Using Turbidity as a surrogate of viscosity in real-time bacteriological water quality assessment at a catchment point: A Case Study of Dang wells

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Abstract:
Turbidity is successful in tracking the movement of various constituents or parameter distribution through a water body plan. This soil particles, algae, suspended solids, flocs or simply turbidity cause materials (TCMs) movement, can modify the flow resistance. Such fluid (water) with complete environment mixing and the concentration after mixing characterizes flocs and particles at their surface. It is the linkage of pathogens germs with their growth to TCMs, that can help estimate bacteria existence. This paper use bacteria attachment to TCMs thorough continuous turbidity monitoring as a relevant rheological (viscosity) parameter surrogate to characterize bacteriological water quality loads in real time at the catchment point. Its innovation aimed to assess the microbiological water quality sampled from domestic water sources. The sampling is done in Adamawa region of Cameroon, from twenty (20) Wells aseptically in the lieu-dit of Dang. At each sampling point, 1000 mL is taken and immediately transported to the laboratory for analysis and in situ tests measure of turbidity is done. The detection of Coliforms bacteria was done using Micro Biological Survey (MBS) method. 1 mL of each sample was inoculated in the Coliforms MBS (Coli MBS) vial initially rehydrated with 10 mL of sterile distilled water. From the in-situ turbidity measures we estimate the viscosity thorough the model and analyzed variations of bacteria in each well corresponding to the turbidity and the corresponding viscosity.

Keywords: Water quality, viscosity, turbidity, Rheological, bacteria

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1. Introduction

Substances contained in the water are either in a dissolved form or in the form of suspended particles, and it is the latter that call for the measurement of the turbidity of the water. Fluid's turbidity can be characterized by changes in its physical, chemical and microbiological properties. These changes can have significant effects on the microbiological quality of water (drinking or any other use purpose) due to the presence of bacteria and viruses. Microbial growth in water is particularly marked on the surface of particles and inside low coherence flocs [1]. There is a coincidence between the existence of pathogenic germs and suspended matter. Wells exposure (to feacally transmitted microbial pathogens) is the primary global health risk associated with contaminated water. Therefore, assessing microbial water quality is important for managing water resources and protecting public consumption. Direct measurements of this water quality are needed to assess water safety information. More generally, water quality monitoring can help to identify contamination events, take corrective actions when needed, and close high-risk water sources. Water quality monitoring thus constitutes a crucial tool for water safety management. Generally carried out by analysis after taking a few liquid samples in laboratories[2], water quality monitoring (WQM) is expensive and tedious as a method of obtaining test results. Researches related to the design[3] of water quality measuring devices [4] on the multiplicity of existing principles and models [5](chemical and electronic), are not easily accessible in poors areas. It is certainly a challenge to select an enough accurate approach for WQM backed on a mechanical model. In this scenario, like most complex functions from the physical point of view some hypotheses are necessary. Every molecule that is suspended in a fluid influences the fluid viscosity as a result of the hydrodynamic interactions [6]. For this reason, the study of the hydrodynamic properties of a medium, and particularly a diluted colloidal suspension of soft particle [7] [8] or and hard one[9] its viscosity, should provide information on the behaviour of biological organisms, as their proliferation influences the viscosity (turbidity too) of the medium. In addition, a higher presence of bacteria in a liquid causes resistance to flow (rigidity) [10]or a change in viscosity . According to Mendoza model[9] viscosity of the suspension can be define by the viscosity of the background solvent, the volume fraction of the colloidal particles(from TCMs), and the volume fraction at maximum packing or the intrinsic viscosity of hard or soft spheres. But in presence of germs pathogens and bacteria in general water is an active fluid or suspension.

To avoid time cost of viscosimeter or Classical viscometers, such as falling ball [11], cone-and-plate[12], rotating disc[13] , and U-tube capillaries such as Ostwald[14] or Ubbelohde[15] with repetitive tests required, large volume consumptions, and complex cleaning procedure[16], which are still used to measure the various fluids in biological fields, moreover, optical technology also that enables viscosity measurements with the use of optical tweezers[17], photoacoustic[18], and fluorescence[19] methods, we have taken a stand .

We consider wells water as active suspensions and viscosities of these ecological resources are priority stakes. This requires a strict program of surveillance of the microbiological quality of water at catchment point. Because of the biological diversity of pathogens, their power and infectious form, the intermittence of their appearance in different concentrations in water environment, and the lack of standardized methods for rapid analysis new approach is needed. Their detection and quantification is difficult, furthermore, the direct monitoring of a single pathogen can only provide specific information about it and does not allow determining the presence of other potential contaminants (unless the degree of co-occurrence is established). Hence, although very promising techniques for pathogen analysis have been developed[20] , the assessment of water safety monitoring still relies on the quantification of surrogate microorganisms, which are usually associated with fecal origin, being so-called fecal

indicator bacteria (FIB). The FIB constitutes a pathogen screening tool, that allows an easy cost-effective monitoring of the microbiological quality changes of water. Unfortunately, FIB monitoring is presently based on cultural methods that give results in 24–48 h, which hinders the provision of real-time information. In that way, timely decisions could not be taken. A great deal of research has been done so as to develop fast methods for both FIB quantification[21] , and the tracking of fecal contamination sources, desirably with the ability for online turbidity monitoring.

This work presents an overview of a global pathogen indicators and quantification methods to ensure the microbiological quality of water from turbidity monitoring and its explanation from the corresponding viscosity and structured into sections. In Section 2 we at first presented the area of study. Secondly, we recall and state the physical, chemical, bacteriological and mathematical problem under consideration. In Section 3 we study the proposed model analytically and we validate its predictions by comparing them against standard experimental data. Some unsteady simulations and their relation to analytical (self-similar) solutions are presented in Section 4 as well. Finally, the main conclusions and perspectives of this study are outlined in Section 4.

2. Materials and Method

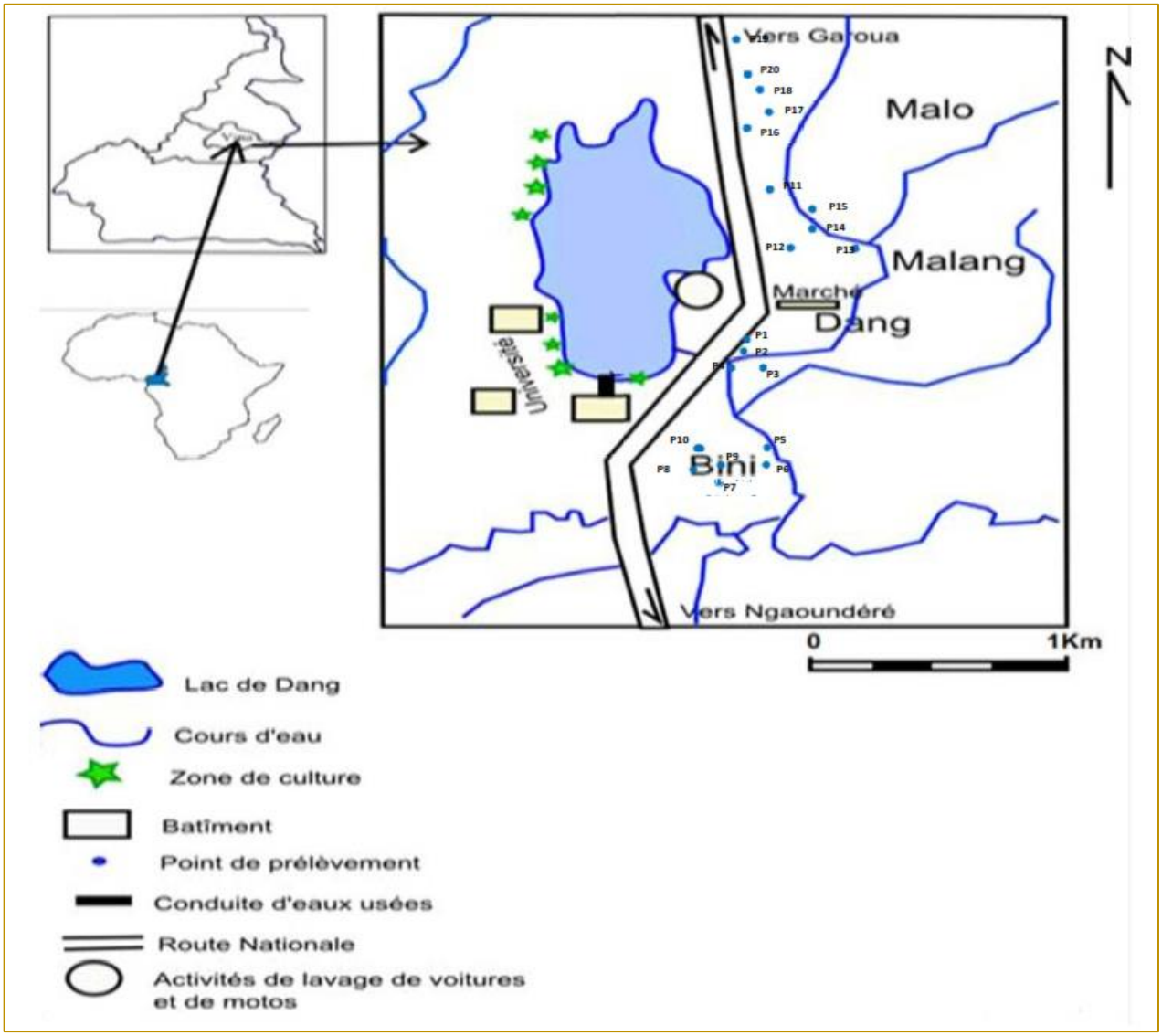

***Figure 1**: Wells localization on maps*

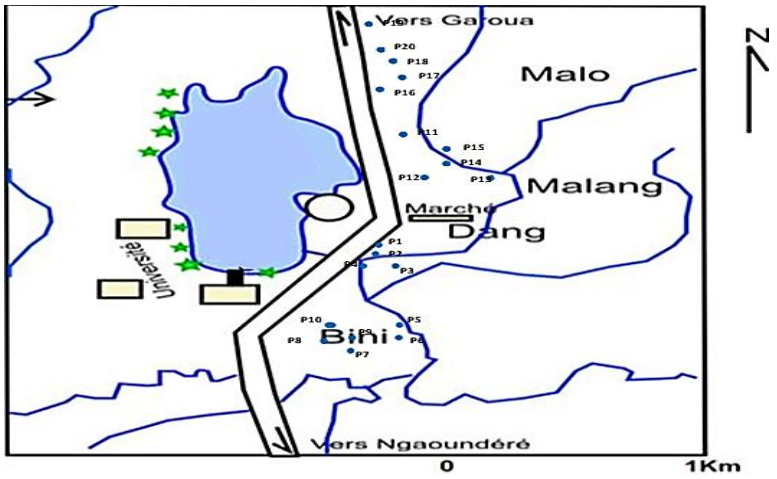

Figure 2: *Site wells distribution*

The chosen study area of Dang, located in the Adamawa Region with ferralitic soil, where twenty wells respectively W_1, W_2, W_3, W_4, W_5, W_6, W_7, W_8, W_9, W_{10}, W_{11}, W_{12}, W_{13}, W_{14}, W_{15}, W_{16}, W_{17}, W_{18}, W_{19}, W_{20}, are chosen in the university neighborhoods (Figure 1), according to their layout, their location in relation to the latrines, pastures and their importance for the population and the activities carried out in their surroundings. They were sampled weekly for three months. 1000 ml of well water per sample was taken aseptically into a sterile glass bottle, transported to the laboratory in a refrigerated chamber at 4°C and analyzed immediately to help us for physico chemical and microbiological standard analyses and mechanical microbiological analyses.

2.1. Standards analyzes

2.1.1. Physico-chemecal analyzes

All the physico-chemical characterizations of the samples were carried out according to the techniques recommended by Rodier [22]. Thus, the water temperature was taken using a thermometer graduated in 1/10 of a degree and the reading was taken after immersion for 10 minutes. The pH and electrical conductivity were measured using a PICCOLO-ATC brand pH meter and a TACUSSEL CD-60 brand resistivity meter, respectively. Suspended solids were determined by filtration, drying and weighing. Turbidity and sulphates were determined by the nephelometric method[23]. Calcium and magnesium were assayed in the samples by the complexometric method. The bicarbonates were determined from the volumetric alkalinity assay. The Mohr method described by Rodier[22] was used to determine the chloride content of the samples. The ammoniacal nitrogen concentration of the samples was determined by the indophenol blue method described by Rodier[22].

2.1.2. Microbiological analyzes

For the bacteriological analyses, a cellulose ester membrane (Millipore, Bedford, MA 01730) with a porosity of 0.45 µm was used to sterile filter 100 ml of the water sample to be analyzed or a dilution thereof using a filtration device connected to a vacuum pump[24]. The enumeration of total aerobic mesophilic flora, total and faecal coliforms, faecal streptococci, vibrios, salmonellae, sulphite-reducing Clostridium and Pseudomonas aeruginosa was performed respectively on Yeast Extract Agar (YEA) medium, Eosin and Methylene Blue (EMB), Slanetz and Bartley medium, Thiosulfate-Citrate-Bile-Sucrose(TCBS)agar, Salmonella-Shigella (SS) agar, Meat-Liver (VF) medium and cetrimide agar[25]. The backgrounds of bacteriological culture used are those of Diagnosis Pasteur (France)[26].

The formaldehyde-ether concentration technique described by has been used to find and enumerate protozoan cysts and helminth eggs[27, 28]. The results are expressed in Colony Forming Unit (CFU) per 100 ml of water for bacteria and number of cysts or of eggs per mm3 for protozoan cysts and helminth eggs.

2.2. Model analyzes

The model developed here base on the Mendoza works, encompasses environment contribution of FIB from pasturages and toilets in the studies zone. According to infiltration diffusion and other mechanisms of contamination, for ferralitic soil that depend(potential in transport) from Darcy's permeability coefficient[29].

2.2.1. Microbiological Mechanical analyzes

The earliest viscosity measurement of the bacterial culture was presented by Jacques Bronfenbrenner[30]. However, as shown recently by Leal's group [31, 32], the viscosity of a bacteria population exhibits non-intuitive alternating behaviour during the exponential growth phase, which depends strongly on the strain type. It is reported that in highly viscous bacterial mixtures, the bacterial mobility is affected and that the drag forces during their swimming are increased[33].Mechanical property of water involved in the swimming, viscosity of water depending on turbidity [9], is define from the modification of Mendoza model[7, 34] model presented below.

$$\eta(\phi) = \eta_0 \left(1 - \frac{\phi}{(1 - A_g \phi)}\right)^{-\kappa} \qquad (1)$$

Where:

$\eta(\phi)$: viscosity of the suspension (apparent viscosity)

η_0 : viscosity of the solvent at the given temperature

ϕ : turbidity

κ : intrinsic viscosity

A_g : overall asperity fitting medias constant related to the critical TCMs volume fraction given by:

$$A_g = \varpi_1 . \varpi_2 . d_{\exp} \quad (2)$$

ϖ_1: fluidity

ϖ_2: Darcy's permeability coefficient

d_{exp}: well contamination exposure index

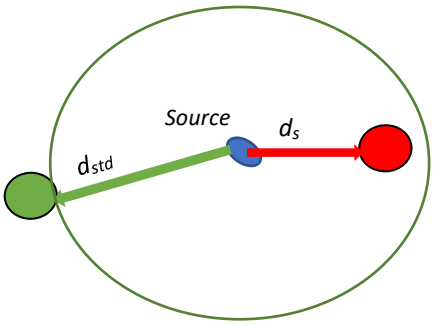

Figure 3: *safety distance according to WHO framework guideline 2017*

$$d_{\exp} = \frac{d_s}{d_{std}} \qquad (3)$$

d_s: distance from source of potential contamination

d_{std}: safe distance allowance between well and potential source of feacal germs

In this condition measuring viscosity is the core of the work. Microfluidics is the most promising technology for measuring the mechanical properties of Biosystems, since its capabilities are nowadays widely explored and described [35, 36]. In addition, the ability to measure the viscosity of chemical systems that change their shapes as a result of chemical factors [37, 38], is also attractive as fluorescence [14] methods.

Herein, we propose a new system that measures by deduction from the model and in real-time, the viscosity from a turbidity sensor data and analyses the variation of the two parameters with the bacteria rate in each well. The device we show is simple and requires only a limited laboratory equipment, while providing measurements that are based solely on the fundamental physical parameters for the flow and light absorbance of TCMs, placed at a catchment point. Hence, knowing the relation of soil porosity and with some calibration required (on overall asperity fitting medias constant related to the critical TCMs volume fraction), we can quickly calculate the viscosity of the solution.

2.2.2. Hypotheses

Water is an active suspension

ϖ_1: fluidity=1

κ : intrinsic viscosity=5/2

3. Results And Discussions

The water quality analysis done here estimates the concentration of physico chemical parameter (temperature and turbidity) and microbiological (total coliforms (TCs) and Escherichia coli, TAMF = total aerobic mesophilic flora; FC = faecal coliforms; FS = faecal streptococci; Pa=Pseudomonas aeruginosa; Cl = sulphite-reducing Clostridium; V = vibrios; S = Salmonella in CFU per 100 ml.

3.1. Experimental standard results

3.1.1. Physico-chemical parameters

Average values obtained for the main physico-chemical parameters of the Dang well water analyzed are from Table 1. It appears from this table that the temperatures measured are between 22.0°C and 24.0°C with an average of 22.64°C. The temperature values obtained, not exceeding 25°C, correspond to ambient atmospheric temperatures and indicate the opening of the aquifer system, and therefore its vulnerability to pollution.

Turbidities analyzed from wells waters varies between 0.64 (W11) and 2.41 NTU (W12), with an average of 1.16 NTU. The average value of the turbidity of these waters is lower than the French and European standards which recommend a turbidity of less than 2 NTU . This results in a clarity observed for some of the well waters of Dang which could be explained by their dilution in rainwater because the studies were carried out during the rainy season. The lowest value of suspended solids concentrations in the well waters studied is that of well W2 (0.32 mg/l), while the highest value is obtained in the case of well W13 (3.42mg/l) with an average of 1.44 mg/l. Iron concentrations fluctuate between 0.12 (W13) and 0.97mg/l (W6). This concentration differs according to the sampling points.

Table 1:*physico-chemical parameters*

Wells	T(°C)	Turbidity (NTU)	pH	SM/SS (mg/L)	X (**µs/cm**)
W_1	23	0,75	5,56	0,68	51,65
W_2	22,3	1,05	5,47	0,32	61,13
W_3	22,4	1,5	5,23	1,42	45,14
W_4	22,5	1,8	5,89	2,03	51,48
W_5	22,4	1,3	6,09	1,5	9,42
W_6	22,4	0,8	5,6	0,88	12,41
W_7	22,5	1,1	5,09	1,33	21,43
W_8	22,5	2,1	5,24	2,42	14,30
W_9	22,4	1,9	5,88	1,59	13,32
W_{10}	22,6	1,33	5,63	0,85	7,01
W_{11}	22,5	0,64	5,55	0,77	17,04
W_{12}	22,13	2,41	5,80	2,35	7,29
W_{13}	22,3	1,31	5,62	3,42	8,41
W_{14}	24	0,85	5,56	1,35	9,45
W_{15}	22	0,75	5,52	1,61	7,85
W_{16}	23,2	0,65	5,68	1,02	7,56
W_{17}	22,8	0,7	5,53	0,54	7,42
W_{18}	23,4	0,75	5,63	0,66	8,54
W_{19}	22,4	0,8	5,44	2,02	10,28
W_{20}	23,2	0,8	5,69	2,12	5,60

3.1.2. Microbiological parameters

The results of the analysis of the microbiological parameters of the water samples taken are recorded in Table 2. It shows that the total mesophilic aerobic flora (TMAF) varies from 162, 00. 10^4 to 1344,00.10^4 CFU/CFU/ 100 /100 ml (W6) ml (W14). The values obtained are higher than those set by the standards (i.e., 100 CFU/100 ml WHO, 2000) and are significantly different (W and W10, respectively. It emerges that well W10 is 5 times more contaminated with total coliforms than well W3. The count of faecal coliforms gives a lower value for well W1 (4,01.10^4 CFU/100 ml), which is higher than those set by the standards (i.e. 20 CFU/100 ml WHO, 2000). The concentration of faecal streptococci ranges from 12.00 CFU/100ml (W10) to 340.00 CFU/100ml (W14). It is higher than

the standards (20 CFU/100 ml), except for wells W3, W6 and W10.

With regard to Pseudomonas aeruginosa, only well W14 where there is an absence of this germ in 100 ml complies with the standards (WHO, 2000). Clostridium concentration sulfite-reducers of all the wells analyzed exceed the standards (1 CFU/100 ml), except for wells W3 and W15. The Vibrios counted number in these wells waters varies from 0 (W3 and W9) to 287.00 CFU/100 ml (W13).

Salmonella concentrations range from $0{,}60.10^4$ (W2) to $32{,}25.10^4$ CFU/100 ml (W19).

Vibrio concentrations are conformed to standards (0 CFU/100 ml), only with regard to wells W3 and W9, while those obtained for the Salmonella are all outside the standards (lack in 100 ml).

Table 2:*standard Microbiological parameters*

Wells	**TC**	**FC**	**FS**	**Pa**	**CI**	**V**	**S**	**TAMF**
	x10^4 **CFU**	x10^4 **CFU**	**CFU**	**CFU**	**CFU**	**CFU**	x10^4 **CFU**	x10^4 **CFU**
W_1	31,1	17,6	101,2	60,8	80,3	80,1	24,6	664
W_2	36,1	20,6	95,6	132,2	41,1	88,5	0,6	885
W_3	10,3	9,1	16,2	43,6	0,0	0,0	8,8	180
W_4	43,1	26,4	210,8	101,5	21,4	22,1	29,8	280
W_5	50,2	22,3	34,1	25,5	40,2	55,8	25,9	450
W_6	13,7	6,6	20,2	27,3	20,1	65,1	4,1	170
W_7	29,8	8,7	85,1	23,3	40,3	2,5	13,7	885
W_8	45,8	11,6	163,4	127,4	60,3	98,4	28,3	970
W_9	48,3	38,1	255,8	19,6	60,2	0,0	18,1	500
W_{10}	51,9	17,2	15,3	58,5	80,1	2,8	27,2	520
W_{11}	11,2	7,1	225,3	184,2	20,4	135,1	6,9	890
W_{12}	27,5	12,6	286,8	286,5	60,2	260,5	21,4	1150
W_{13}	24,3	12,1	325,6	84,4	50,4	287,3	30,9	1300
W_{14}	38,6	17,6	365,5	0,5	20,2	236,1	27,2	1350
W_{15}	15,6	4,6	75,52	267,6	0,0	21,1	14,2	300
W_{16}	32,1	15,5	144,6	1,2	35,5	48,4	26,7	950
W_{17}	25,6	10,8	170,3	37,4	30,4	48,5	13,4	970
W_{18}	21,2	9,6	146,6	1,6	60,5	13,2	25,7	1060
W_{19}	18,9	8,6	231,69	46,2	80,2	19,1	32,4	750
W_{20}	35,1	14,2	119,9	4,9	40,6	7,4	16,6	800

3.2 Model response

The result here concern physico-chemical, microbiological water parameters (table 3) and soil characteristics (table 4).

Tableau 3: *wells sample specific and organized data*

Wells ID	Turbidity ϕ NTU	Bacteriax 10^8 (CFU)	Viscosity η(ϕ)x10^{-4}(Pa·s)
W_2	1,05	0,024	0,002
W_7	1,1	0,024	0,014
W_5	1,3	0,014	0,128
W_{13}	1,31	0,034	0,137
W_{10}	1,33	0,016	0,15
W_3	1,5	0,516	0,266
W_4	1,8	0,937	0,468
W_9	1,9	0,014	0,523
W_8	2,1	0,026	0,622
W_{12}	2,41	0,031	0,748
W_{11}	0,64	0,023	7,13
W_{16}	0,65	0,026	7,343
W_{17}	0,7	0,025	8,404
W_{18}	0,75	0,029	8,733
W_1	0,75	0,019	8,8
W_{15}	0,75	0,86	8,942
W_{14}	0,85	0,036	8,991
W_{20}	0,8	0,022	9,041
W_6	0,8	0,465	9,05
W_{19}	0,8	0,021	9,252

Table 5: *environment and soil neighborhood parameters*

Wells	ϖ_1	ϖ_2	d_s	d_{std}	$d_{\exp}$	A_g
W_1	1	0,000036	8	15	0,54	192.10^{-7}
W_2	1	0,000036	9	15	0,60	216.10^{-7}
W_3	1	0,000036	3	15	0,20	72.10^{-7}
W_4	1	0,000036	10	15	0,67	240.10^{-7}
W_5	1	0,000036	13	15	0,87	312.10^{-7}
W_6	1	0,000036	11	15	0,74	264.10^{-7}
W_7	1	0,000036	13	15	0,87	312.10^{-7}
W_8	1	0,000036	12	15	0,80	288.10^{-7}
W_9	1	0,000036	7	15	0,47	168.10^{-7}
W_{10}	1	0,000036	6	15	0,40	144.10^{-7}
W_{11}	1	0,000036	9	15	0,60	216.10^{-7}
W_{12}	1	0,000036	11	15	0,74	264.10^{-7}
W_{13}	1	0,000036	11	15	0,74	264.10^{-7}
W_{14}	1	0,000036	6	15	0,40	144.10^{-7}
W_{15}	1	0,000036	2	15	0,14	48.10^{-7}
W_{16}	1	0,000036	1,5	15	0,10	36.10^{-7}
W_{17}	1	0,000036	0,9	15	0,06	216.10^{-7}
W_{18}	1	0,000036	3,5	15	0,24	84.10^{-7}
W_{19}	1	0,000036	8	15	0,54	192.10^{-7}
W_{20}	1	0,000036	8	15	0,54	192.10^{-7}

From the tables 3 and 4 we have the graphs given below, showing the variation of observed parameters (turbidity, viscosity and bacteria) in situ that can enable the use of turbidity as surrogate of viscosity to explain or forecast the bacteriological potentiality status of wells water. This is made possible by knowing some environmental parameters given in Table 4.

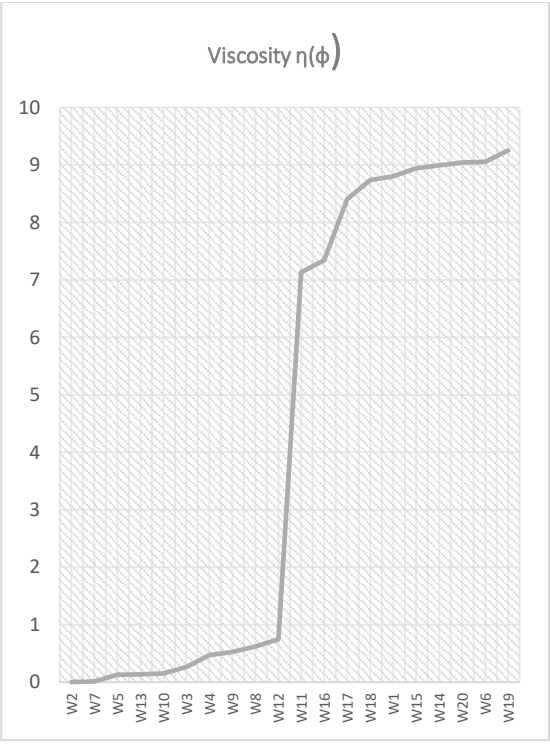

Figure 4: *variation of viscosity with turbidity*

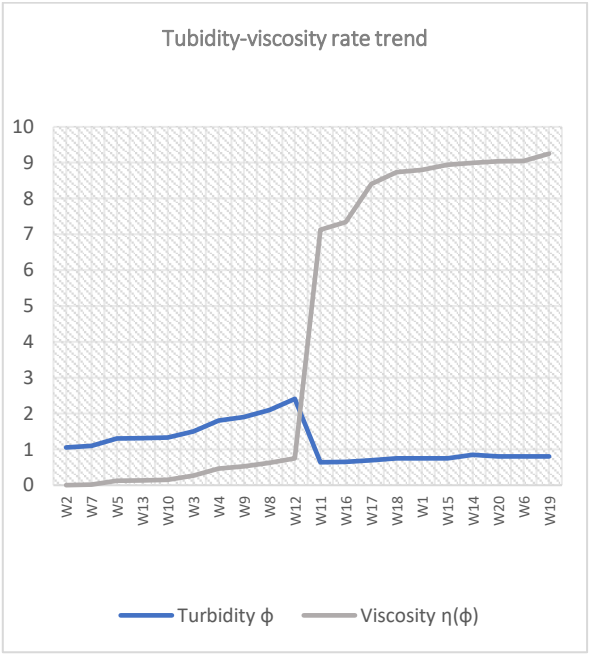

Figure 5: *Tubidity-viscosity rate trend*

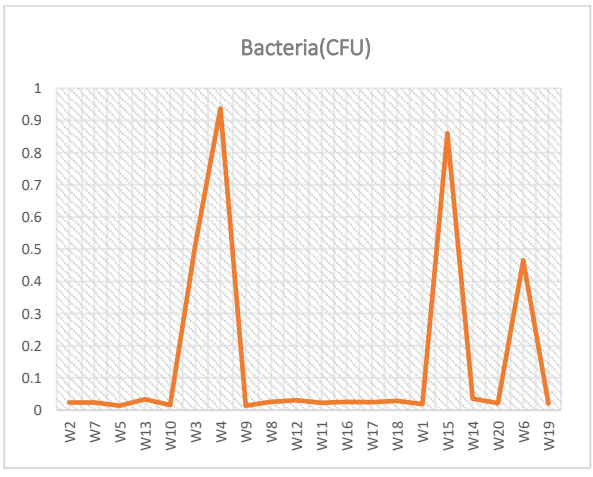

Figure 6: *Bacteria variqtion with turbidity*

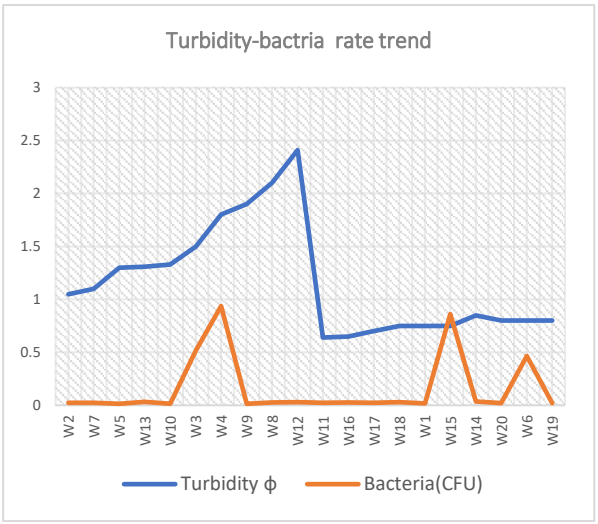

Figure 7: *turbidity-viscosity rate trend*

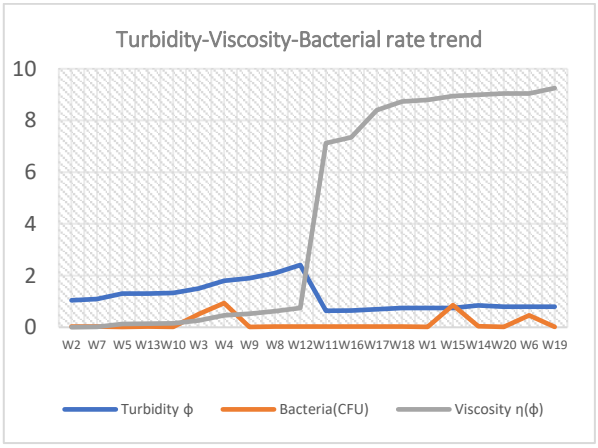

Figure 8: *Turbidity-Viscosity-Bacterial rate trend*

3.3 Discussion

The above result gives us the difference from experimental and the model response on the field. Table 3 shows that the variation of viscosity, turbidity and the number of bacteria in wells water are linked. The increase of turbidity implies the decrease of viscosity and the increase of bacteria as shown in figs.4, 5, 6. Chemical are the same in the model but bacteria are not far from the total of all the germs given in the standard experimental.

4. Conclusion

Turbidity (thorough TMCs) has shown it ability to help evaluate parameter state in wells water. In the approach presented, the relationship of turbidity to different parameters (viscosity and bacteria) introduces a practical building block that provides a simplified path to bacteriogical water quality analysis. It also consumes considerably low time.

There is a significant improvement in the speed of analysis. The observed production of data can allow monitoring of a body of water and a significant advantage for water mapping. it can be very suitable for water quality monitoring application.

We can notice the weakness of it use on the specification on the type of germs or bacteria but for global information on the water state it works.

We hope by the way started in this work to major germs (bacteria) thorough an equation or model analyses

5. References

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