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In-silico molecular analysis of rabies virus across regions

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Abstract Rabies is a preventable viral disease of mammals most often transmitted through the bite of a rabid animal. Almost all human deaths caused by rabies occur in Asia and Africa. There are approximately 55000 human deaths annually from rabies worldwide. The disease affects domestic and wild animals and is spread to people through close contact with infected materials usually saliva via bites and scratches. The objective of this study wasi to determine the phylogenic structure of rabies viruses across species and geographical locations. A total of 22 Rabies virus sequences from 5 species (Dog, Cat, Cow, Wolf and Fox) across 8 locations (Nigeria, India, Ghana, Pakistan, Niger, Brazil, Argentina and Texas) were obtained from the GenBank. A Neighbor-joining tree on the basis of genetic distances depicting phylogenetic relationship among Rabies viruses was constructed using the complete deletion and p-distance option using the MEGA VERSION 5 SOFTWARE. The phylogenic analysis revealeds a strong subdivision of rabies viruses by geographical location. The phylogenic groups also formed clusters associated with species from which the virus is isolated.

Keywords Rabies virus; Phylogeny; In-silico; Across regions

Introduction

The rabies virus of the Rhabdoviridae family is the major Lyssavirus responsible for majority of human and animal rabies cases. Rabies is a preventable viral disease of mammals most often transmitted through the bite of a rabid animal (CDC). The rabies virus infect the central nervous system, ultimately causing disease and death. All specie of mammals are susceptible to rabies infection but only a few specie are important as reservoirs for the disease. Almost all human deaths caused by rabies occur in Asia and Africa.There are approximately 55000 human deaths annually from rabies worldwide. The disease affect domestic and wild animals and is spread to people through close contact with infected materials usually saliva via bites and scratches (WHO).Rabies is a neglected disease of poor and vulnerable populations whose deaths are rarely reported. Under reporting of rabies also prevents mobilization of resources from the international community for the elimination of human –dog mediated rabies. The rabies viral genome is a nonsegmented single-stranded negative-sense RNA of approximately 12 kb, which encodes a nucleoprotein (N), a phosphoprotein (P), a matrix protein (M), a glycoprotein (G), and a polymerase (L) (Wunner et al., 1988). Understanding the transmission dynamics and genetic diversity of rabies provides useful information for establishing a rabies control strategy (Denduangboripant et al., 2005). As a group, the lyssaviruses are characterized by their ecological association with specific mammalian species, which act as vectors for their transmission, such that a number of phylogenetic lineages co-circulate among a range of mammalian hosts (Davis et al., 2005). Lyssaviruses are zoonotic infections that invariably spill over into non-reservoir hosts (humans, bovines, small ruminants, cats etc). Onward transmission within these dead-end hosts is not sustained, so the successful transmission of RABV in new host species is likely to represent a major adaptive challenge (Kuiken et al., 2006).The objective of this study is to determine the phylogenic structure of rabies viruses

across specie and geographical locations.

Materials and Methods

A total of 22 Rabies virus sequences from 5 species (Dog, Cat, Cow, Wolf and Fox) across 8 locations (Nigeria, India, Ghana, Pakistan, Niger, Brazil, Argentina and Texas) were obtained from the GenBank. The GenBank accession nos are FJ228677.1, FJ228678.1, FJ228681.1, FJ228683.1 (Fox): HM368163.1 (Cat), DQ105964.1 (Wolf), DQ105964.1 (Cow), EU038108.1 EU038106.1 EU038105.1 EU038103.1, HM368162.1 HM368160.1 FJ545679.1 FJ545678.1 FJ545674.1, FJ545678.1 FJ545674.1, DQ105963.1, AY654585.1 JN106463.1 AY233451.1, AY233450.1 (Dog). Sequence alignments were carried out using clusterW w (Larskin et al., 2007). A Neighbor-joining tree on the basis of genetic distances depicting phylogenetic relationship among Rabies viruses was constructed using the complete deletion and p-distance option using the MEGA VERSION 5 SOFTWARE (Tamara et al., 2011) (Figure 1).

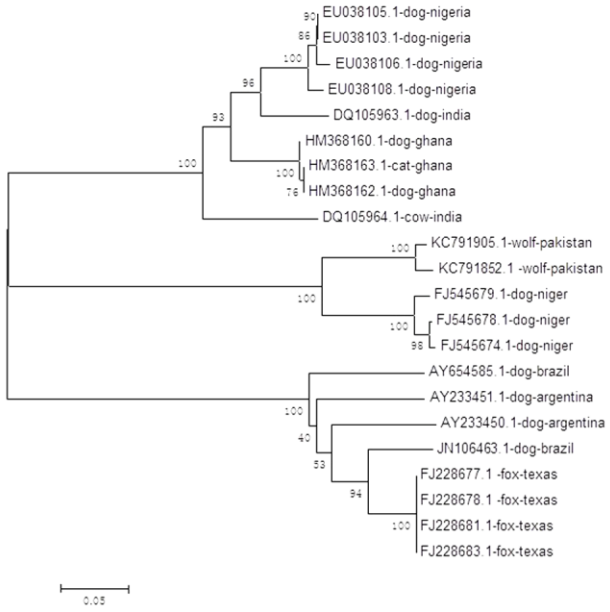

Figure 1 Phylogenetic tree derived from nucleotide sequences of rabies viruses using the Neighbor-Joining method

Results and Discussion

The phylogenic analysis reveals a strong subdivision of rabies viruses by geographical location (Table 1). The phylogenic groups also form clusters associated with species from which the virus is isolated. It has been reported that the lyssaviruses are characterized by their ecological association with specific mammalian species, which act as vectors for their transmission, such that that a number of phylogenic lineages co-circulate among a range of mammalian hosts (Davies et al., 2005). The phylogenic structure may be explain by the importance of geographical barriers to gene flow as previously demonstrated for rabies virus in Europe (Bourhy et al., 1999). The closest relationship is seen between virus isolates from a dog and a Cat both from Ghana, followed by isolates from a Dog and Cow from India (Table 2).

References

Bourhy H., Kissi B., Audry L., Smreczak M., Sadkowska-Todys M., Kulonen K., Tordo N., Zmudzinski J.F.,and Holmes E.C.,1999, Ecology and evolution of rabies virus in Europe. J Gen Virol. 80:2545-2557

Davis P.L., Holmes E.C., Larrous F., Van der Poel W.H., Tjornehoj K., Alonso W.J., andBourhy H.,2005, Phylogeography, population dynamics, and molecular evolution of European bat lyssaviruses. J Virol. 79:10487-10497
http://dx.doi.org/10.1128/JVI.79.16.10487-10497.2005

Denduangboripant J., Wacharapluesadee S., Lumlertdacha B., Ruankaew N.,and Hoonsuwan W., 2005 ,Transmission dynamics of rabies virus in Thailand: implications for disease control. BMC Infect Dis 5: 52
http://dx.doi.org/10.1186/1471-2334-5-52

Kuiken T., Holmes E.C., McCauley J., Rimmelzwaan G.F., Williams C.S.,and Grenfell B.T., 2006,Host species barriers to influenza virus infections. Science. 312:394-397
http://dx.doi.org/10.1126/science.1122818

LarkinM.A.,2007 ,ClusterW and Clusterx version. Bioinformatics, 23:2947-2948
http://dx.doi.org/10.1093/bioinformatics/btm404

Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S., 2011) ,MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Molecular Biology and Evolution 28: 2731-2739
http://dx.doi.org/10.1093/molbev/msr121

WHO Expert consultation on rabies:first report,2005

Wunner W.H., Larson J.K., Dietzschold B.,and Smith C.L., 1988 ,The molecular biology of rabies viruses. Rev Infect Dis 10 Suppl 4: S771-784
http://dx.doi.org/10.1093/clinids/10.Supplement_4.S771

Table 1 Sequences used for phylogenic analysis identified by region and specie

S/N	Accession number	Location	Host	Base pairs
1	FJ228677.1	Texas	Fox	264
2	FJ228678.1	-Texas	Fox	264
3	FJ228681.1	Texas	Fox	264
4	FJ228683.1	Texas	Fox	264
5	EU038108.1	Nigeria	Dog	1350
6	EU038106.1	Nigeria	Dog	1350
7	EU038105.1	Nigeria	Dog	1350
8	EU038103.1	Nigeria	Dog	1350
9	HM368163.1	Ghana	Cat	405
10	HM368162.1	Ghana	Dog	405
11	HM368160.1	Ghana	Dog	405
	FJ545679.1			
12	FJ545678.1	Niger	Dog	1575
13	FJ545674.1	Niger	Dog	1575
14		Niger	Dog	1575
15	KC791905.1	Wolf	Pakistan	1572
16	KC791852.1	Wolf	Pakistan	1572
17	DQ105964.1	Cow	India	446
18	DQ105963.1	Dog	India	446
19	AY654585.1	Dog	Brazil	320
20	JN106463.1	Dog	Brazil	320
21	AY233451.1	Dog	Argentina	320
22	AY233450.1	Dog	ARgentina	320

Table 2 Estimates of Evolutionary Divergence between Sequences

	Fox Texas	Dog Nigeria	Cat Ghana	Dog Ghana	Dog Niger	Wolf Pakistan	Cow India	Dog India	Dog Brazil	Dog Argentina
Fox Texas	-									
Dog Nigeria	.605 (.030)	-								
Cat Ghana	.590(.029)	.130(.020)	-							
Dog Ghana	.590(.029)	.130(.020)	.000	-						
Dog Niger	.670(.029)	.613(.029)	.613(.029)	.613(.029)	-					
Wolf Pakistan	.682(.029)	.613(.020)	.605(.029)	.605(.029)	.146(.023)	-				
Cow India	.594(030)	.165(.022)	.149(.022)	.149(.022)	.617(.029)	.609(.031)	-			
Dog India	..613(.030)	.069(.015)	.107(.019)	.107(.019)	.628(.029)	.625(.030)	.146(.021)	-		
Dog Brazil	.192(.025)	.594(.029)	.586(.029)	.586(.029)	.621(.030)	.617.030)	.605(.030)	.617(.030)	-	
Dog Argentina	.146(,022)	.613(029)	.594(.029)	.594(.029)	.678(.029)	.655(.030)	.598(.020)	.625(.029)	.150(.024)	-

Note: The number of base differences per site from between sequences are shown with Standard error estimate(s). The analysis involved 10 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 261 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 (Tamura et al., 2011)