

Evolutionary analysis of *Fasciolopsis buski* isolated from a human in India

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Background

Fasciolopsiasis, caused by the giant intestinal fluke, *Fasciolopsis buski* (*F. buski*), is a significant cause of morbidity and mortality in South and South-east Asia. Importantly, *F. buski* is found in multiple hosts species, including pigs, and the genetic diversity of this parasite isolated from these hosts is largely unknown. The site of study is Uttar Pradesh, India where fasciolopsiasis has been emerging since recent times.

Methodology

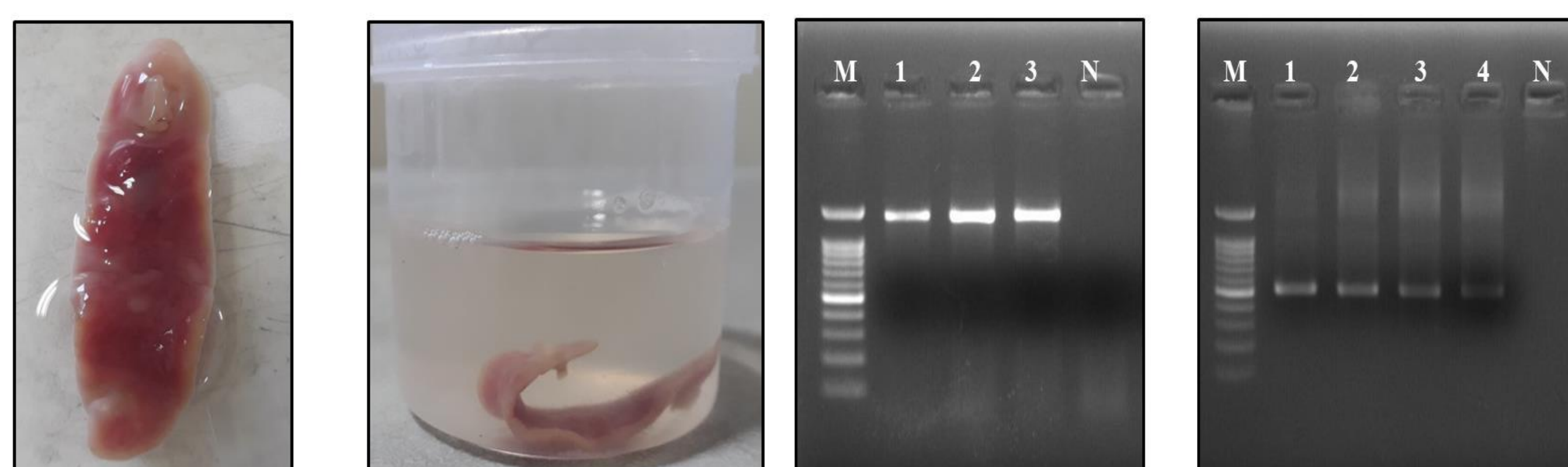
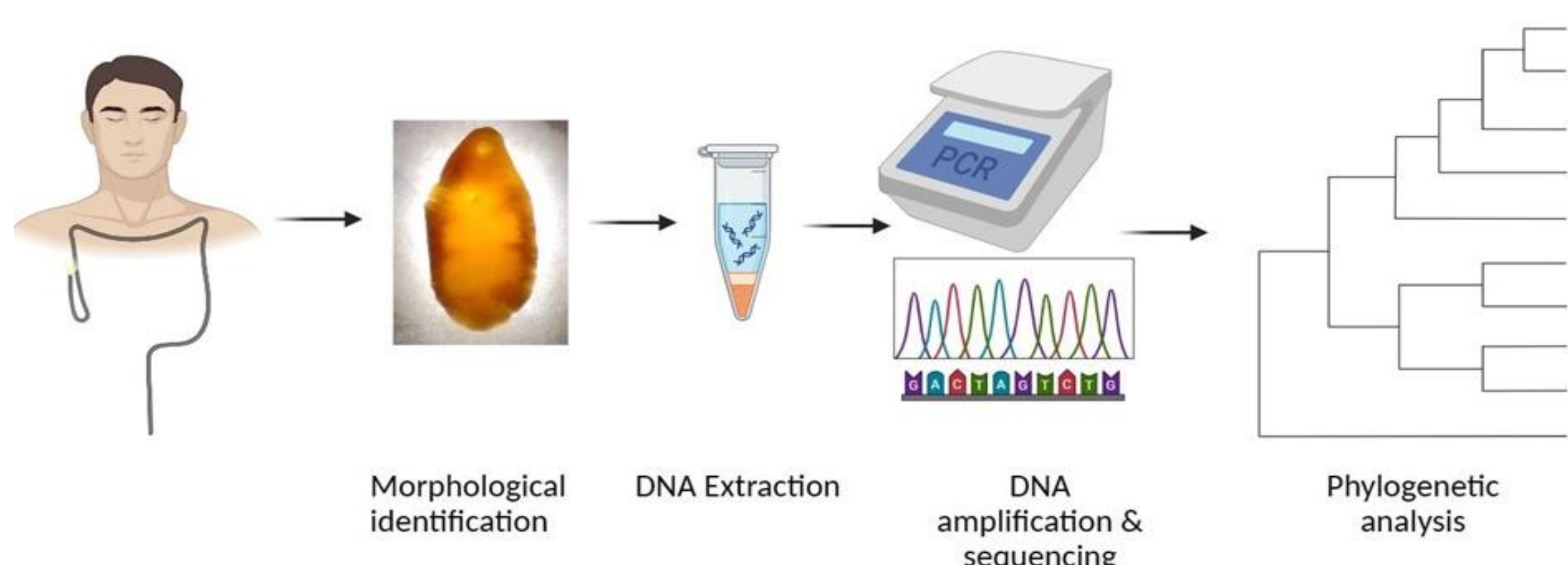
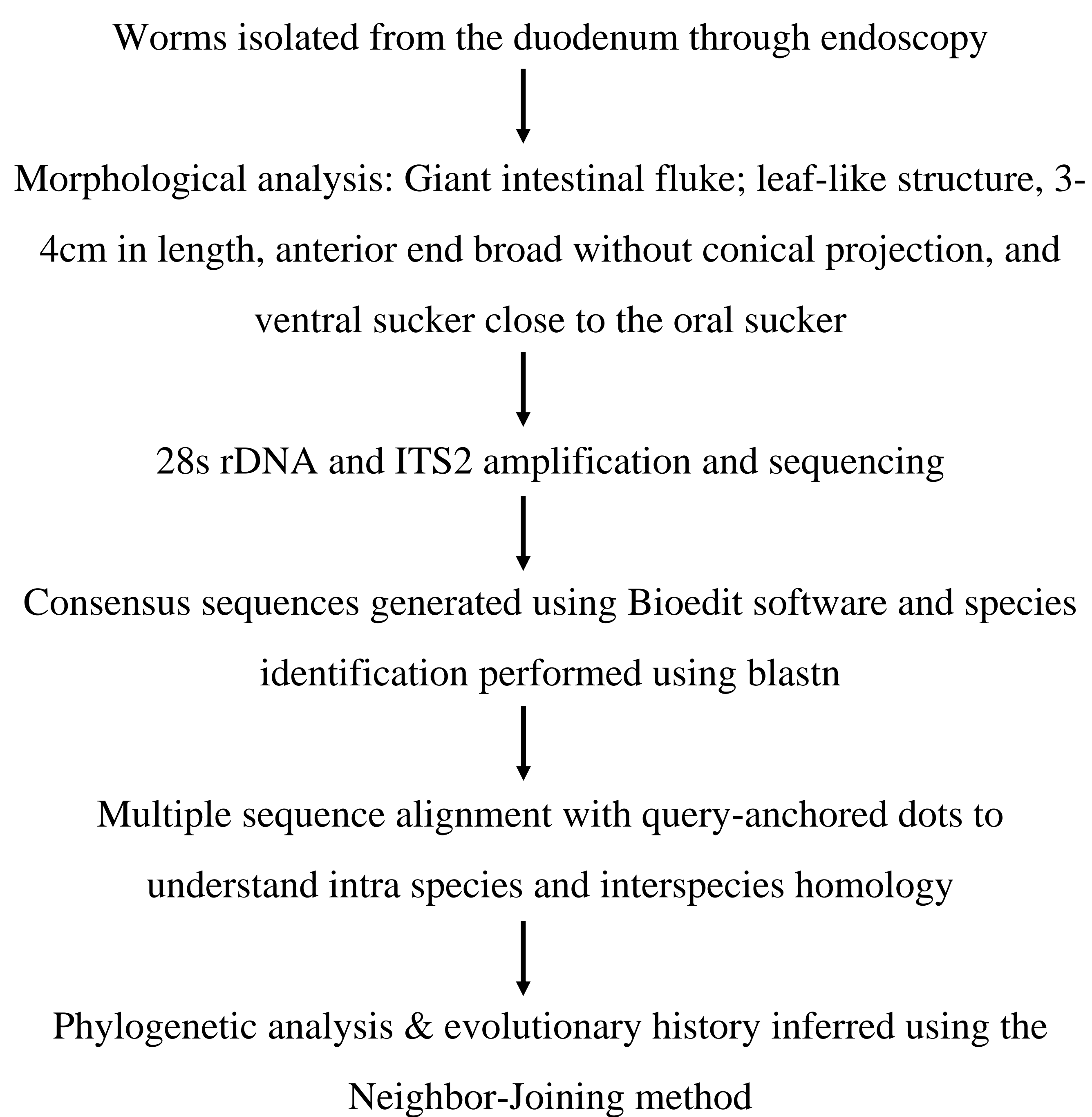


Figure 1: *Fasciolopsis buski* isolated during endoscopy in human host **Figure 2:** Amplified products of 28s rDNA and ITS regions

Results

Parasite showed close similarity to an isolate from pig in one of the north-eastern states in India, Meghalaya.

Intra species genetic variation for 28S rDNA of *F. buski* was 1-3% from the isolates of India, 5% from Vietnam and 8-11% with other related trematodes.

For ITS2, intra-species genetic variation 1-2% from isolates of India while 17% from Vietnam and 3-28% among other trematodes.

On phylogenetic analysis, *F. buski* isolated from humans or pigs from India were closely related, to those from Vietnam and China, which were grouped into separate clades.

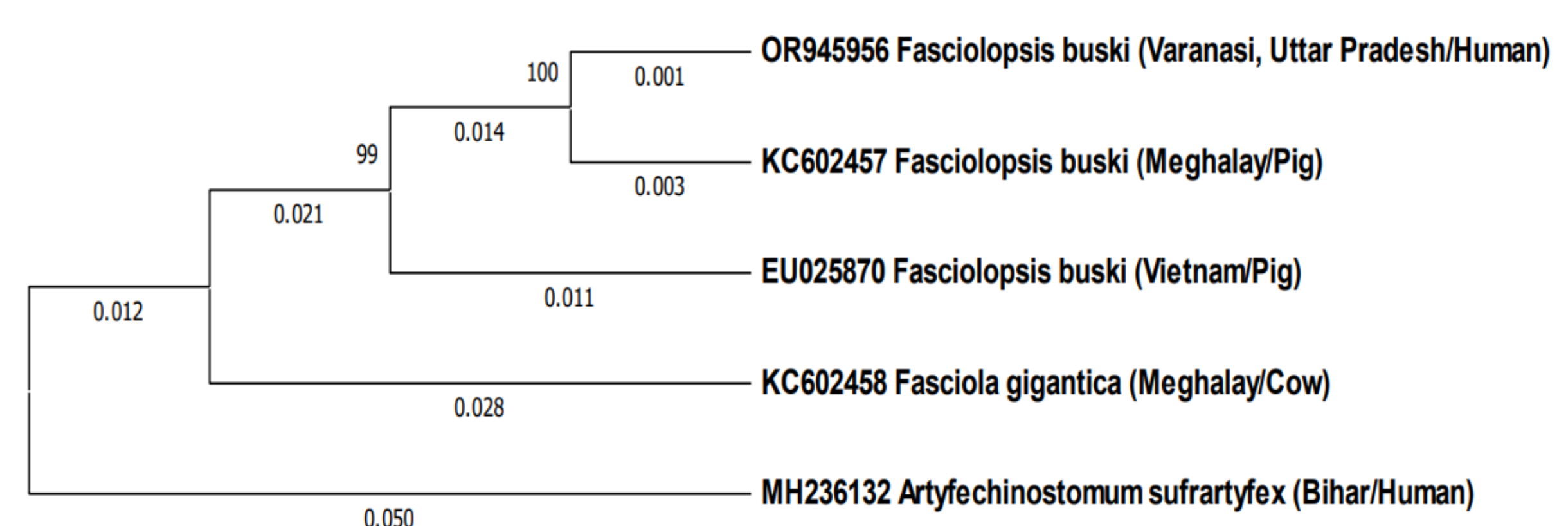


Figure 3: Tree depicting relationships *F. buski* and other related trematodes inferred from 28S rDNA data

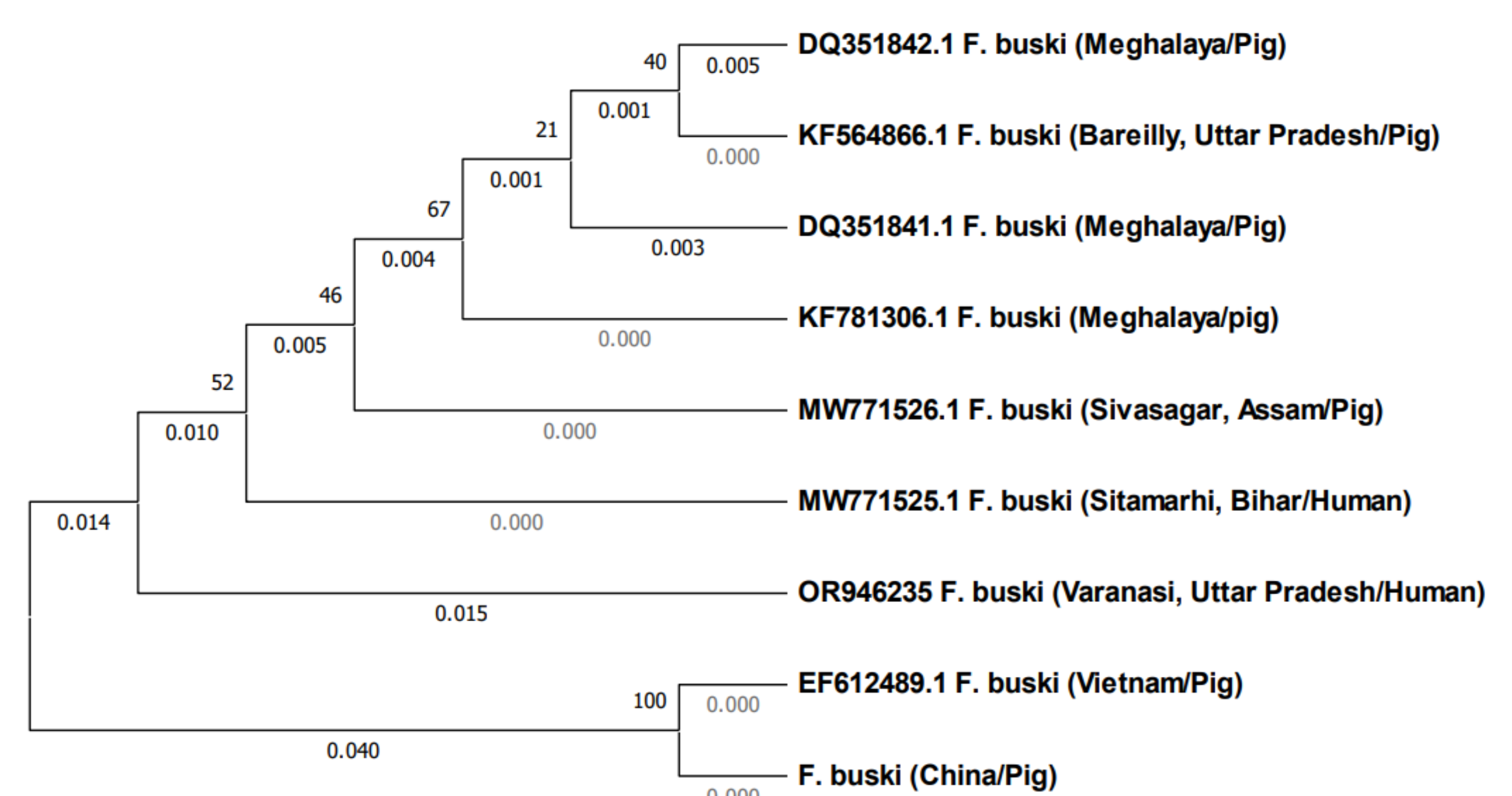


Figure 4: Tree depicting relationships among *F. buski* inferred from ITS2 data

Table 1: Sequence similarity based on ITS2 gene region

Gene	Species	Location	Host	Accession no.	Similar
ITS2	<i>F. buski</i>	Meghalaya	Pig	DQ351842	100%
	<i>F. buski</i>	U. P. (Bareilly)	Pig	KF564866	99.77%
	<i>F. buski</i>	Bihar (Sitamarhi)	Human	MW771525	99.66%
	<i>F. buski</i>	Assam (Sivasagar)	Pig	MW771526	99.66%
	<i>F. buski</i>	Meghalaya	Pig	KF781306	98.86%
	<i>F. buski</i>	Vietnam	Pig	EF612489	83.00%

Conclusions

Isolated fluke matched the sequence of *F. buski* found in Indian pigs, thus affirming the zoonotic cross-transmission of this parasite.

F. buski from India may represent a distinct clade different than those Vietnam and China, hinting at distinct evolutionary adaptations based on geographical locations