

2009/02/18

2009/11/03

2007 /12 - 1

26.06

 $(\text{fgC.cell}^{-1})^3 \times 10 \times 178.14$ $(\text{fgC.cell}^{-1})^3 \times 10 \times$

EC

/ 15

TOC

/ 11

*Actinomycetes Pseudomonas**Salmonella-Shigella Total coliform Bacillus*

listwise

Pearson correlation

. one way ANOVA

:

Heterotrophic Bacterial Populations Dynamics and Role in Food Web in the Room Reservoir (Sweeda)

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ABSTRACT

Heterotrophic Bacterial populations Dynamics were studied in the Room and Jueleen reservoirs in Sweeda through 2007. The biovolume and biomass as carbon biomass was assessed where the maximum value of biomass were $178.14 \times 10^3 \text{ fgC.cell}^{-1}$ in the Room reservoir in June and $26.06 \times 10^3 \text{ fgC.cell}^{-1}$ in the Jueleen reservoir in August, the role of heterotrophic bacterial community in food web was assessed by relation between bacterial populations and total organic carbon (TOC), where the maximum value of TOC was 15 mg.l^{-1} in the Room reservoir in June and 11 mg.l^{-1} in the Jueleen reservoir in August. The physicochemical parameters temperature, electrical conductivity, pH, and total organic carbon (TOC) were determined; also total count, viable counts and dynamics populations of *Pseudomonas*, *Actinomycetes*, *Bacillus*, Total coliform, *Salmonella-Shigella*, were determined. In the statistical analysis we applied standard deviation, Pearson correlation, listwise, and one way ANOVA.

Key words: *Heterotrophic bacterial, Bacterial populations, Bacterial Dynamics, Food web.*

Community

Lindstrom 2000, Gasol]
et al., 2002, David C. Sigee 2005, Goddard *et al.*, 2005, Magnuson
et al., 2005

Heterotrophic

Geochemical cycles

Biofilms

Allman *et al.*, 1992, Alfreider *et al.*, 1996, David C. Sigee. 2005,]
 (*Escherichia coli*) [Mark Skidmore *et al.* 2005
 .[Donald Scavia *et al.*, 1986, David C. Sigee. 2005]

Food web

Fuhrman & Azam. 1980, Malinsky &]
 [Legrand 1996, Fuhrman 1999
 Primary production %50-10

Goldman *et al.*, 1996, Wommack & Colwell 2000, Hewson &]
 [Fuhrman 2004

Bacterial [Azam *et al.* 1983]
 productivity

.

:

.1

.2

.3

.4

(1)

345
20
75 1515
[2007]
1
(2007) (1)

54200	²	1440	
6.400 ³		18	
72.50		631	
0.450	³	30 ²	
³ 6.400	1980	400	
150 - 128	f^3	1977	

7

5 :1
3 :2
1 :3
1 :4
(Potamogeton)
3 :5
5 :6
12 :7
25 :

5

50

Bathometer

Montagna] 5

[1982, Donegan *et al.* 1991



Google Earth

(1)

5016

(2007 /12 - 1)

12

pH

Total Counts

(/ %2)

()

4'6-diamidino-2- DAPI

390

DNA

phenylindol

/

25

Epifluorescence microscope (EFM)

5 mg.l⁻¹ DAPI

Porter & Feig 1980, Schallenberg *et al.*, 1989, Donegan *et al.*, 1991,]
Baleux & Monfort, 1992, Kepner & Pratt 1994, Epstein & Rossel
: [1995, Nanna & Mark 2002

$$V = (w^2 \times \pi/4) \times (l - w) + (\pi \times w^{3/6})$$

l (μm^3) V)

Fry 1988, Psenner 1993, Haldal *et al.*] (μm) W (μm)
1994, Koch *et al.*, 1996, Posch *et al.*, 1997, Robertson *et al.*, 1998,
400 [Bernard *et al.*, 2000

0.75 1

0.33 μm^3

fg) C) $C = 120 \times V^{0.72}$:

Norland, 1993, Robertson *et al.*] (V (of C per cell
54.01 fgC.cell⁻¹ [1998, Posch *et al.*, 2001
) viable counts
()

nutrient agar

pseudomonas agar base, Actinomycete isolated agar, salmonella
Shigella agar, eosin methylene blue agar, bacillus selective agar

colony forming units (CFU).ml⁻¹ /

Greenberg *et al.*, 1992, Wintzingerode *et al.*]. 37 30 25
1997, Denisova *et al.*, 1999, Schauer *et al.*, 2000, Gaidos *et al.*, 2004,
Kemp and Aller, 2004, Koizumi *et al.*, 2004, Lysnes, *et al.*, 2004,
.[David C. Sigee, 2005.

Physicochemical characteristics**:Temperature**

4

24.4

.1

4.5

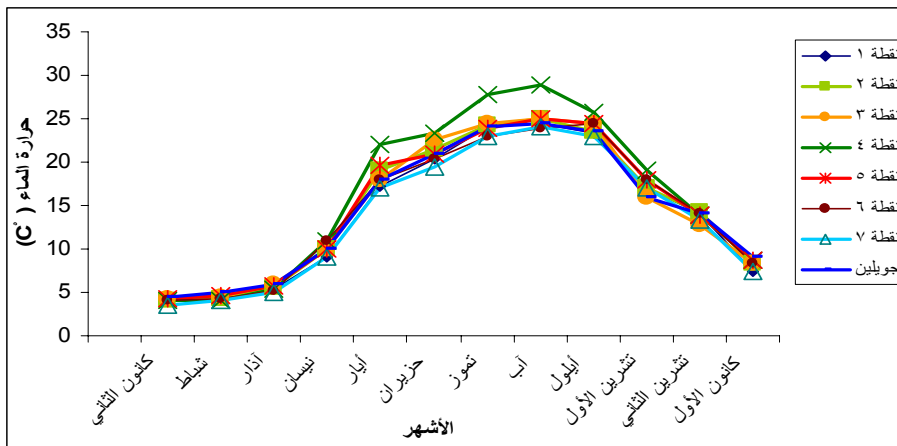
28

Worm *et al.*,]

(2)

[2001, David C. Sigeo, 2005, Lindstrom *et al.*, 2005

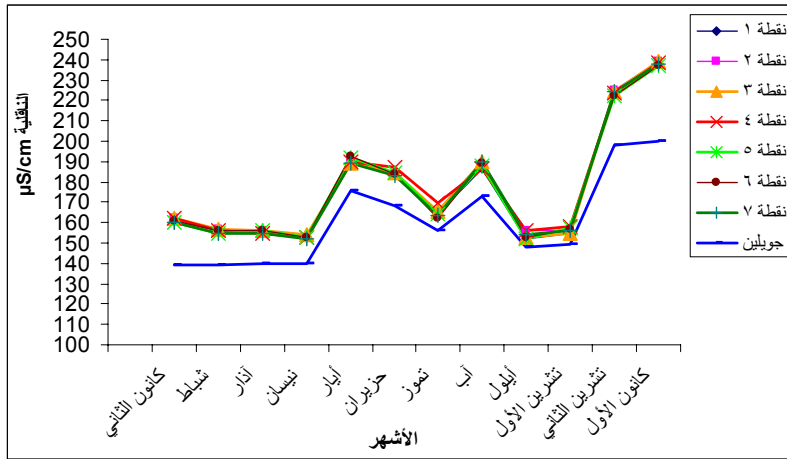
4



(2)

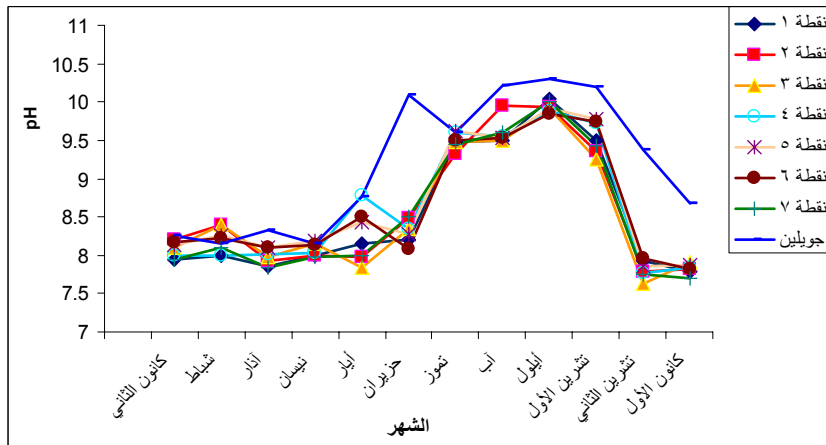
:Electrical conductivity (EC)**.2** $\mu\text{S/cm}200$ $\mu\text{S/cm}139$ $\mu\text{S/cm}239.5$ $\mu\text{S/cm}152$

(3)



(3)

8.15 :pH 3
 10.04 7.63 10.22
 pH 4



pH (4)

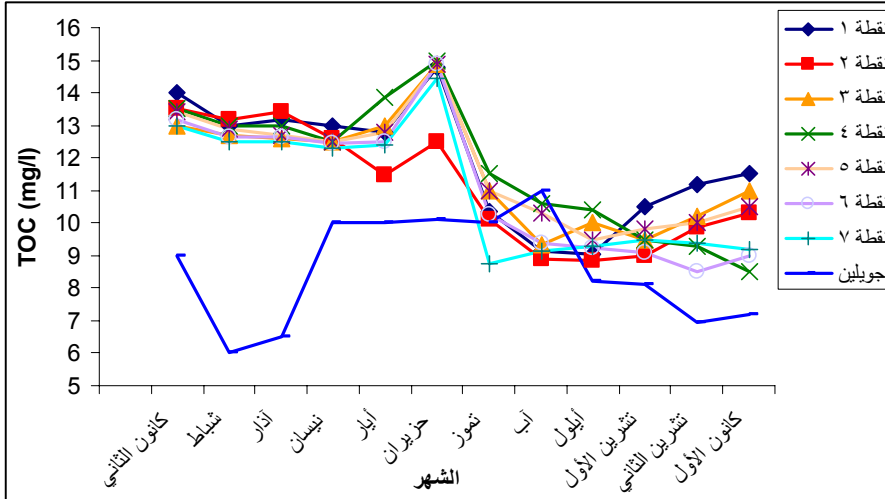
:Total Organic Carbon (TOC) .4

/ 11 / 6
/ 15 / 8.75

Goldman *et al.*, 1996, Pernthaler *et al.*, 1998, Crump, 2003, Hullar *et*]

(5) [*al.*, 2006, Newton *et al.*, 2006

TOC



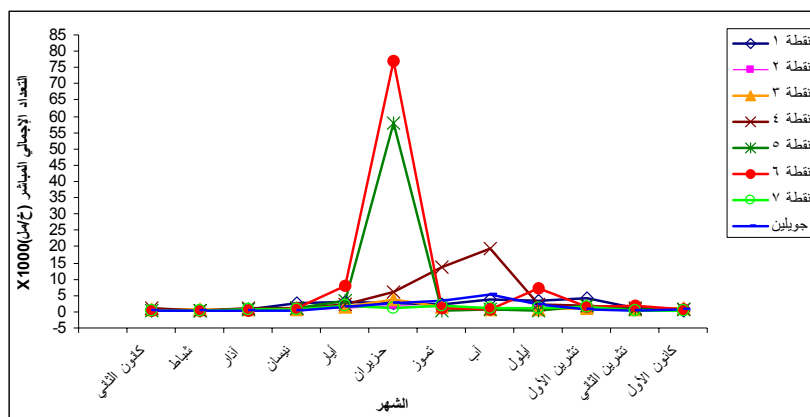
(TOC) (5)

:Total Count

$$\left(\frac{\quad}{\quad} \right)^3 10 \times 77 \quad \left(\frac{\quad}{\quad} \right)^3 10 \times 0.201$$

$$\left(\frac{\quad}{\quad} \right)^3 10 \times 5.33 \quad \left(\frac{\quad}{\quad} \right)^3 10 \times 0.212$$

(6)



(6)

:Viable Counts

[David C. Sigeer, 2005]

$$0.041 \times 10^3 (\text{CFU}).\text{ml}^{-1}$$

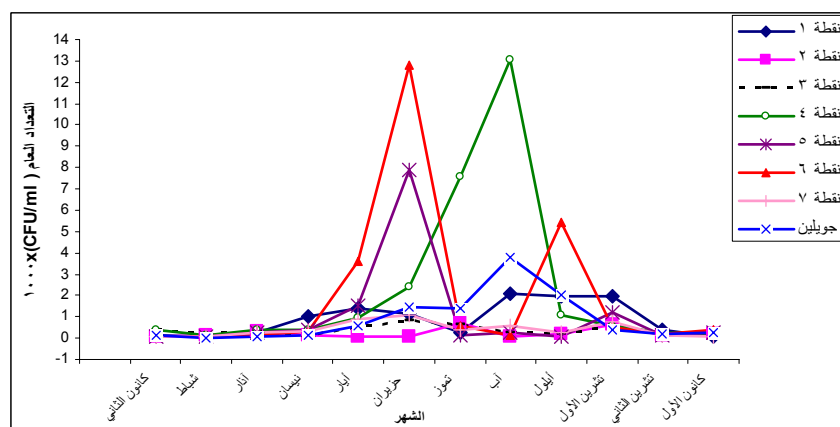
nutrient agar

$$13.040 \times 10^3 (\text{CFU}).\text{ml}^{-1}$$

$$3.767 \times 10^3 (\text{CFU}).\text{ml}^{-1}$$

$$0.035 \times 10^3 (\text{CFU}).\text{ml}^{-1}$$

(7)

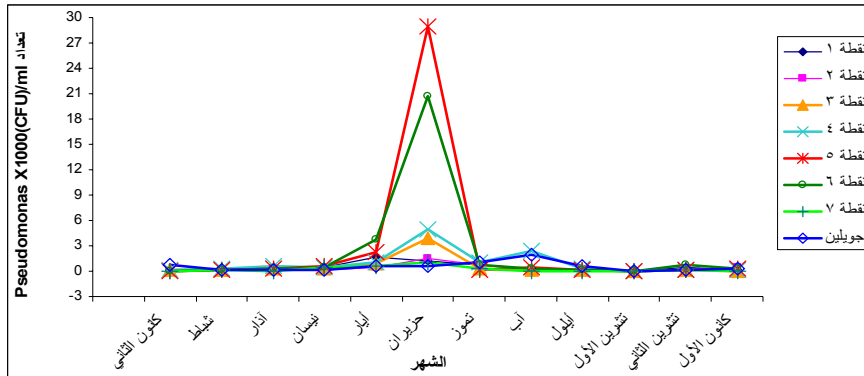


(7)

pseudomonas 2×10^3 (CFU). ml⁻¹ *Pseudomonas* .1
 29×10^3 (CFU). ml⁻¹ 0.04×10^3 (CFU). ml⁻¹
 TOC 0.018×10^3 (CFU). ml⁻¹

8

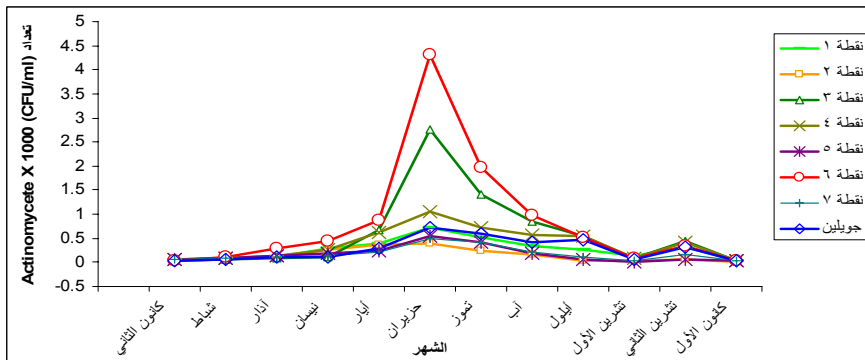
pseudomonas



pseudomonas (8)

Actinomycetes 0.72×10^3 (CFU). ml⁻¹ *Actinomycetes* .2
 0.018×10^3 (CFU). ml⁻¹ 0.031×10^3 (CFU). ml⁻¹
 9 4.3×10^3 (CFU). ml⁻¹

Actinomycetes



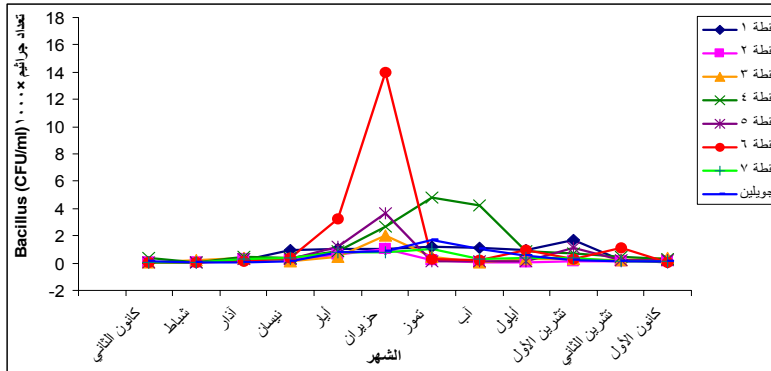
Actinomycetes (9)

Bacillus

1.68×10^3 (CFU). ml⁻¹
 14×10^3 (CFU). ml⁻¹
Bacillus

Bacillus

0.046×10^3 (CFU). ml⁻¹
 0.03×10^3 (CFU). ml⁻¹
(10)



Bacillus (10)

Total

0.312×10^3 (CFU). ml⁻¹

Total coliform

0 (CFU). ml⁻¹

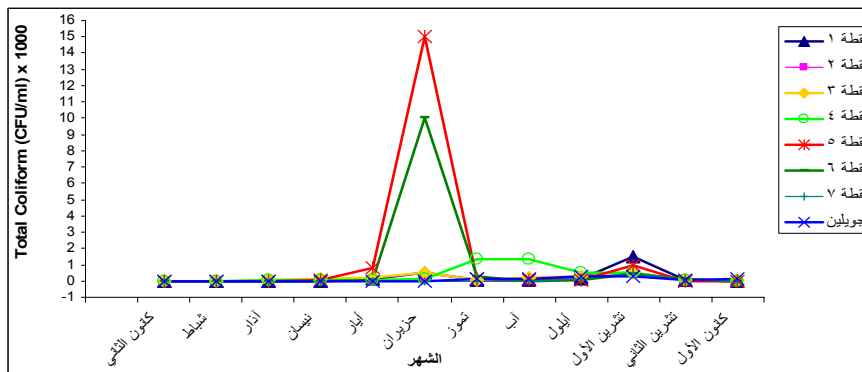
.4

coliform

0 (CFU). ml⁻¹

15×10^3 (CFU). ml⁻¹

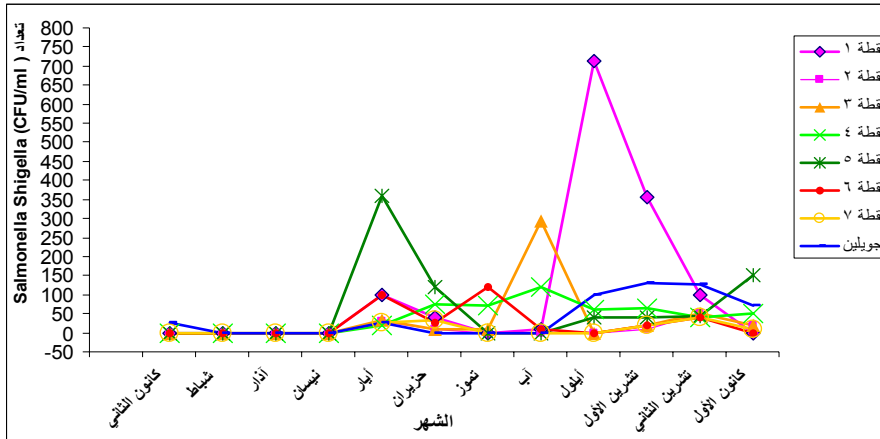
()
.Total coliform (11)



.Total coliform (11)

Salmonella-Shigella .5

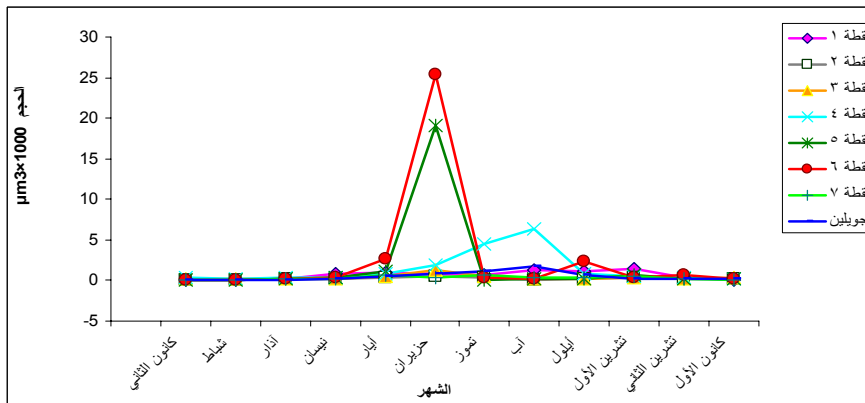
0 (CFU). ml⁻¹ Salmonella-Shigella
 0 (CFU). ml⁻¹ Salmonella-Shigella
 715(CFU). ml⁻¹ -
 130(CFU). ml⁻¹ -
 .Salmonella-Shigella



.Salmonella-Shigella (12)

$$\frac{(\mu\text{m}^3)^3 10 \times 25.41}{(\mu\text{m}^3)^3 10 \times 1.76} \quad \frac{(\mu\text{m}^3)^3 10 \times 0.066}{(\mu\text{m}^3)^3 10 \times 0.0699}$$

.13



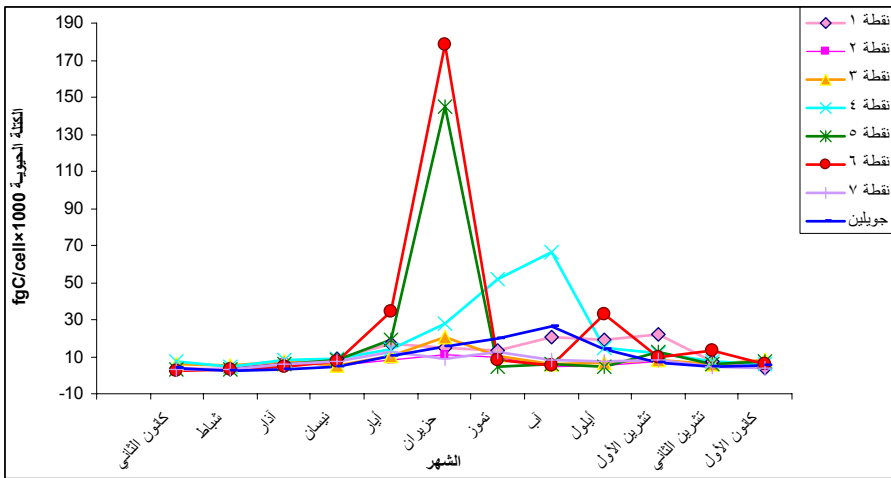
(13)

$$(fgC.cell^{-1})^3 \times 10 \times 2.55$$

$$(fgC.cell^{-1})^3 \times 10 \times 178.14$$

$$(fgC.cell^{-1})^3 \times 10 \times 26.06 \quad (fgC.cell^{-1})^3 \times 10 \times 2.55$$

.(14)



(14)

Pearson standard deviation
 one way listwise correlation
 [Kirchman *et al.*, 1982, Hughes *et al.*, 2001, Idakwo, 2004] ANOVA

		0.832	<i>Pseudomonas</i>
<i>Actinomycete</i>	0.768	<i>Bacillus</i>	
		0.717	0.396
	0.738	0.752	0.534
	0.114-	-	
<i>Pseudomonas</i>			
	15	3 2	<i>Bacillus</i>

Pseudomonas
Actinomycete *Bacillus*

:

Listwise Correlations (2)
Listwise Correlations

	Biomass	Total count	ViablecountNA	Total coliform	pseudomonas	Bacillus	Actinomycete	SS	TOC	pH	temper	EC
Biomass	1											
Total count	.991	1										
ViablecountNA	.923	.882	1									
Total coliform	.964	.982	.819	1								
pseudomonas	.966	.985	.807	.970	1							
Bacillus	.991	.974	.911	.944	.954	1						
Actinomycete	.424	.326	.552	.196	.299	.506	1					
SS	.243	.142	.389	.121	.070	.233	.386	1				
TOC	.738	.752	.534	.717	.832	.768	.396	-.114	1			
pH	.130	.043	.418	.027	-.115	.119	.307	.584	-.380	1		
temper	.529	.425	.747	.351	.303	.543	.701	.735	.054	.768	1	
EC	.066	.072	.012	.037	.108	.065	.045	.177	-.022	-.390	.031	1

Pearson Correlation (3)
Correlations^a

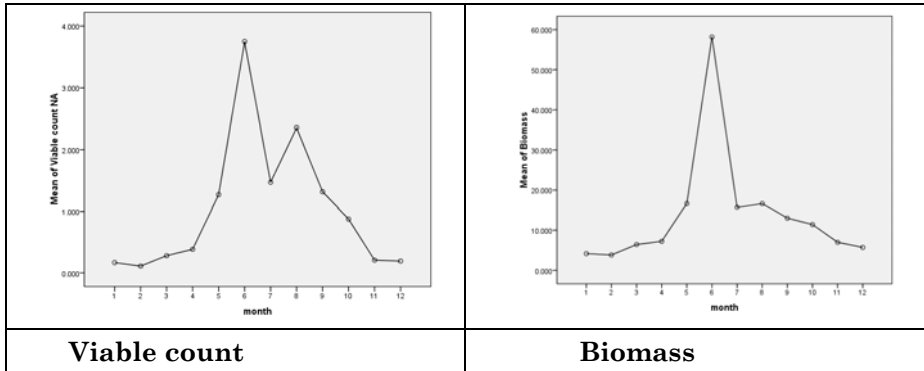
	Biomass	Total count	Viable count NA	Total coliform	pseudomonas	Bacillus	Actinomyceete	S-S	TOC	pH	temper	EC	
Biomass	Pearson Correlation	1	.991**	.923**	.964**	.966**	.991**	.424	.243	.738**	.130	.529	.066
	Sig. (2-tailed)		.000	.000	.000	.000	.000	.169	.446	.006	.686	.077	.838
	Sum of Squares and Cross-products	2.395E3	936.798	165.540	164.320	389.199	154.833	19.466	1.567E3	171.322	16.892	699.249	308.154
	Covariance	217.738	85.163	15.049	14.938	35.382	14.076	1.770	142.419	15.575	1.536	63.568	28.014
Total count	Pearson Correlation	.991**	1	.882**	.982**	.985**	.974**	.326	.142	.752**	.043	.425	.072
	Sig. (2-tailed)	.000		.000	.000	.000	.000	.301	.660	.005	.896	.168	.825
	Sum of Squares and Cross-products	936.798	373.204	62.449	66.074	156.723	60.057	5.909	360.935	68.941	2.175	222.032	132.192
	Covariance	85.163	33.928	5.677	6.007	14.248	5.460	.537	32.812	6.267	.198	20.185	12.017
Viable count NA	Pearson Correlation	.923**	.882**	1	.819**	.807**	.911**	.552	.389	.534	.418	.747**	.012
	Sig. (2-tailed)	.000	.000		.001	.002	.000	.063	.211	.073	.176	.005	.969
	Sum of Squares and Cross-products	165.540	62.449	13.433	10.458	24.343	10.659	1.899	187.810	9.296	4.058	73.979	4.367
	Covariance	15.049	5.677	1.221	.951	2.213	.969	.173	17.074	.845	.369	6.725	.397
Total coliform	Pearson Correlation	.964**	.982**	.819**	1	.970**	.944**	.196	.121	.717**	.027	.351	.037
	Sig. (2-tailed)	.000	.000	.001		.000	.000	.542	.709	.009	.933	.263	.909
	Sum of Squares and Cross-products	164.320	66.074	10.458	12.141	27.814	10.497	.639	55.303	11.856	.253	33.062	12.272
	Covariance	14.938	6.007	.951	1.104	2.529	.954	.058	5.028	1.078	.023	3.006	1.116

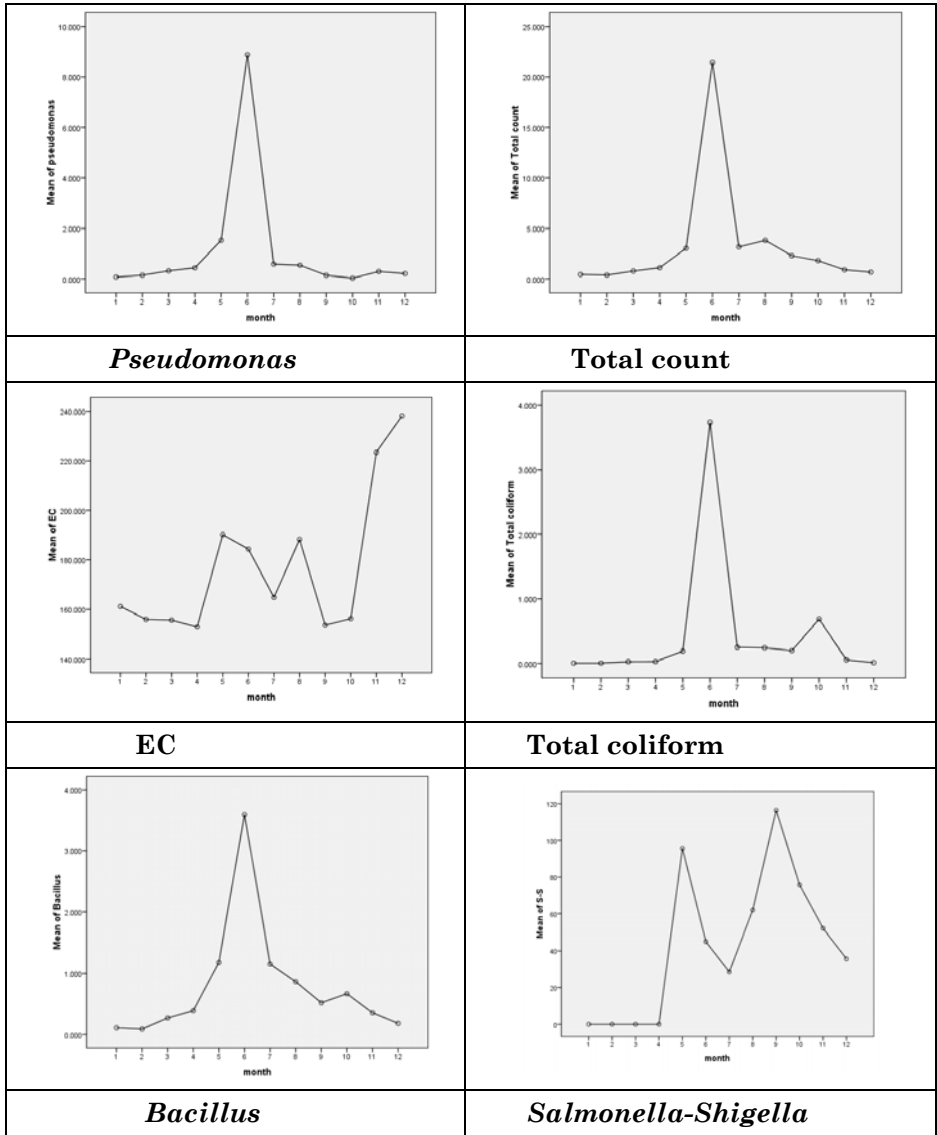
pseudomonas	Pearson Correlation	.966**	.985**	.807**	.970**	1	.954**	.299	.070	.832**	-.115-	.303	.108
	Sig. (2-tailed)	.000	.000	.002	.000		.000	.345	.828	.001	.723	.338	.739
	Sum of Squares and Cross-products	389.199	156.723	24.343	27.814	67.786	25.079	2.307	76.141	32.507	-2.502-	67.450	84.455
	Covariance	35.382	14.248	2.213	2.529	6.162	2.280	.210	6.922	2.955	-.227-	6.132	7.678
Bacillus	Pearson Correlation	.991**	.974**	.911**	.944**	.954**	1	.506	.233	.768**	.119	.543	.065
	Sig. (2-tailed)	.000	.000	.000	.000	.000		.093	.466	.004	.712	.068	.841
	Sum of Squares and Cross-products	154.833	60.057	10.659	10.497	25.079	10.189	1.514	97.839	11.631	1.010	46.835	19.824
	Covariance	14.076	5.460	.969	.954	2.280	.926	.138	8.894	1.057	.092	4.258	1.802
Actinomycete	Pearson Correlation	.424	.326	.552	.196	.299	.506	1	.386	.396	.307	.701*	.045
	Sig. (2-tailed)	.169	.301	.063	.542	.345	.093		.215	.202	.331	.011	.890
	Sum of Squares and Cross-products	19.466	5.909	1.899	.639	2.307	1.514	.879	47.643	1.763	.763	17.763	3.997
	Covariance	1.770	.537	.173	.058	.210	.138	.080	4.331	.160	.069	1.615	.363
S-S	Pearson Correlation	.243	.142	.389	.121	.070	.233	.386	1	-.114-	.584*	.735**	.177
	Sig. (2-tailed)	.446	.660	.211	.709	.828	.466	.215		.724	.046	.007	.582
	Sum of Squares and Cross-products	1.567E3	360.935	187.810	55.303	76.141	97.839	47.643	1.733E4	-71.397-	203.761	2.613E3	2.224E3
	Covariance	142.419	32.812	17.074	5.028	6.922	8.894	4.331	1.575E3	-6.491-	18.524	237.537	202.158
TOC	Pearson Correlation	.738**	.752**	.534	.717**	.832**	.768**	.396	-.114-	1	-.380-	.054	-.022-
	Sig. (2-tailed)	.006	.005	.073	.009	.001	.004	.202	.724		.223	.868	.947
	Sum of Squares and Cross-products	171.322	68.941	9.296	11.856	32.507	11.631	1.763	-71.397-	22.519	-4.779-	6.905	-9.743-
	Covariance	15.575	6.267	.845	1.078	2.955	1.057	.160	-6.491-	2.047	-.434-	.628	-.886-

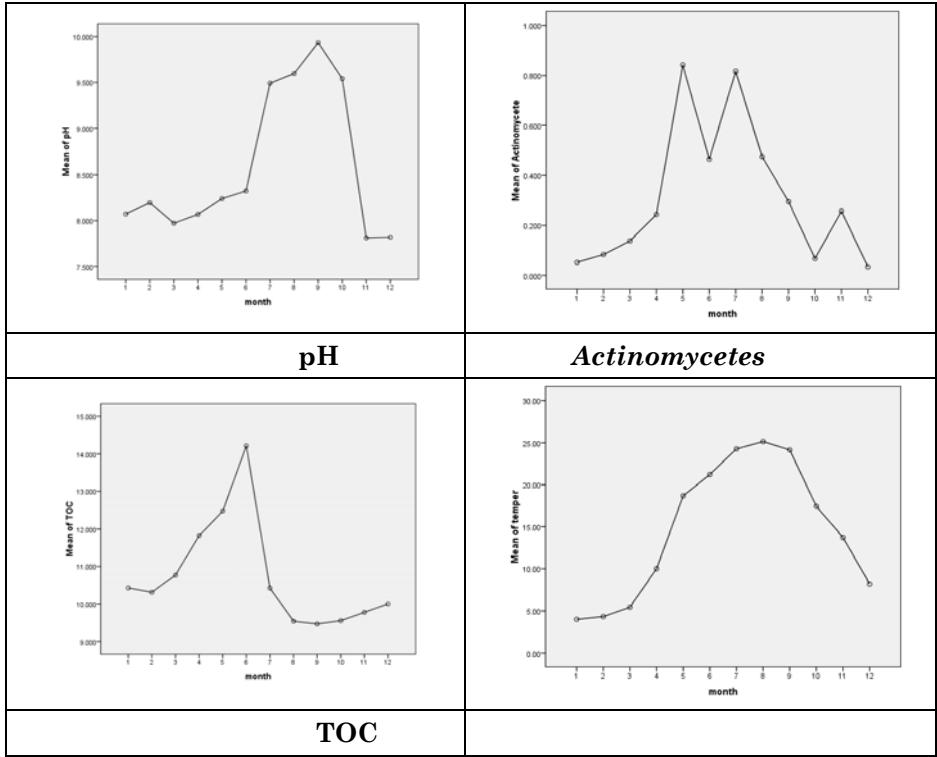
pH	Pearson Correlation	.130	.043	.418	.027	-.115-	.119	.307	.584*	-.380-	1	.768**	-.390-
	Sig. (2-tailed)	.686	.896	.176	.933	.723	.712	.331	.046	.223		.004	.211
	Sum of Squares and Cross-products	16.892	2.175	4.058	.253	-2.502-	1.010	.763	203.761	-4.779-	7.014	54.955	-98.356-
	Covariance	1.536	.198	.369	.023	-.227-	.092	.069	18.524	-.434-	.638	4.996	-8.941-
temper	Pearson Correlation	.529	.425	.747**	.351	.303	.543	.701*	.735**	.054	.768**	1	.031
	Sig. (2-tailed)	.077	.168	.005	.263	.338	.068	.011	.007	.868	.004		.923
	Sum of Squares and Cross-products	699.249	222.032	73.979	33.062	67.450	46.835	17.763	2.613E3	6.905	54.955	730.123	81.051
	Covariance	63.568	20.185	6.725	3.006	6.132	4.258	1.615	237.537	.628	4.996	66.375	7.368
EC	Pearson Correlation	.066	.072	.012	.037	.108	.065	.045	.177	-.022-	-.390-	.031	1
	Sig. (2-tailed)	.838	.825	.969	.909	.739	.841	.890	.582	.947	.211	.923	
	Sum of Squares and Cross-products	308.154	132.192	4.367	12.272	84.455	19.824	3.997	2.224E3	-9.743-	-98.356-	81.051	9.087E3
	Covariance	28.014	12.017	.397	1.116	7.678	1.802	.363	202.158	-.886-	-8.941-	7.368	826.106

one way ANOVA

(15)







REFERENCES

- [1] Baleux, B. and Monfort, P. 1992. Comparison of flow cytometry and epifluorescence microscopy for counting bacteria in aquatic ecosystems. *Cytometry* 13:188–192.
- [2] Bernard, L., C. Courties, P. Servais, M. Troussellier, M. Petit, and P. Lebaron. 2000. Relationships among bacterial cell size, productivity, and genetic diversity in aquatic environments using cell sorting and flow cytometry. *Microb. Ecol.* 40:148–158.
- [3] Epstein SE, Rossel J (1995) Enumeration of sandy sediment bacteria: search for optimal protocol. *Mar Ecol Prog Ser* 117:289–298.
- [4] Gaidos, E. J., B. D. Lanoil, T. Thorsteinsson, A. Graham, M. L. Skidmore, S. Han, T. Rust, and B. Popp. 2004. A viable microbial community in a subglacial volcanic crater lake, Iceland. *Astrobiology* 4:327–344.
- [5] Goddard, V. J., A. C. Baker, J. E. Davy, D. G. Adams, M. M. DE Ville, S. J. Thackeray, S. C. Maberly, and W. H. Wilson. 2005. Temporal distribution of viruses, bacteria and phytoplankton throughout the water column in a freshwater hypereutrophic lake. *Aquat. Microb. Ecol.* 39: 211–223.
- [6] Hewson, I., and J. A. Fuhrman. 2004. Richness and diversity of bacterioplankton species along an estuarine gradient in Moreton Bay, Australia. *Appl. Environ. Microb.* 70: 3425–3433.
- [7] Hughes, J. B., J. J. Hellmann, T. H. Ricketts, and B. J. M. Bohannan. 2001. Counting the uncountable: statistical approaches to estimating microbial diversity. *Appl. Environ. Microbiol.* 67:4399–4406.
- [8] Hullar, M. A. J., L. A. Kaplan, and D. A. Stahl. 2006. Recurring seasonal dynamics of microbial communities in stream habitats. *Appl. Environ. Microb.* 72: 713–722.
- [9] Idakwo, P Y; ABU, G O. 2004 Distribution and Statistical Analysis of Bacteria in Lake Alau in the Arid Northern Nigeria. *J. Appl. Sci. Environ. Mgt.* 2004 Vol. 8 (1) 5 – 9 JASEM ISSN 1119-8362. All rights reserved.
- [10] Kemp, P. F., and J. Y. Aller. 2004. Bacterial diversity in aquatic and other environments: what 16S rDNA libraries can tell us. *FEMS Microbiol. Ecol.* 47:161–177.
- [11] Kepner, R. L., and J. R. Pratt. 1994. Use of fluorochromes for direct enumeration of total bacteria in environmental samples: past and present. *Microbiol. Rev.* 58:603–615.
- [12] Koch, A. L., B. R. Robertson, and K. Button. 1996. Deduction of the cell volume and mass from forward scatter intensity of bacteria analyzed by flow cytometry. *J. Microbiol. Methods* 27:49–61.
- [13] Koizumi, Y., H. Kojima, and M. Fukui. 2004. Dominant microbial composition and its vertical distribution in saline meromictic Lake Kaiike (Japan) as revealed by quantitative oligonucleotide probe membrane hybridization. *Appl. Environ. Microbiol.* 70:4930–4940.
- [14] Lindstrom, E. S., M. P. Kamst-van Agterveld, and G. Zwart. 2005. Distribution of typical freshwater bacterial groups is associated with pH, temperature, and lake water retention time. *Appl. Environ. Microb.* 71: 8201–8206.

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- [15] Lysnes, K., I. H. Thorseth, B. O. Steinsbu, L. Ovreas, T. Torsvik, and R. B. Pedersen. 2004. Microbial community diversity in seafloor basalt from the arctic spreading ridges. *FEMS Microbiol. Ecol.* 50:213-230.
- [16] Magnuson, J. J., T. K. Kratz, and B. J. Benson. 2005. Long term dynamics of lakes in the landscape. Oxford Univ. Press.
- [17] Mark Skidmore, Suzanne P. Anderson, Martin Sharp, Julia Foght, and Brian D. Lanoil, 2005. Comparison of Microbial Community Compositions of Two Subglacial Environments Reveals a Possible Role for Microbes in Chemical Weathering Processes. *APPLIED AND ENVIRONMENTAL MICROBIOLOGY*, Nov. 2005, p. 6986–6997 Vol. 71, No. 110099-2240/05/\$08.00_0 doi:10.1128/AEM.71.11.6986–6997.2005. Copyright © 2005, American Society for Microbiology. All Rights Reserved.
- [18] Montagna PA (1982) Sampling design and enumeration statistics for bacteria extracted from marine sediments. *Appl Environ Microbiol* 43:1366–1372.
- [19] Nanna Buesing, Mark O. Gessner. 2002. Comparison of detachment procedures for direct counts of bacteria associated with sediment particles, plant litter and epiphytic biofilms. *AQUATIC MICROBIAL ECOLOGY* Aquat Microb Ecol, Vol. 27: 29–36, 2002.
- [20] Norland, S. 1993. The relation between biomass and volume of bacteria, p. 303–308. In P. Kemp, B. F. Sherr, E. B. Sherr, and J. J. Cole (ed.), *Handbook of methods in aquatic microbiology*. Lewis Publishers, Boca Raton, FL.
- [21] Posch, T., J. Pernthaler, A. Alfreider, and R. Psenner. 1997. Cell-specific respiratory activity of aquatic bacteria studied with the tetrazolium reduction method, cyto-clear slides, and image analysis. *Appl. Environ. Microbiol.* 63:867–873.
- [22] Posch, T., M. Loferer-Kroßbacher, G. Gao, A. Alfreider, J. Pernthaler, and R. Psenner. 2001. Precision of bacterioplankton biomass determination: a comparison of two fluorescent dyes, and of allometric and linear volume-to-carbon conversion factors. *Aquat. Microb. Ecol.* 25:55–63.
- [23] Robertson, B. R., D. K. Button, and A. L. Koch. 1998. Determination of the biomass of small bacteria and low concentrations in a mixture of species with forward light scatter measurements by flow cytometry. *Appl. Environ. Microbiol.* 64:3900–3909.
- [24] Schauer, P., Sarvala, J., K. Salonen, M. Jarvinen, E. Aro, T. Huttula, P. Kotilainen, H. Kurki, V. Langenberg, M., R. Massana, and C. Pedros-Alio. 2000. Spatial differences in bacterioplankton composition along the Catalan coast (NW Mediterranean) assessed by molecular fingerprinting. *FEMS Microbiol. Ecol.* 33:51-59.
- [25] Sigeo, D.C., 2005. *Freshwater Microbiology, biodiversity and dynamic interactions of microorganisms in aquatic environment*. University of Manchester, UK, John Wiley & Sons, LTD.
- [26] Wommack, K.E., and Colwell, R.R. 2000. Virioplankton: viruses in aquatic ecosystems. *Microbiol. Mol. Biol. Rev.* 64:69–114.
- [27] Worm, J., K. Gustavson, K. Garde, N. H. Borch, and M. Sondergaard. 2001. Functional similarity of attached and free-living bacteria during freshwater phytoplankton blooms. *Aquat. Microb. Ecol.* 25: 103–111.

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