LETTER TO THE EDITOR

Discovery of 20 Novel Bio-Flocculants Producers and 19 New Bacterial Strains from Three Surface Water In Ilorin, Kwara State, Nigeria

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doi.org/10.36283/PJMD9-1/024

Dear Editor,

Plummeting the burden that is increasingly posed by water related diseases is amongst the major public health goals for a developing country. The required growth and development experienced in developing countries will always weigh on this important component of earth from either industrial waste, sewage or domestic waste. A general estimate from WHO global evidence synthesis on water related complications and diseases posits that about 94% could be preventable through environmental modification and application of simple techniques to treat water[1,2]. Amongst other explored purification protocols, flocculation and chlorination as a chemical process has been linked to few health conditions after long time of exposure[3]. This has been largely adduced to the synthetic source and thus the need to explore flocculants of biological origin that can effectively purify water and presents little or no health risk. Surface water, which is often categorized as harbor of large numbers of microorganisms amongst other characteristics was, explored for the presence of bacteria flocculants producers from three surface water in Ilorin, Kwara State in Nigeria.

Water samples were collected with a sterile bottle in duplicate from Asa, Agba and Oyun river of Ilorin metropolis. The samples were respectively inoculated on pre-labelled Nutrient agar plates for isolation and sub-culturing to obtain pure isolate. Biochemical and morphological characteristics were employed for preliminary screening and identification following standard microbiological protocols[4]. Each isolate was exposed to fermentation medium, incubated for 7 days and centrifuged to obtain cell free supernatants, which was used to assay for bio-flocculant production determined from the flocculating activity in kaolin clay suspension[5]. Furthermore, to optimize the production of the bio-flocculants, the fermentation medium was varied across different carbon source (glucose, lactose and starch), and cation source ($FeSO_4$, KCl and $CaCl_2$) at different pH (2 to 12). The flocculants producing bacterium was processed for molecular analysis and 16S rRNA sequence.

Amongst others, the result yielded twenty bio-flocculants producing bacteria that had not been previously reported to possess such characteristic. Furthermore, the 16S rRNA sequence analysis revealed that nineteen out of the twenty bio-flocculants producers were new bacteria strains not existing in the world genomic bank database. Table 1 shows the respective names of the bio-flocculants producers and the assigned accession numbers by the National Center for Biotechnology Information (NCBI). The table further shows the range of the flocculating activity of each organism recorded across different fermentation culture conditions. Most of the identified organisms are from the genus of enteric bacteria and this can be adduced to the nature of the water source been an open water that is also characterized with several domestic and anthropogenic activities at the surroundings.

The flocculating activity was noticed to be as high as 99.50% with *Aeromonas caviae* MTK12 and conversely as low as -67.94% with *Pseudomonas aeruginosa* MTK10. The organisms with highly significant activities were noticed to be expressed with glucose and lactose carbon source with $CaCl_2$ as cation source. *Raoultella ornithinolytica* MTK04, which was not a new strain, had an activity of 77.71 to 25.95% but this is the first report on its flocculant production ability. Conclusively, glucose and lactose revealed to be the most supporting carbon source in comparison to starch while the most supportive cation source ranged from $CaCl_2$ to KCl and $FeSO_4$. The recorded flocculating rate offers harmless flocculant as an alternative treatment strategy, which can be adopted, optimized and commercially synthesized for incorporation into treatment regimen.

Table 1: Bio-flocculent producers and the Accession Numbers.

Number	Identification	Accession Number	Flocculating Activity (Highest - Lowest) %
1	*Pseudomonas otitidis* MTK01	MK263227	92.00 to 23.67
2	*Aeromonas caviea* MTK02	MK2 63228	82.65 to -14.50
3	*Providencia alcalifaciens* MTK03	MK263229	88.60 to 45.50
4	*Providencia* sp MTK05	MK263230	83.90 to -2.00
5	*Alcaligenes* sp. MTK06	MK263231	90.00 to 13.40
6	*Klebsiella pneumoniae* MTK07	MK263232	80.30 to 38.85
7	*Klebsiella sp.* MTK08	MK263233	78.29 to -54.50
8	*Comamonas aquatica* MTK09	MK288112	74.49 to13.44
9	*Pseudomonas aeruginosa* MTK10	MK288113	69.65 to -67.94
10	*Aeromonas* sp. MTK11	MK288114	88.30 to 6.80
11	*Aeromonas caviae* MTK12	MK288115	99.50 to 27.80
12	*Pseudomonas* sp. MTK13	MK288116	75.30 to 15.00
13	*Aeromonas veronii* MTK14	MK288117	89.00 to -6.30
14	*Aeromonas* sp. MTK15	MK288118	86.36 to -34.96
15	*Lysinibacillus sphaericus* MTK16	MK288119	81.96 to14.20
16	*Pseudomonas sp.* MTK17	MK288120	65.69 to14.51
17	*Aeromonas veronii* MTK18	MK288121	73.00 to18.20
18	*Aeromonas sp.* MTK19	MK288122	86.00 to -11.00
19	*Lysinibacillus sphaericus* MTK20	MK288123	98.00 to -18.00
20	*Raoultella ornithinolytica* MTK04	ASM36742v1	77.71 to 25.95

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ACKNOWLEDGEMENTS

We appreciate the support of the Institute of Molecular Science and Biotechnology and the department of Microbiology, University of Ilorin, Ilorin, Kwara state, Nigeria.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

AUTHORS' CONTRIBUTIONS

OMK was involved in the design of the study, collection and analysis of samples and submission to genbank. AAA was involved in the design of the study and submission to genbank

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