

Supplementary Material



Short Communication: Molecular Characterization and Epitope Mapping of Fusion (F) and Hemagglutinin (HN) Genes of Avian Paramyxovirus Serotype I from Peacocks in Pakistan

Sameera Akhtar^{1*}, Muhammad Akram Muneer¹, Khushi Muhammad¹, Muhammad Yasin Tipu¹, Muhammad Anees², Imran Rashid¹, Raza-ur-Rehman³ and Irshad Hussain¹

¹University of Veterinary and Animal Sciences, Lahore 54000, Pakistan

²Veterinary Research Institute, Lahore 54000, Pakistan

³Poultry Research Institute, Rawalpindi 46000, Pakistan

* Corresponding author: sameera.akhtar@uvas.edu.pk

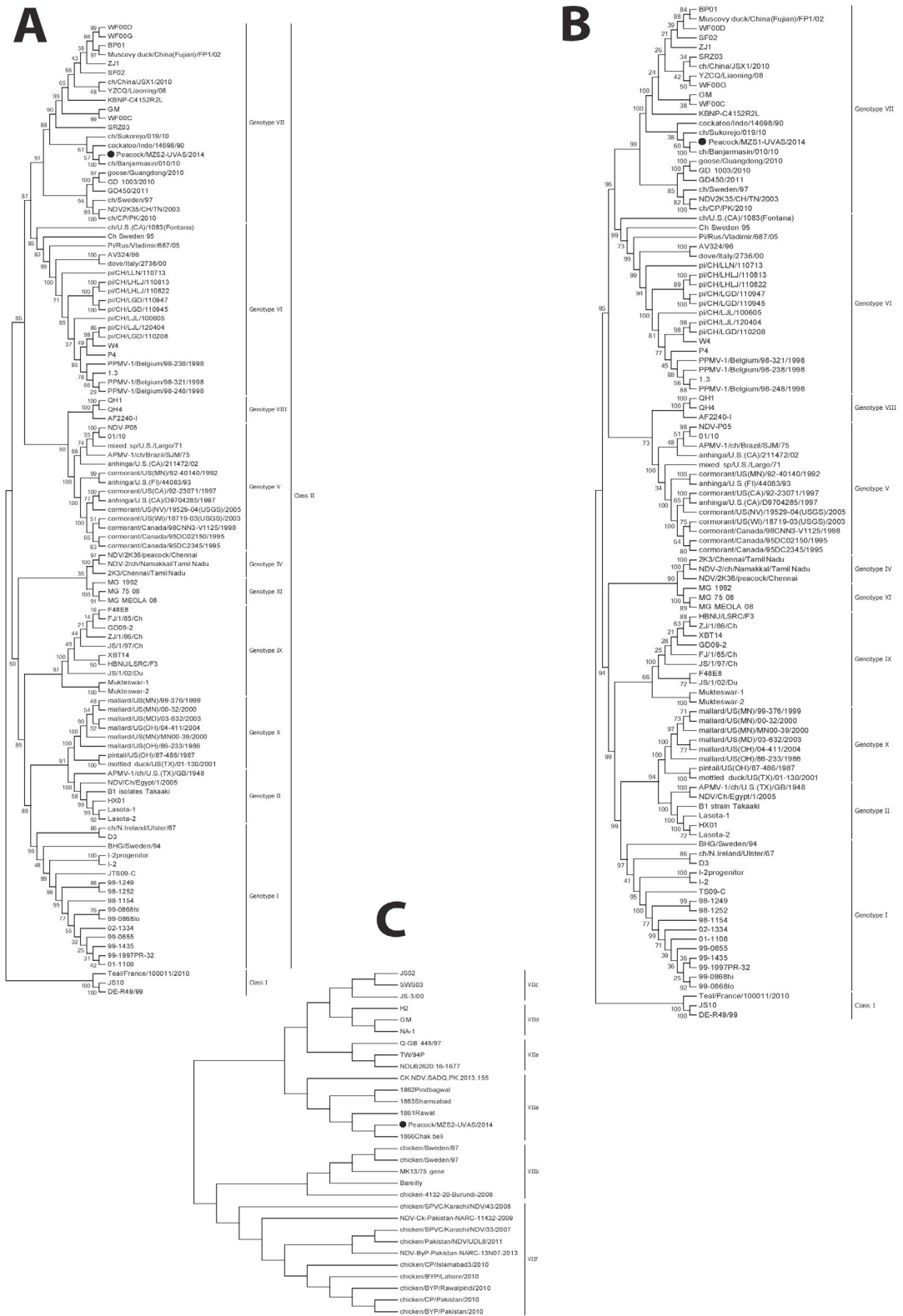
0030-9923/2016/0004-1161 \$ 8.00/0

Copyright 2016 Zoological Society of Pakistan

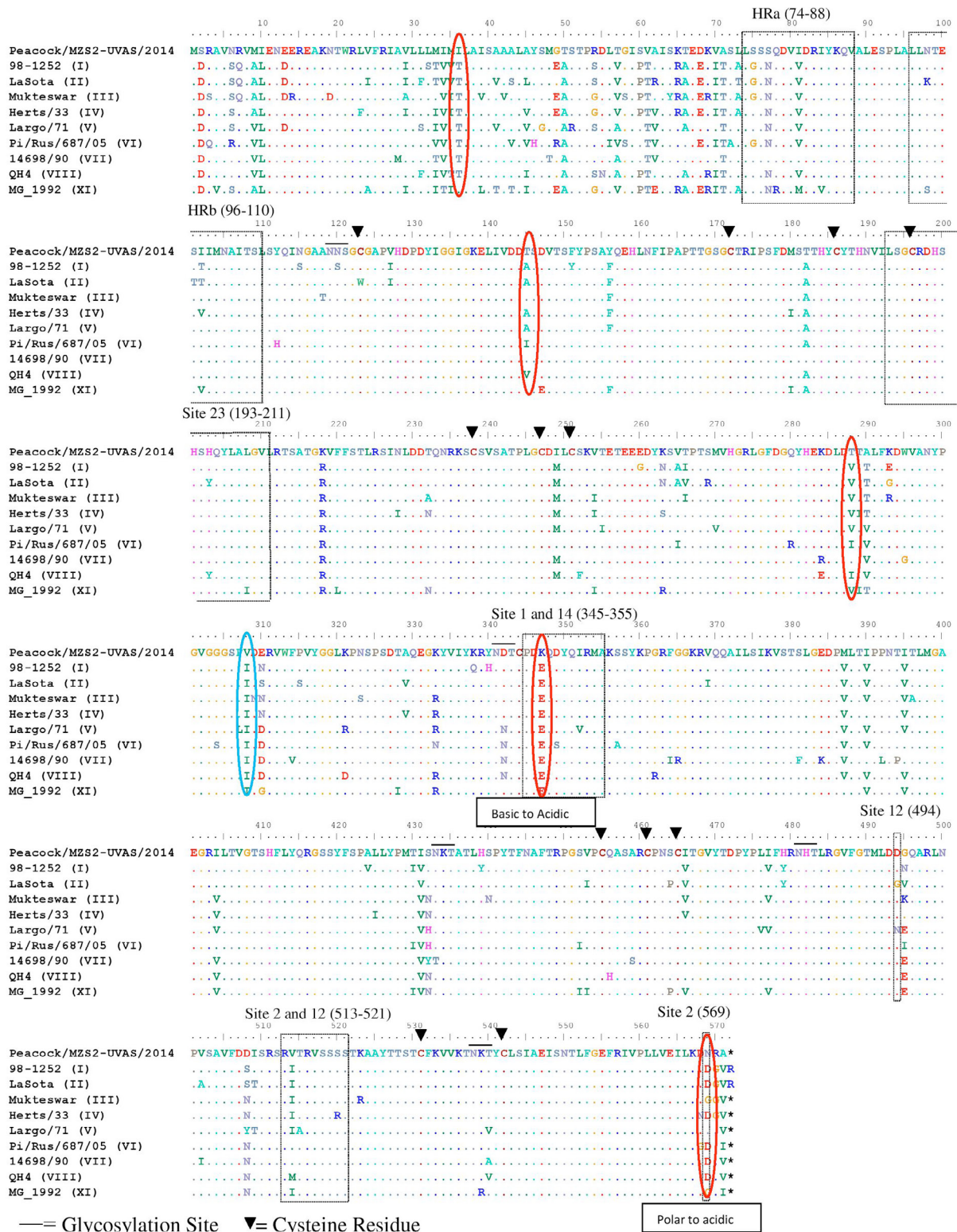
Supplementary Table I.- Primer sequences used for identification and amplification of Fusion and Hemagglutinin gene along with their expected product sizes.

No.	Primer sequences (5' - 3')	Position on viral genome	Product size (bp)	Reference
1	Sense: GTGAAYTTTGTCTCCTTGAC Anti-sense: GAGGCATGTGCRAAAGC	3833-3852 to 4814- 4798	965 bp	Munir et al., 2012
2	Sense: TTGAYGGCAGGCCTCTTG Anti-sense: GTGATAGAAGARCTTGACACCTC	4673-4690 to 5585-5563	890 bp	
3	Sense: ATAATATGCGTGCCACCTA Anti-sense: ATAYACGGGTAGAACGGT	5465-5483 to 6370-6353	888 bp	
4	Sense: TGGCTTGGGAAYAATACCCT Antisense: TGCAGTGTGAGTGCAACT	6190-6209 to 7176-7159	969 bp	
5	Sense: GGGAGGCATACAACAGGACA Antisense: TGGTTGCAGCAATGCTCTC	289-308 to 512-530	242 bp	Ling et al., 1997

Primer 1 to 4, used for amplification of F and HN gene of study isolate; Primer 5, used for the identification of NDV isolate.



Supplementary Fig. 1 Phylogenetic consensus tree for the pigeon-originated NDV isolate for fusion gene (A), hemagglutinin gene (B) and hyper-variable region of F gene (C). The nucleotide sequences of study isolate for each gene were compared with corresponding genes of representative strains reported previously to public database, the GenBank. The evolutionary history was inferred using the Neighbor-Joining method with 1000 bootstrap value in MEGA version 6.0.



Supplementary Fig. 3. Alignment of deduced amino acid sequence of complete HN gene of pigeon isolate. The residue profile of study isolate is compared with strains of NDVs representing different genotypes including the vaccine strains. Structurally and functionally important residues are boxed and highlighted. sequence of complete HN gene of pigeon isolate. The residue profile of study isolate is compared with strains of NDVs representing different genotypes including the vaccine strains. Structurally and functionally important residues are boxed and highlighted.