



## Direct sequencing of hepatitis A virus strains isolated during an epidemic in France

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Auteur	Apair-Marchais, Véronique [1], Robertson, B H [2], Aubineau-Ferre, V [3], Le Roux, M.G. [4], Leveque, F [5], Schwartzbrod, L [6], Billaudel, S. [7]
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Résumé en anglais	Direct sequencing of PCR products was used to study the VP1 region of the hepatitis A virus (HAV) genome (position 2199 to 2356) of nine strains isolated from human stools collected during a hepatitis A epidemic (western France, 1992), three strains from environmental samples (1990, 1991, and 1992), and two HAV cell culture isolates (the French strain CF53/Lyon and strain CLF). These viruses differed from CF53/Lyon (genotype I) by between 1 and 10.3%, and results indicated the existence of two groups of strains belonging to two different subgenotypes (IA and IB). With this sequencing technique it was possible to monitor the epidemiology of HAV and study its relations.
URL de la notice	<a href="http://okina.univ-angers.fr/publications/ua7630">http://okina.univ-angers.fr/publications/ua7630</a> [29]
Lien vers le document	<a href="http://aem.asm.org/content/61/11/3977.short">http://aem.asm.org/content/61/11/3977.short</a> [30]
Autre titre	Appl. Environ. Microbiol.
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## Liens

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