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Annals of Biological Research, 2011, 2 (3) : 4-6
(http://scholarsresearchlibrary.com/archive.html)

Annals of Biological Research
Scholars Research Library

ISSN 0976-1233
CODEN (USA): ABRNBW

The biolog system and the gallery api20e in identifying *Aeromonas* Original Clinic

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ABSTRACT

The genus Aeromonas belong s to the family Aeromonadaceae and the class of γ-proteobacteria Harf-Monteil and Monteil, (2007). It includes 17 species distributed. Aeromonas species are widely distributed in aquatic environments; in freshwater and wastewater. They are also detected in various foods.

Key words: Aeromonas, Clinical, Biolog, Api20.

INTRODUCTION

The genus *Aeromonas* belong s to the family Aeromonadaceae and the class of γ-proteobacteria Harf-Monteil and Monteil, (2007). It includes 17 species distributed. *Aeromonas* species are widely distributed in aquatic environments(Abbey and Etang,1988 a ; Abbey and Etang, 1988b ; Nam and Joh,2007)) in freshwater (Wu *and al*.,2007)) and wastewater (Sechi *and al*.,2002). They are also detected in various foods (Clity *and al*., 2003).

The three species of *Aeromonas* clinical relevance and causing more than 85% of human infections are: *Aeromonas hydrophila*, *Aeromonas caviae* and *Aeromonas veronii bv sobria* (Harf-Monteil and Monteil, 2007; Janda, 1991; Janda and Abbott, 1998).

Due to the complexity of identifying what kind of bacteria, our study focused on the biochemical identification of 108 strains of clinical origin collected through the collaboration of the College of Bacteriology Virology and Hospital Hygiene, which brings together many hospitals in France. This identification is based on a new system: The system ID Omnilog (BIOLOG, Hayward CA, USA).

MATERIALS AND METHODS

After cultivation and storage of strains, they were subcultured twice in succession to obtain a pure culture. The protocol was carried out as specified by the supplier "organic" by the laboratory Chemunex AES (Bruz, France). The BIOLOG system relies on the ability of a strain to metabolize each substrate. This ability is measured by the presence or absence of a violet color over time. This coloration is due to oxidation of tetrazolium violet by cellular respiration of bacteria. The result of the identification was obtained by comparing the profile of each strain with the profile of strains of each species of *Aeromonas* in this database. The results were recorded on the ID of the computer software BIOLOG and printed at the end of the confirmation of the species from the 4th hour of incubation until the 22nd hour maximum.

RESULTS AND DISCUSSION

The results of the 3 species of clinical interest are present in the table below with those obtained by the API 2oth always comparing himself with the identification by sequencing of the gene *rpoB* (beta subunit RNA polymerase).

Table 1: Comparison of three techniques for identifying clinical *Aeromonas* home

RpoB	Gallery api20E	Omnilog ID (%)
***A.hydrophila* N=37**	27 *A.hydrophila/A.caviae/A.sobria 1* 10 *A.hydrophila/A.caviae/A.sobria 2*	**28 A.hydrophila (75.68%)** 5 *A.media* 2 *A.allosaccharophila* 2 *A.enteropelogenes* 2 *A.veronii*
***A.veronii* N=35**	32 *A.hydrophila/A.caviae/A.sobria2* 2 *A.hydrophila/A.caviae/A.sobria 1* 1 *Vibrio cholerae*	**25 *A.veronii* (71.43%** 7 *A.allosaccharophila* 2 *A.media* 1 *A.sobria*
***A.caviae* N=30**	25 *A.hydrophila/A.caviae/A.sobria 1* 5 *Vibrio fluvialis*	**26 *A.caviae* (86.67%)** 4 *A.media*

All these results show that the identification of *Aeromonas* appears problematic in using the system of the gallery API20E. Indeed, the API 20E system software includes very few species of *Aeromonas* (*A.hydrophila*, *A.caviae*, *A.sobria*, *A.salmonicida subsp salmonicida*) unlike the system Omnilog. The system seems Omnilog outperform gallery API20E is what corresponds to the results of the study by Watts *and al*., 2000. Furthermore, reading is fast (4-22h), but the system remains costly for medical bacteriologylaboratory.

Compared to the molecular identification, the system is less efficient since Omnilog its database does not systematically change which corresponds to the results of studies by Watts *and al*.,2000 and De Paolis and Lippi,2008 worked on Corynebacterium and *Bacillus*,respectively.

CONCLUSION

We can conclude that the biochemical identification by the system allows the identification Omnilog the rank of the species and gives the result with a detailed data sheet on the strain identified (probability, percentage of similarity and distance with existing strains in database software and is updated after each use of the system). Despite this, the system Omnilog we have not identified a number of strains studied mostly they are of clinical interest. In addition, the system remains a Omnilog important and expensive investment for a routine laboratory.

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