

**WHOLE GENOME
CHARACTERIZATION OF PORCINE
ROTAVIRUS A COLLECTED IN
SOUTHERN MOZAMBIQUE, REVEALS
G9P[13] AND G4P[6] STRAINS WITH A
WA-LIKE BACKBONE**

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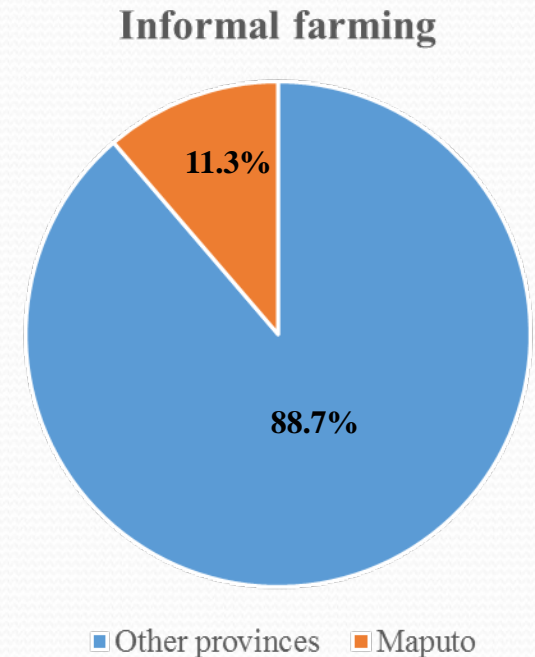
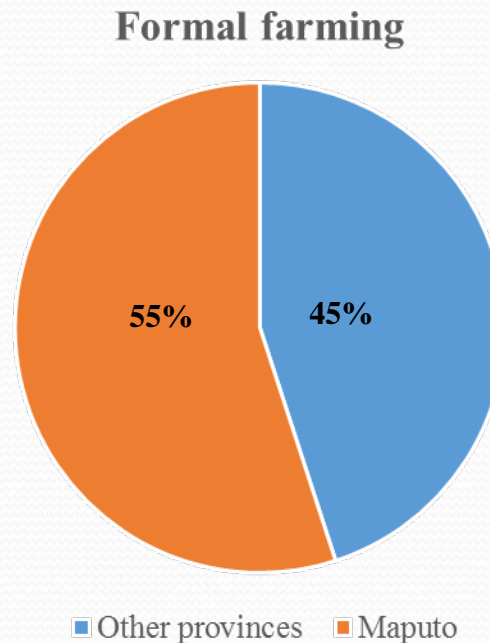
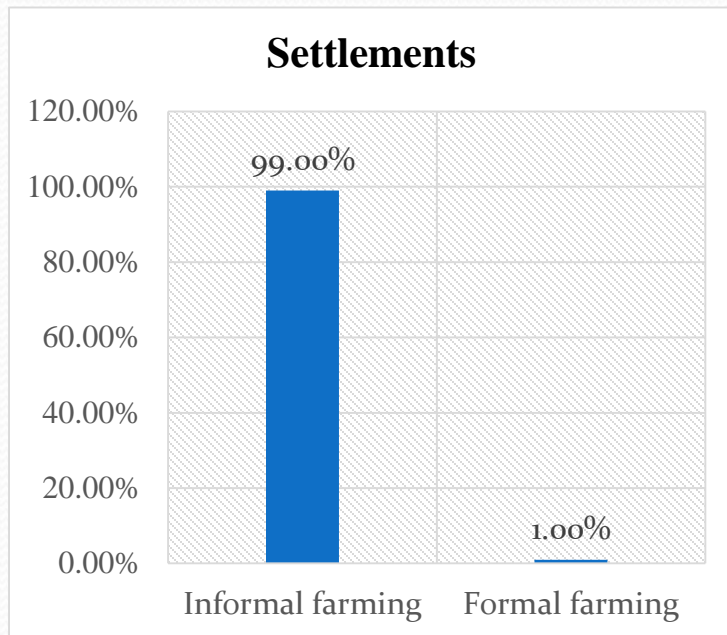
Introduction

- Rotavirus Group A (RVA) is an important cause of diarrhea in the young of many species, including pigs and humans
- Causes severe gastroenteritis which contributes to reduced production and productivity in pigs
- RVA has implications in the field of public health (reassortments)
- RVA genotypes (G3, G8, G9, P[6] and P[8]) are usually detected in children and pigs

(Amimo *et al.*, 2013; Jing *et al.*, 2018)

Motivation

- In Mozambique, only limited information is available about RVA infections in animals
- Pig is the 3rd most produced mammalian species for consumption (1,588,325 pigs in Mozambique)



- **No previous studies investigated the prevalence or genotypes of RVA in pigs.**

(Official report of the Ministry of Agriculture, 2017)
12th ARS, 2019

Aim and objectives

Aim:

- Detection and molecular characterization of porcine rotavirus A in Maputo, Southern Mozambique in 2016.

Objectives:

- Determine the prevalence of rotavirus A in pigs;
- Identify rotavirus A genotype in pigs;
- Determine phylogenetic relationships for selected rotavirus type A strains.

Methodology

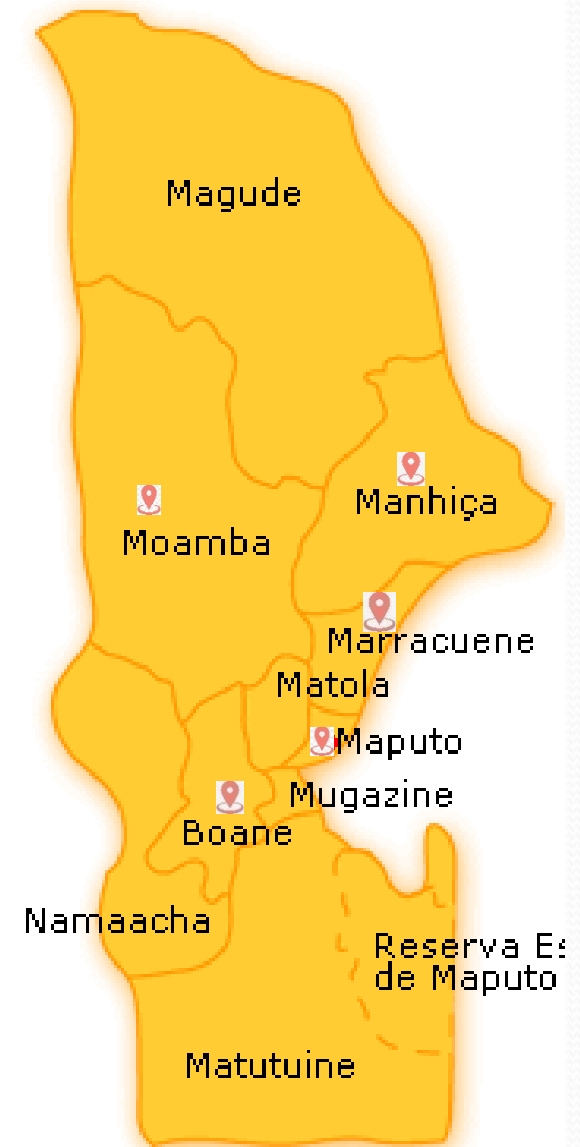
Location of the study



Southern Mozambique



Maputo province



Methodology

Lab tests

ELISA

Prospect rotavirus A kit (Oxoid, UK)



Extraction of RNA and synthesis of cDNA

Trizol (Sigma) and Maxima H Minus double-stranded cDNA kit (Thermofisher)



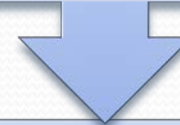
Sequencing

Illumina MiSeq platform (V300 Cartridge)

Data analysis

Data Assembly

CLC Bio Genomics Workbench (9.0)



Genotype constellation

BLAST & ViPR



Phylogenetic analyses

MEGA X

Results and discussion

Local of collection		n	Positive (ELISA)	Prevalence (%)
Formal farming settlements	Manhiça	47	8	17.02
	Marracuene	68	5	7.35
	Boane	22	0	0.00
	Moamba	20	9	45.00
	Maputo city	24	0	0.00
Subtotal		181	22	12.15
Informal farming settlements	Manhiça	68	12	17.65
	Maputo city	39	0	0.00
Subtotal		107	12	11.21
Total		288	34	11.81

**Amimo et al.,
2015 – 26.2%
East Africa**

**Amimo et al.,
2017 – 46.2%
Western Kenya**

**Collins et al.,
2010 – 6.5%
Ireland**

**Amimo et al.,
2013 – 9.4%
USA**

Results and discussion

Genome constellation

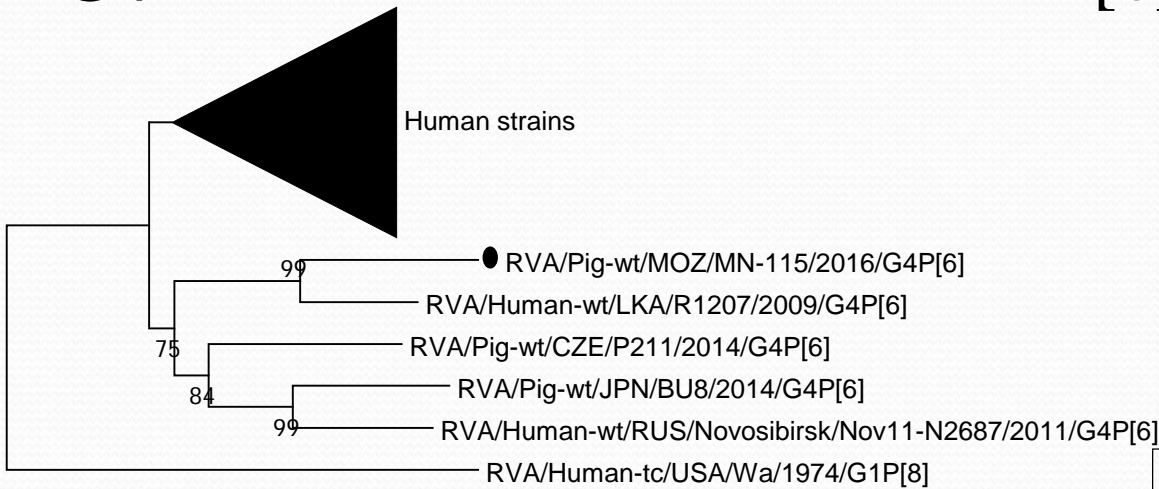
Strain	Area	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5/6
MN-115	Manhiça	G4	P[6]	I1	R1	C1	M1	A8	N1	T7	E1	H1
MB-192	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
MB-193	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
MB-194	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
MB-195	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
MB-198	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
MB-199	Moamba	G9	P[13]	I5	R1	C1	M1	A8	N1	T1	E1	H1
Gottfried		G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1
OSU		G5	P[7]	I5	R1	C1	M1	A8	N1	T1	E1	H1

Genotype constellations with wa-like backbone typical for pigs and possible reassortment with bovine RVA strains

(Bwogi *et al.*, 2017; Amimo *et al.*, 2017; Matthijssens *et al.*, 2008)

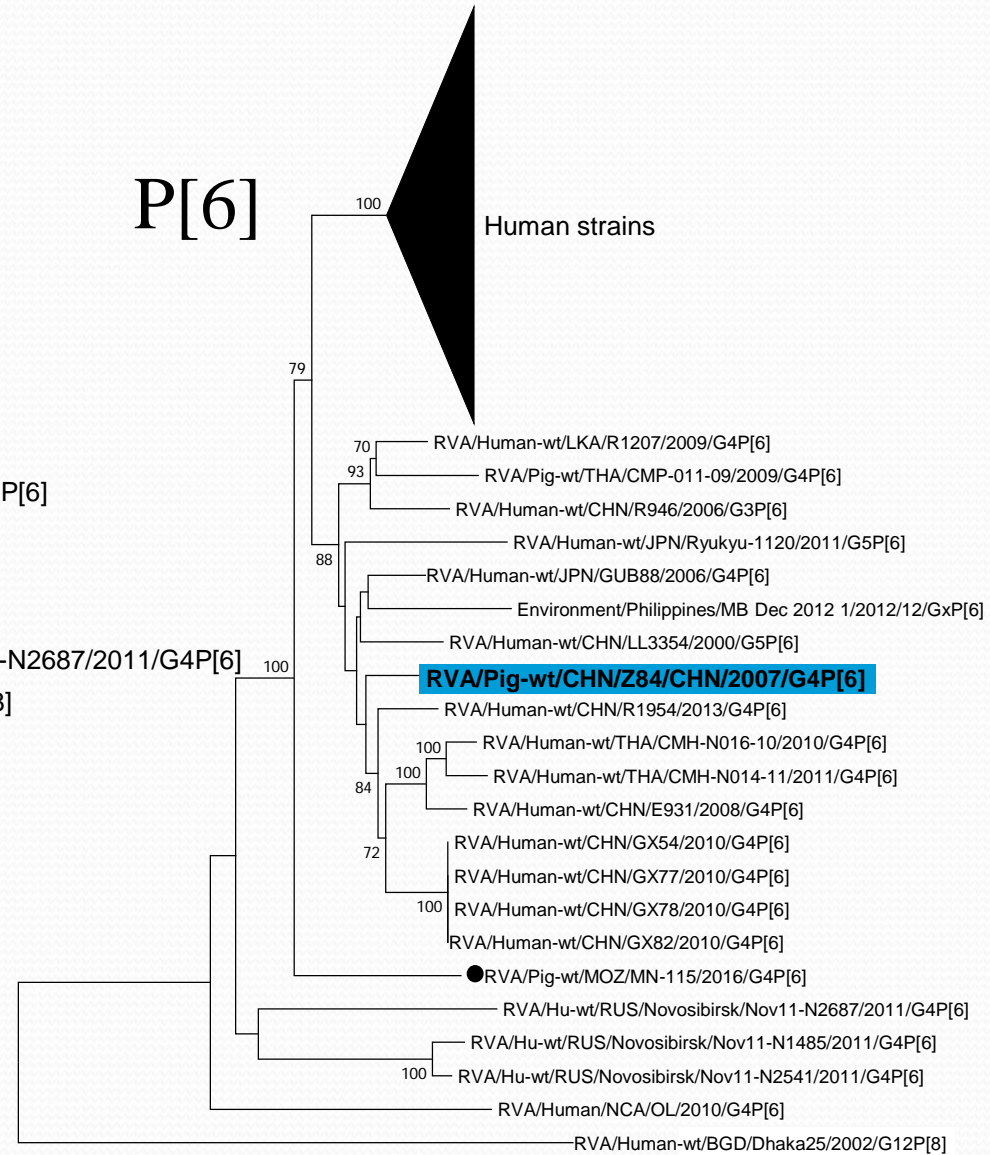
Phylogenetic analysis

G4



0.05

P[6]

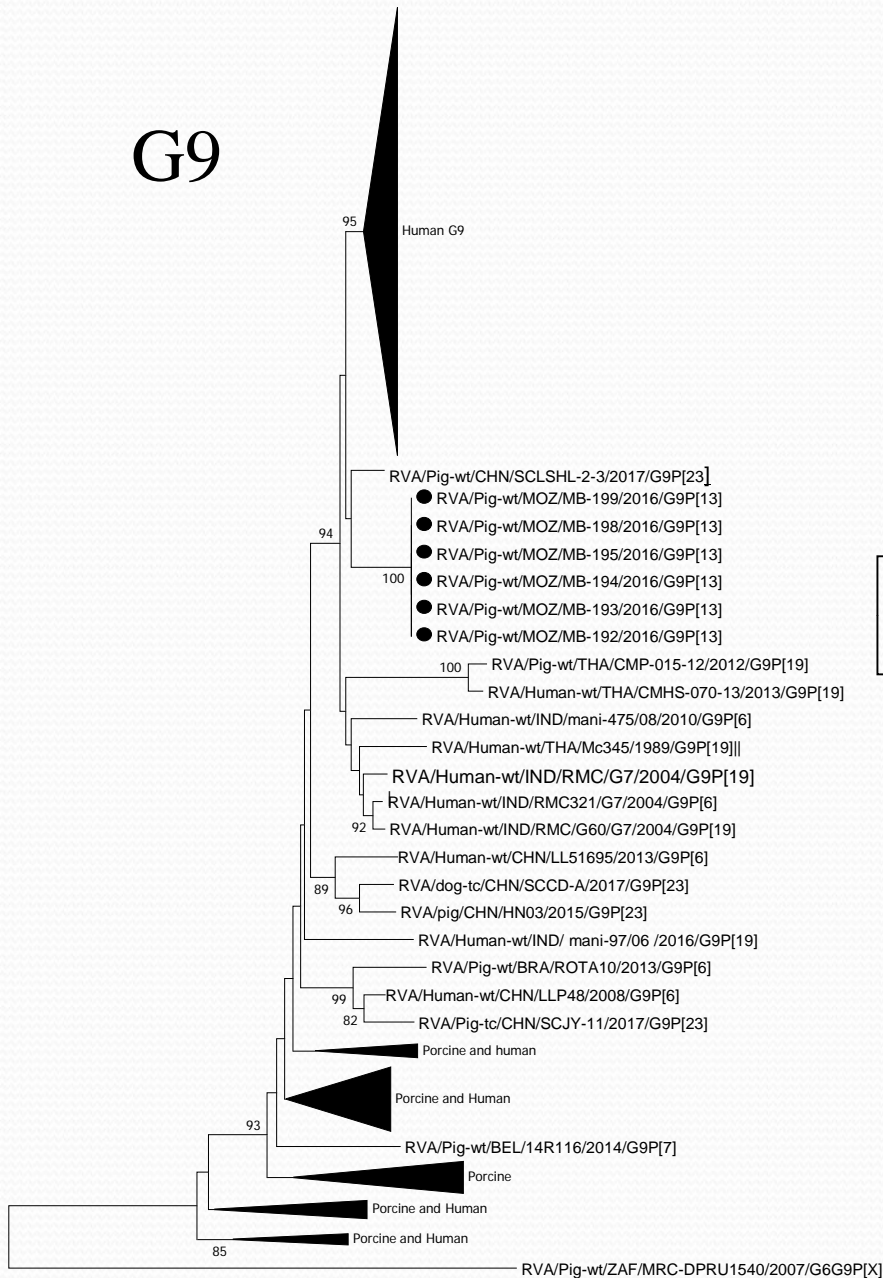


0.05

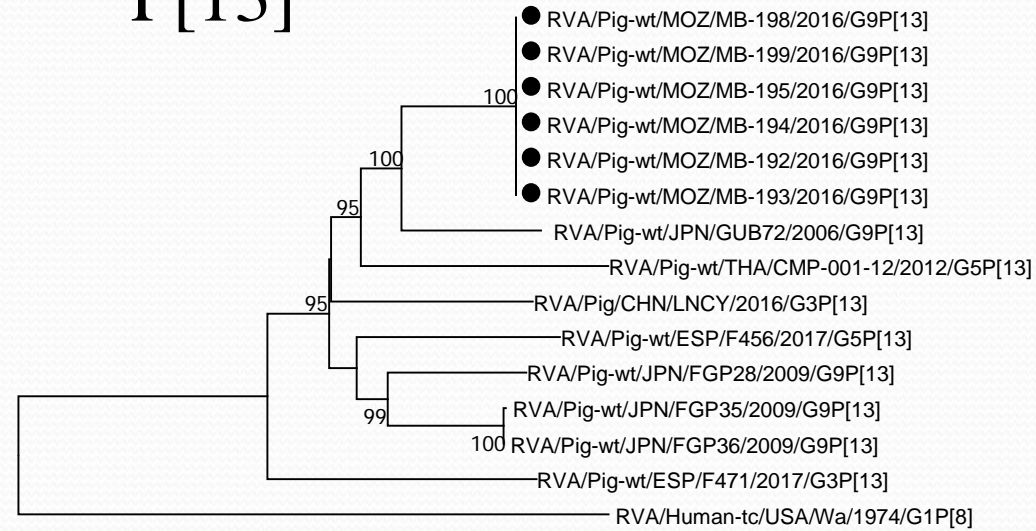
Blast results

VP7	90.9	RVA/Pig-wt/JPN/HLJ/15/1/2015/G4P[6]
VP4	92.2	RVA/Pig-wt/CHN/Z84/CHN/2007/G4P[6]

G9



P[13]



Closest relatives are Asian RVA

P[13]- Genotype mostly restricted to pigs (Amimo *et al.*, 2013)

Conclusion

- Prevalence of RVA in pigs was 11.8% and was detected in formal and informal farming in Maputo province
- A G4P[6] and six G9P[13] RVA strains were identified with porcine-like backbones
- G9P[13] preliminary analysis based on VP7 and VP4 encoding sequences indicate that the strains might be the same as they were collected in the same farm
- The study contribute to understand the diversity of RVA for Southern Africa.

Next steps

- Finalize the phylogenetic analysis
- Extend the study to other provinces of Mozambique
- Analyze samples of other animal species (bovines and caprines)

Acknowledgements

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DFG Deutsche
Forschungsgemeinschaft



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**THANK YOU VERY MUCH FOR THE
ATTENTION!
OBRIGADO!**