL: <http://epa.maps.arcgis.com/explorer/?open=c1a99f34073541d0b976065466b44d97>. The application title is "Soil Bacterial Survey Version 2". The map shows a topographic view of the Southeastern United States, including parts of Tennessee, Mississippi, Alabama, Georgia, and Louisiana. Numerous blue circular markers represent soil sampling locations across the region. A popup window titled "Soil_Sampling_Locations" is open over a specific site in Alabama, displaying the following information:

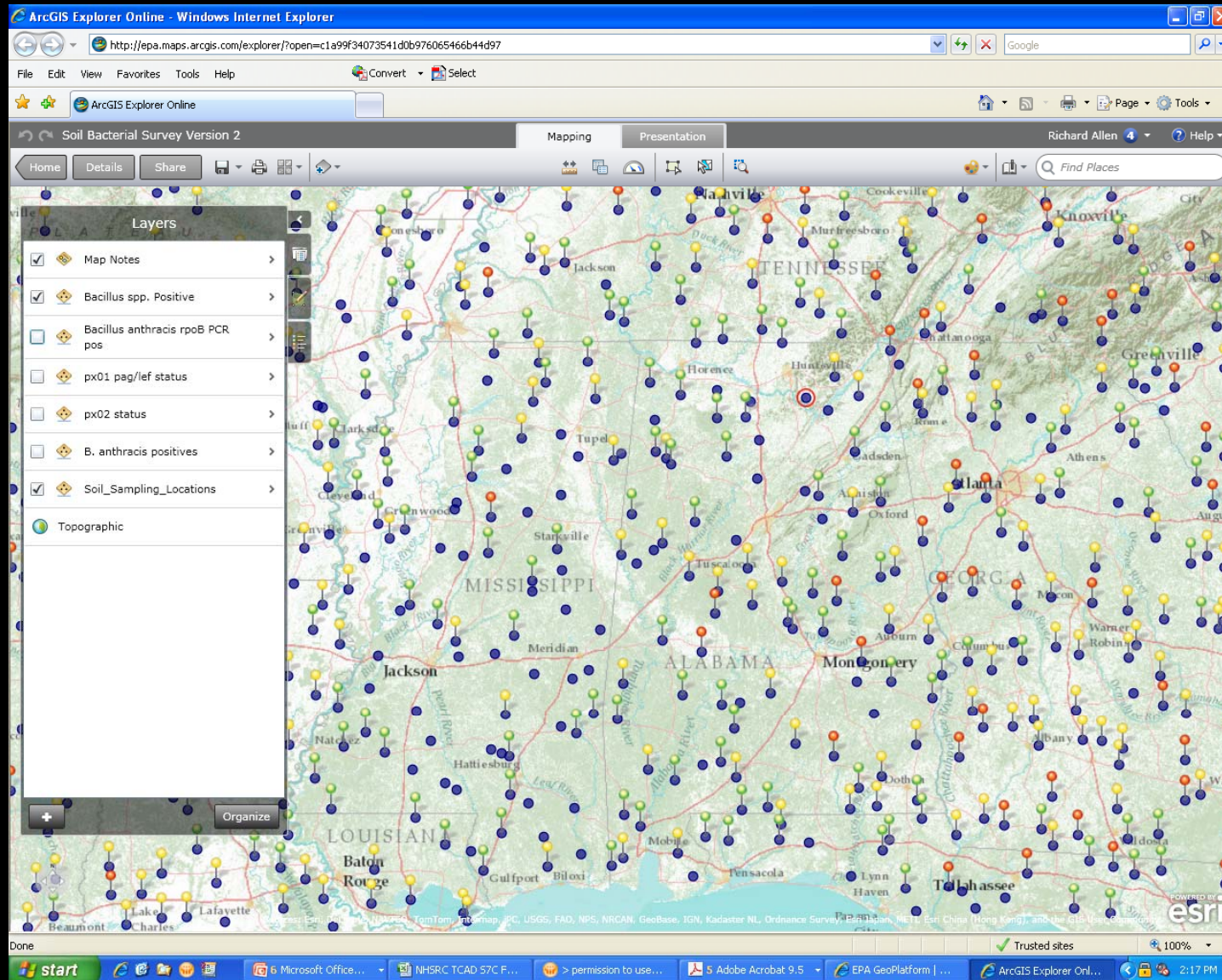
Soil_Sampling_Locations	
State	AL
Final ID	AL 3984
Bacillus species status	n
B. anthracis rpoB PCR status	
USF CBD px01 pag/lef status	
USF CBD px02 status	

The popup window also includes "Zoom To" and "Edit" options. The Layers panel on the left shows the following layers:

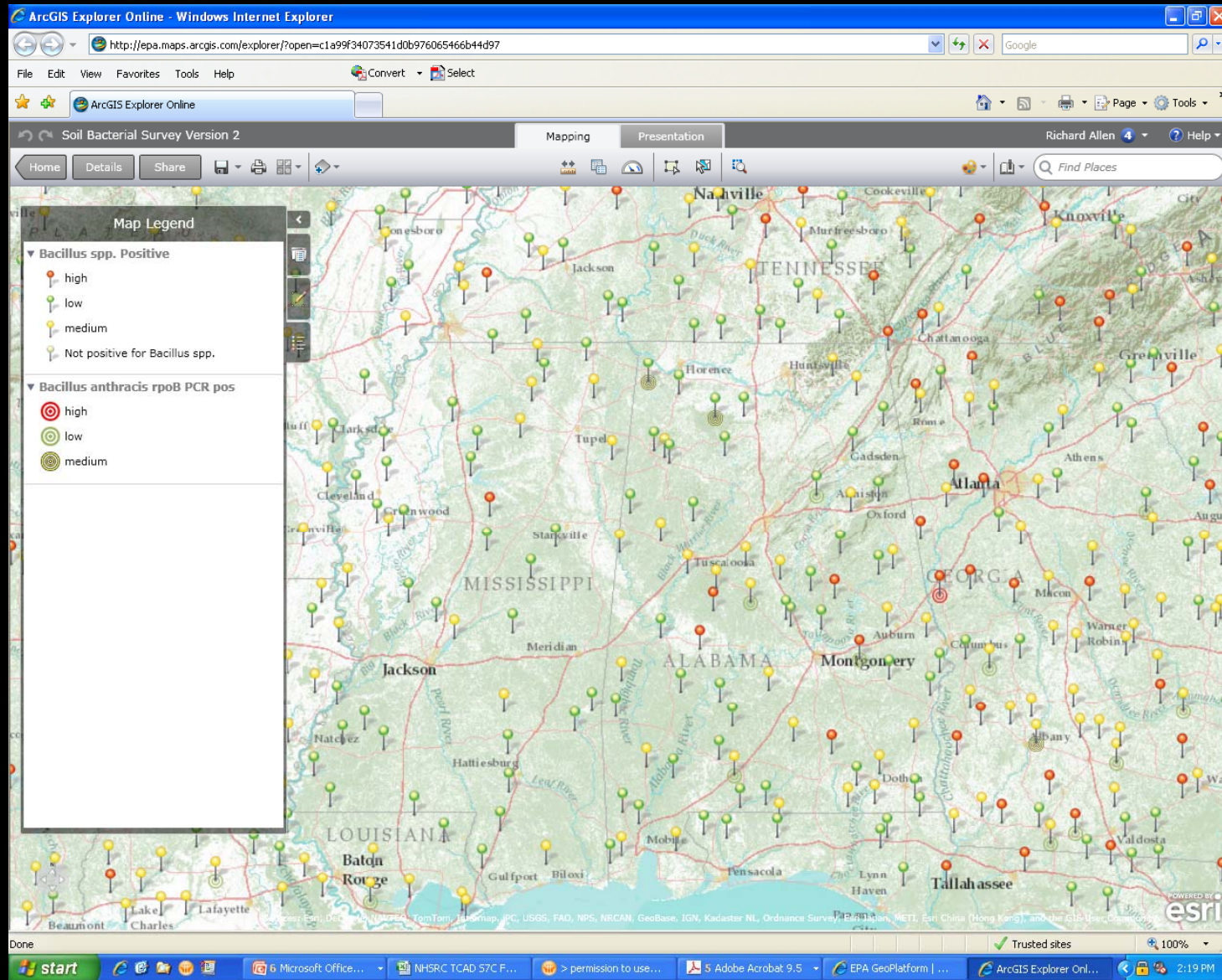
- Map Notes
- Bacillus spp. Positive
- Bacillus anthracis rpoB PCR pos
- px01 pag/lef status
- px02 status
- B. anthracis positives
- Soil_Sampling_Locations
- Topographic

The Windows taskbar at the bottom shows several open applications, including Microsoft Office, NHSRC TCAD 57C F..., Adobe Acrobat 9.5, EPA GeoPlatform, and ArcGIS Explorer Online. The system clock indicates the time is 2:16 PM.

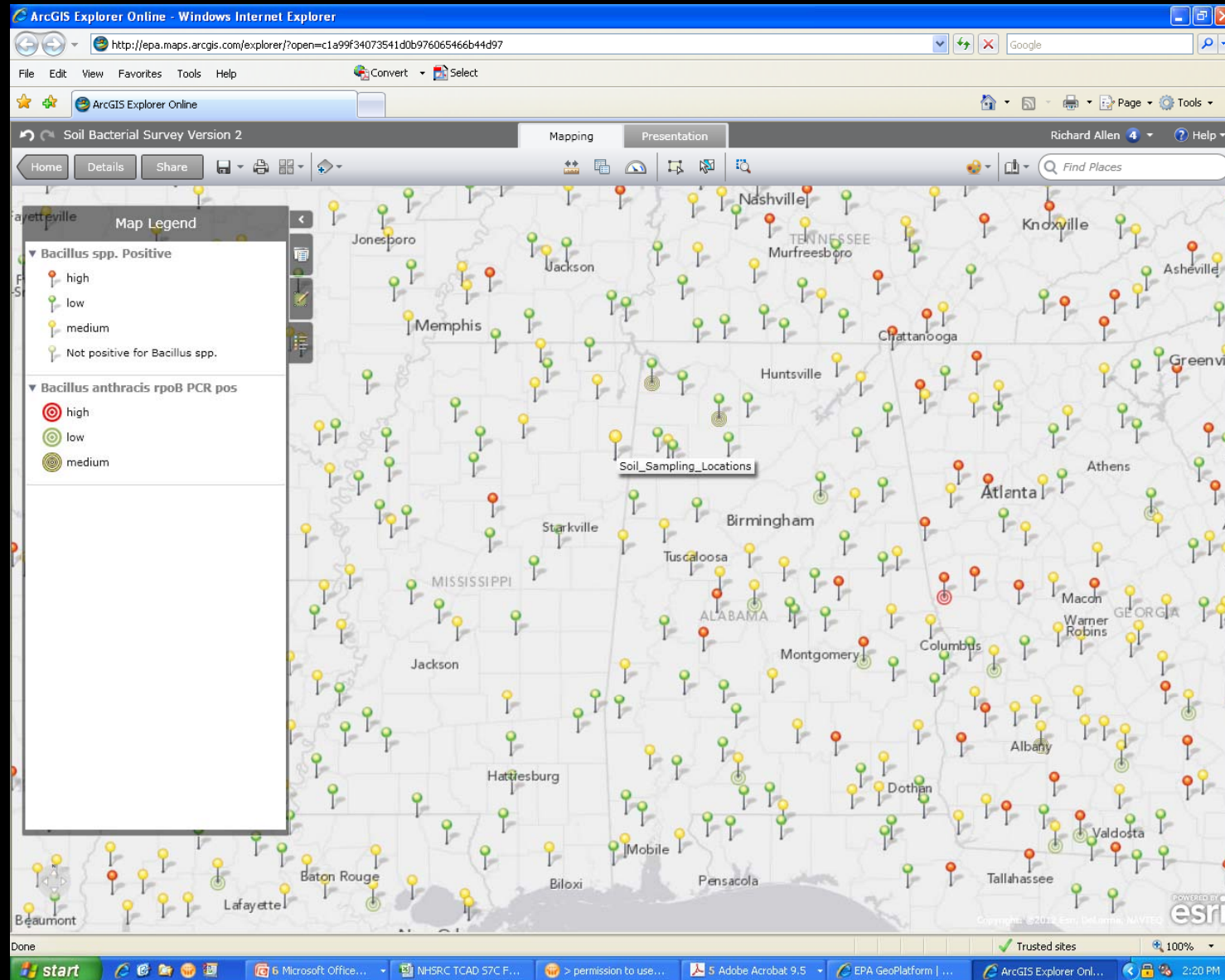
USGS-USEPA *Bacillus* sp. positive layer – Color coded for strength of PCR signal



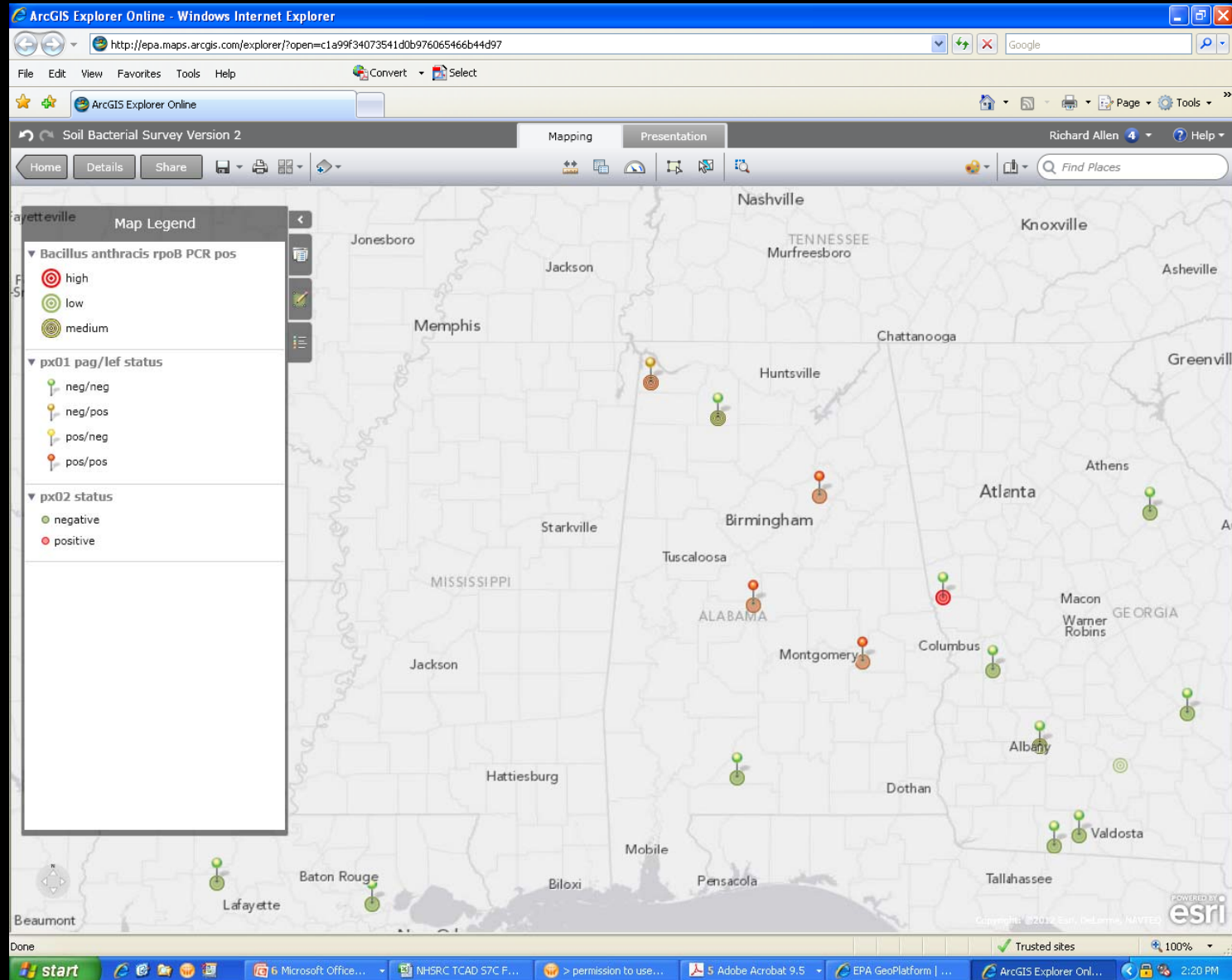
USGS-USEPA *Bacillus* sp. and *B. anthracis* positive layer – Color coded for strength of PCR signal, w/topo



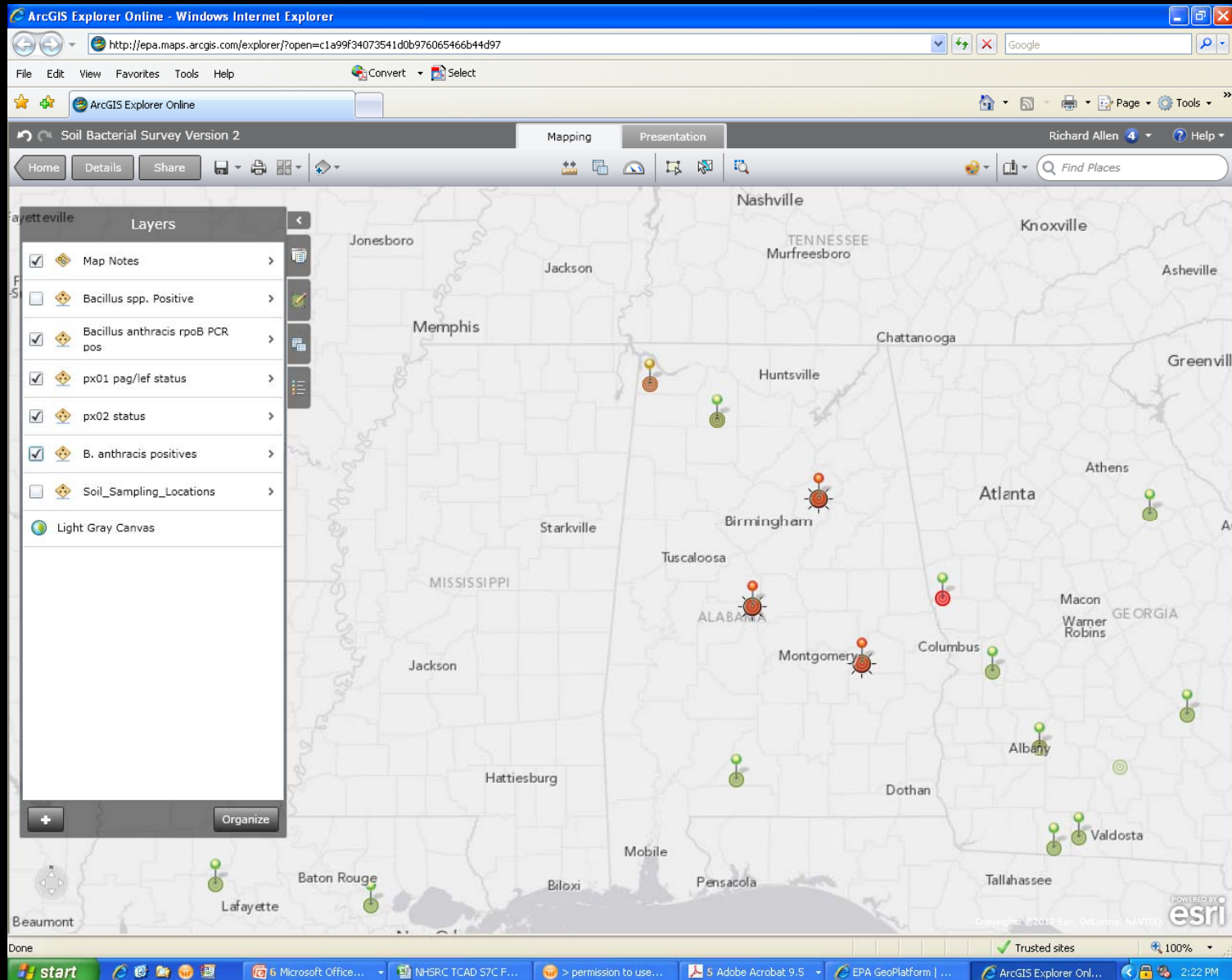
USGS-USEPA *Bacillus* sp. and *B. anthracis* positive layer – Color coded for strength of PCR signal, w/o topo



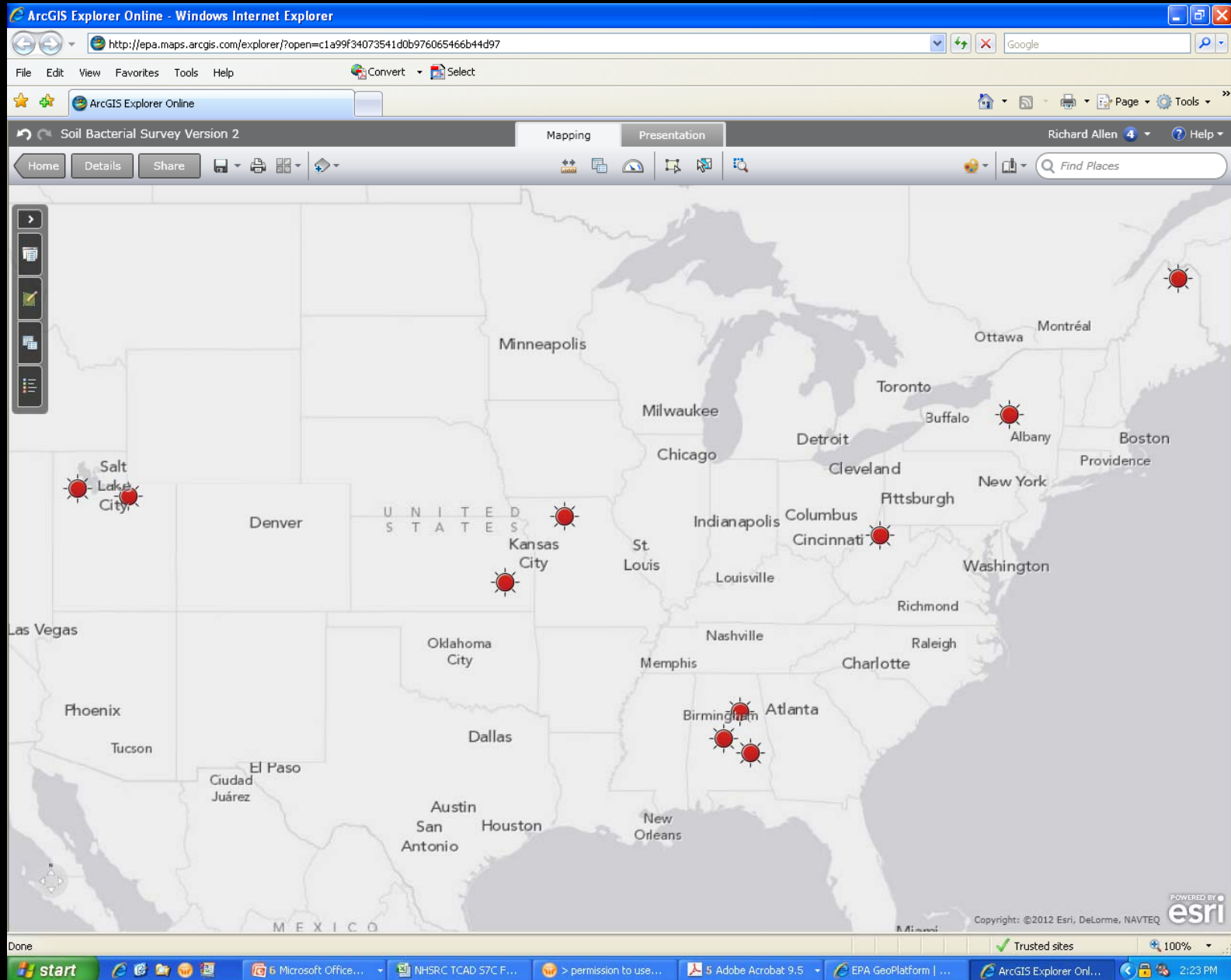
USGS-USEPA *B. anthracis*/plasmid positive layer – Color coded for strength of PCR signal and presence or absence of plasmid genes



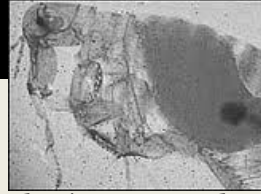
USGS-USEPA *B. anthracis* positive layer –Color coded for strength of PCR signal, presence or absence of plasmid genes and highlighted red star for all positive



USGS-USEPA *B. anthracis* positive layer – All genetic markers screened present



Yersinia pestis



Gram negative, rod-shaped, facultative anaerobe. A flea-borne category A pathogen. Causative agent of the death of ~ 1/3 of European population in the 14th Century, ~ 75 million worldwide 19th Century outbreak killed

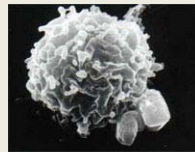
~ 12 million in China and India

Annually, about 12 cases in the US, 2,000 worldwide.

"I was fifteen years old at the time, and I remember everything clearly. The Japanese plane spread something that looked like smoke. A few days later we found dead rats all over the village. At the same time, people came down with high fevers and aches in the lymph nodes. Every day, people died....."



Fransicella tularensis



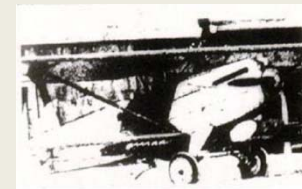
Gram negative, facultative intracellular (infects macrophages).

A highly virulent category A pathogen. Inhalation can lead to lethal pneumonic rabbit fever.

Previously developed as a biological weapon (easily spread via aerosols and low infectious dose 10-50 CFU).

Widespread disease (USA) in animals, ~ 200 US human cases per year.

"People who inhale an infectious aerosol would generally experience severe respiratory illness, Including life-threatening pneumonia and systemic infection, if they are not treated. The bacteria that causes tularemia occur widely in nature and could be isolated and grown in quantity in a laboratory, although manufacturing an effective aerosol weapon would require considerable sophistication"



WWW.BT.CDC.GOV

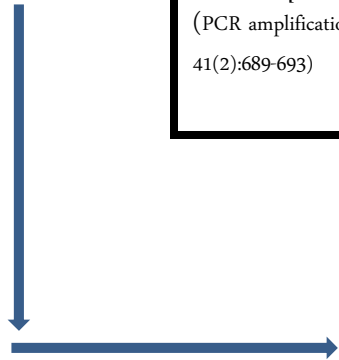
Yersinia pestis and *Fransicella tularensis* Detection Protocols

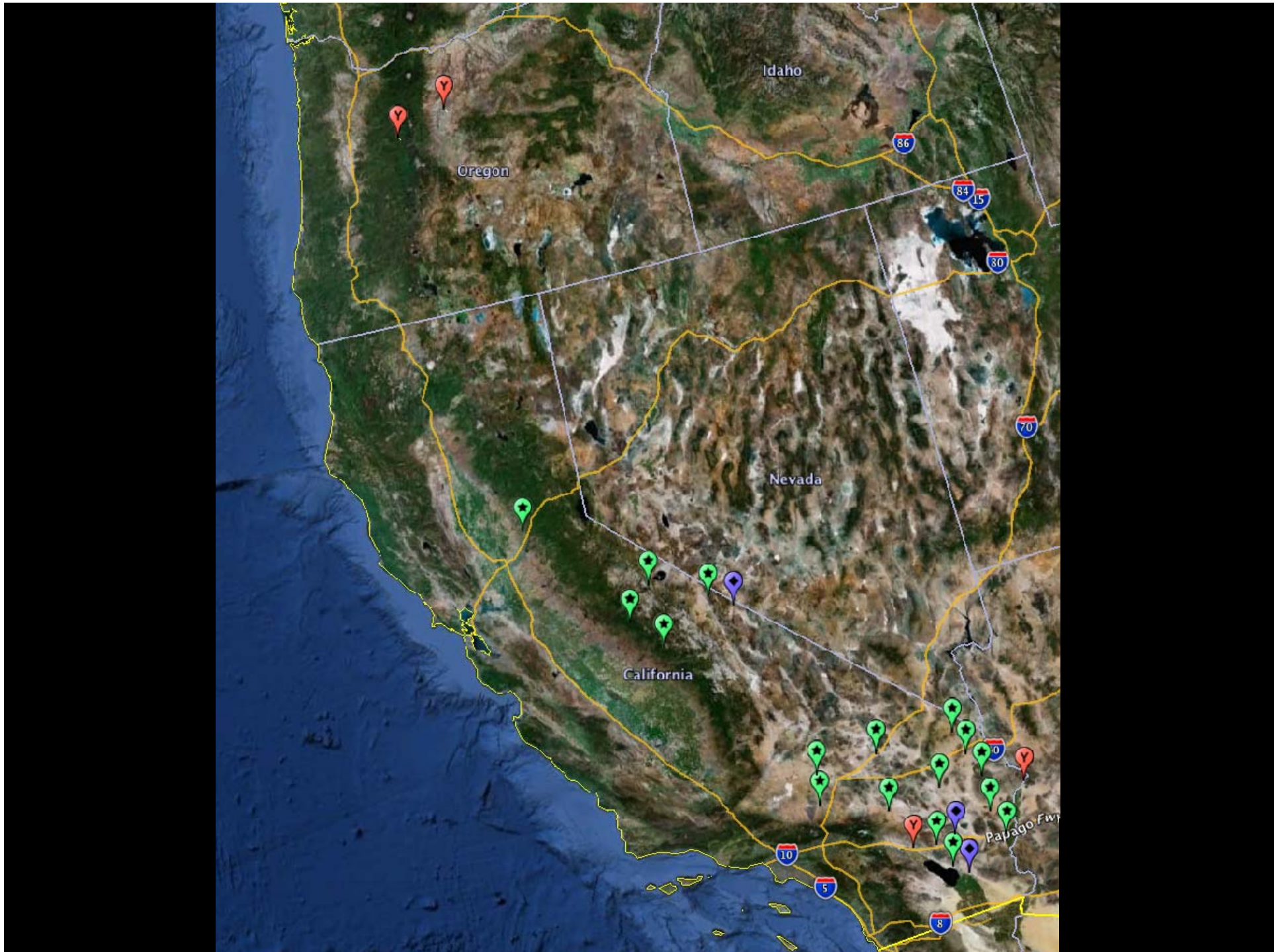
~0.25g of soil

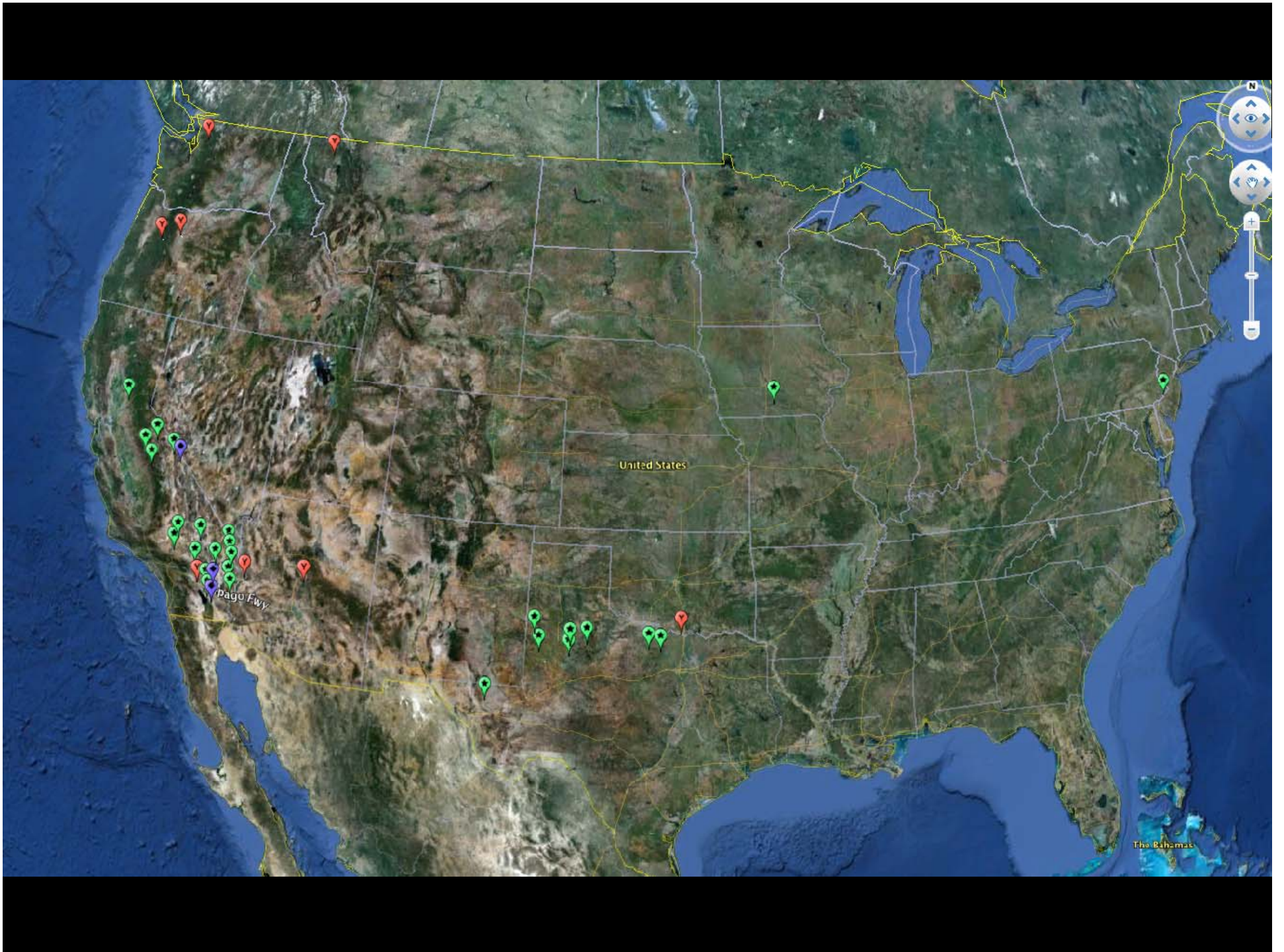


Yersinia pestis
 67bp amplicon, located between two common genomic *Yersinia* insertion elements (1541 and 285)...ID'd via suppression subtractive hybridization
 3aF - GGACGGCATCACGATTCTCT, 3aR - CCTGAAAACCTTGGCAGCAGTT
 3a Probe - [6~FAM]AAACGCCCTCGAATCGCTGGC[BHQ1a~6FAM]
 (Primers – Radnedge et al., 2001. AEM. 67:3759-3762. Probe - Qu et al., 2010. PLOS Neglected Tropical Diseases. 4(3)e629...modified amplification profile...AB TaqMan start then Qu et al. cycles)

Fransicella tularensis
 86bp amplicon of the fopA gene (encodes an outer membrane protein).
 Up - AACAAATGGCACCTAGTAATATTTCTGG,
 Dn - CCACCAAAGAACCATGTAAACC,
 Probe - [6~FAM]TGGCAGAGCGGGTACTAACATGATTGGT[BHQ1a~6FAM]
 (PCR amplification profile and primer/probe sequences from – Emanuel et al., 2003. Journal of Clinical Microbiology. 41(2):689-693)







Summary/Conclusions

- 4,851 sites analyzed for *Bacillus* species.
- ~ 50% positive for the genus *Bacillus*.
- 79 PCR positive for *B. anthracis*.

10 PCR positives verified by USF.

62 PCR positives pending verification and reassessment

Presumptive prevalence rate at ~1.0% of sites at this point in the study

- *Yersinia pestis* was detected in 9 of 2133 samples (0.4%).
 - *Fransicella tularensis* was detected in 30 of 2133 samples (1.4%).
-
- As the New Orleans post-Katrina data demonstrates, *B. anthracis* is more readily detected following flood events. Surprisingly, post flood isolates could not be detected several years later.
 - *B. anthracis* post flood surveys are needed as well as survival experiments in surface and subsurface environments.
 - This study will provide ‘natural occurrence data’ that will be valuable in site specific risk assessments conducted during future events.

Acknowledgements

U.S. Environmental Protection Agency collaborators:
Tonya Nichols and Sarah Perkins

Disclaimer:

This presentation has been reviewed by the Agencies but does not necessarily reflect the Agencies' views. No official endorsement should be inferred.

