

Rotavirus infections in Amerindian children from western Brazil: characterization of uncommon human G8P[6] genotype with similarity to bovine and bat strains

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INTRODUCTION

Rotavirus (RV) is an important etiologic agent of gastroenteritis in humans and animals. RV usually exhibit host species restriction, although interspecies transmission or reassortment between animals and humans viruses can occur. Sequence analysis of the genes that code for the 2 outer capsid proteins VP7 (G-type) and VP4 (P-type) is useful for gathering epidemiologic information and tracing the origin of unusual RV strains. Gastroenteritis is the leading problem in indians communities, and indigenous populations are known to maintain close interactions with animals together with the poor hygienic conditions. During national RV surveillance 2008-2011 G2P[4], G3P[8] and G8P[6] genotypes were detected in native children ≤3 years from indigenous villages in western region of Brazil. The aim of this work was to carry out sequence analysis of VP4 and VP7 proteins in order to obtain further information on the genetic relationship between human and animal RV.

MATERIAL E METHODS

This study was carried out with 19 Brazilian indian communities from the city of Dourados, State of Mato Grosso do Sul (MS) with convenient surveillance specimens (Fig 1). RV were detected using ELISA, PAGE, and genotyped by RT-PCR. The genetic relationship was performed with MEGA software version 4.0 by sequencing of selected strains: two G2 (IAL-RN191, IAL-RN71094), one G8 (IAL-RN376), two P[6] (IAL-RN376, IAL-RN377), and one G3 (IAL-R2758).



FIGURE 1. Map representing the location of the city of Dourados, Mato Grosso do Sul, Brazil.

RESULTS

IAL G2 RV sequences showed 79%-78.6% similarity compared to animal representative strains. IAL-R2758 G3 sequence share the highest nucleotide similarity to human strains (98.6-99%), however, demonstrated moderate-to-low nucleotide identity to animal strains (90-70.5%), highlighting two feline strains: Cat2 (89.5%) and BA222 (90%). IAL-RN376 G8 sequence shares a clade with bovine and human strains, displaying highest nucleotide identity to African human strains (DRC86-98%, DRC88-97.9%), following by the African bovine NGRBg8 strain (95.1%) (Fig 2). IAL-RN376 and IAL-RN377 P[6] sequences showed the highest identity to human R330 strain (99.6%). In addition, IAL P[6] sequences were also closely related to an African fruit bat RV strain (KE4852/07) (94.6%) (Fig 3).

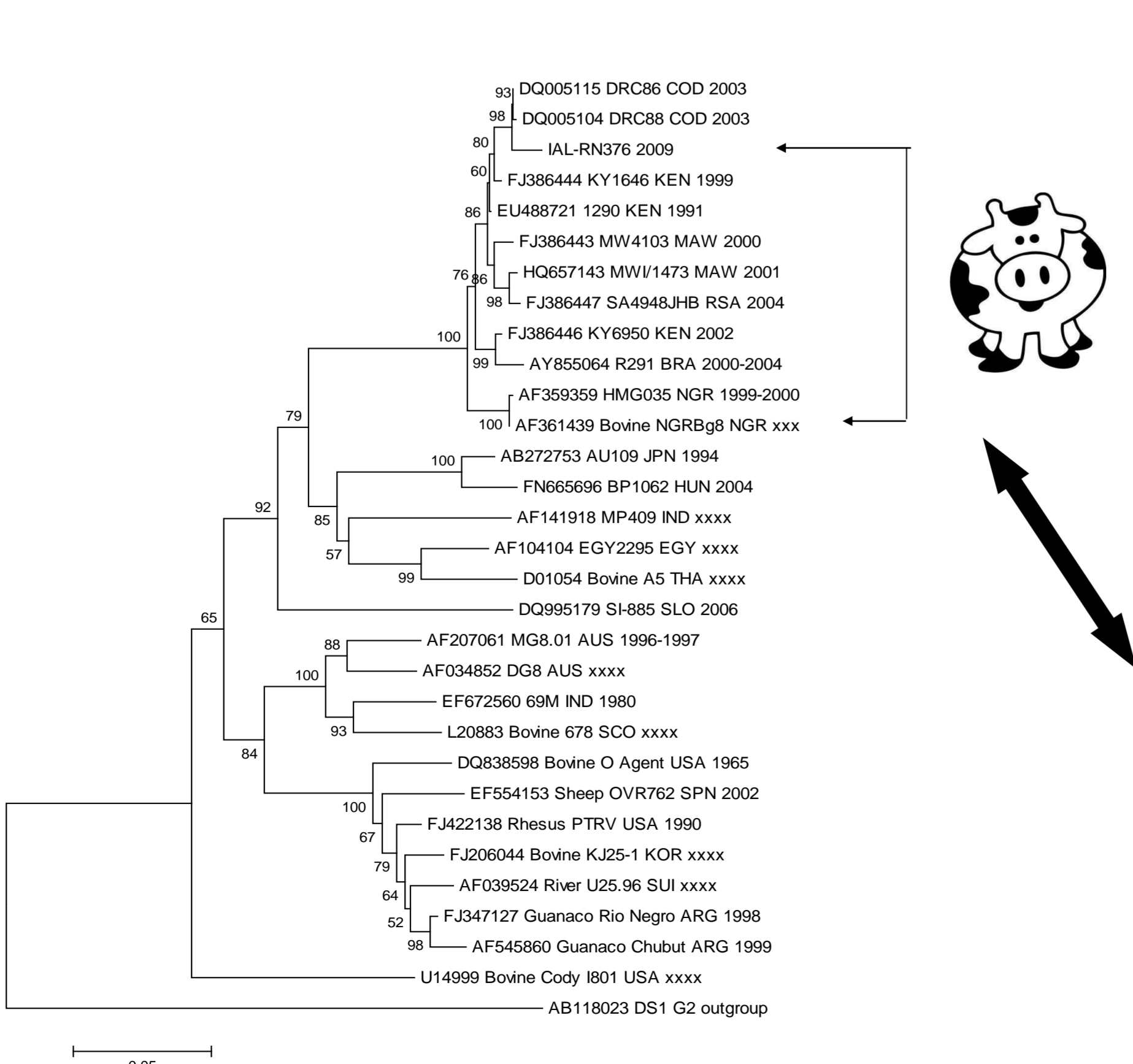


FIGURE 2. Neighbor-Joining phylogenetic tree of the partial G8 nucleotide sequence generate with MEGA 4.0 software of the IAL-RN376 strain detected in native Brazilian children ≤3 years with acute gastroenteritis in the state of Mato Grosso do Sul, Brazil.



FIGURE 3. Neighbor-Joining phylogenetic tree of the partial P[6] nucleotide sequences generate with MEGA 4.0 software of the IAL-RN376 and IAL-RN377 strains detected in native Brazilian children ≤3 years with acute gastroenteritis in the state of Mato Grosso do Sul, Brazil.

DISCUSSION

Genotype G8 strains have been reported globally in humans, and has also a wide distribution in animal species, including pigs, horses, and cattle. The origin of G8 strains in the human population has been investigated in the recent years, and interspecies transmission from a bovine source has been suggested. Although genotype P[6] can circulate reasonably efficient in the human population, recent findings strongly suggest interspecies transmission of RV P[6] strains. This study may suggests that a supposed reassortment event between bovine G8 and bat P[6] RV could have occurred in animal host(s) preceding the transmission to human host; however, on the other hand, recent findings strongly suggests that the P[6] strain had a porcine origin, and it is clear to also suggest that humans may served as a reservoir and transmitted the P[6] strain to bats, which can result in anthrozoootic transmission of RV genes. Fruit bats often live near human habitats, and there are various opportunities for bats and humans to contact each other and their respective RV. In an indigenous population, an anthrozoootic transmission, is probably fairly frequent as many of the inhabitants live in poor hygienic conditions, in close proximity with animals, and often share a common source of drinking water. Moreover, children could be more exposed to infection than adults because of their close interactions with pets together with limited hygiene habits characteristic of the age. The findings of this study reinforce the theory that there is a forceful interaction between RV of human and animals, however, simultaneous surveillance of animal (including wildlife) and human RV infections is therefore vital for the understanding of the evolution of these viruses.



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