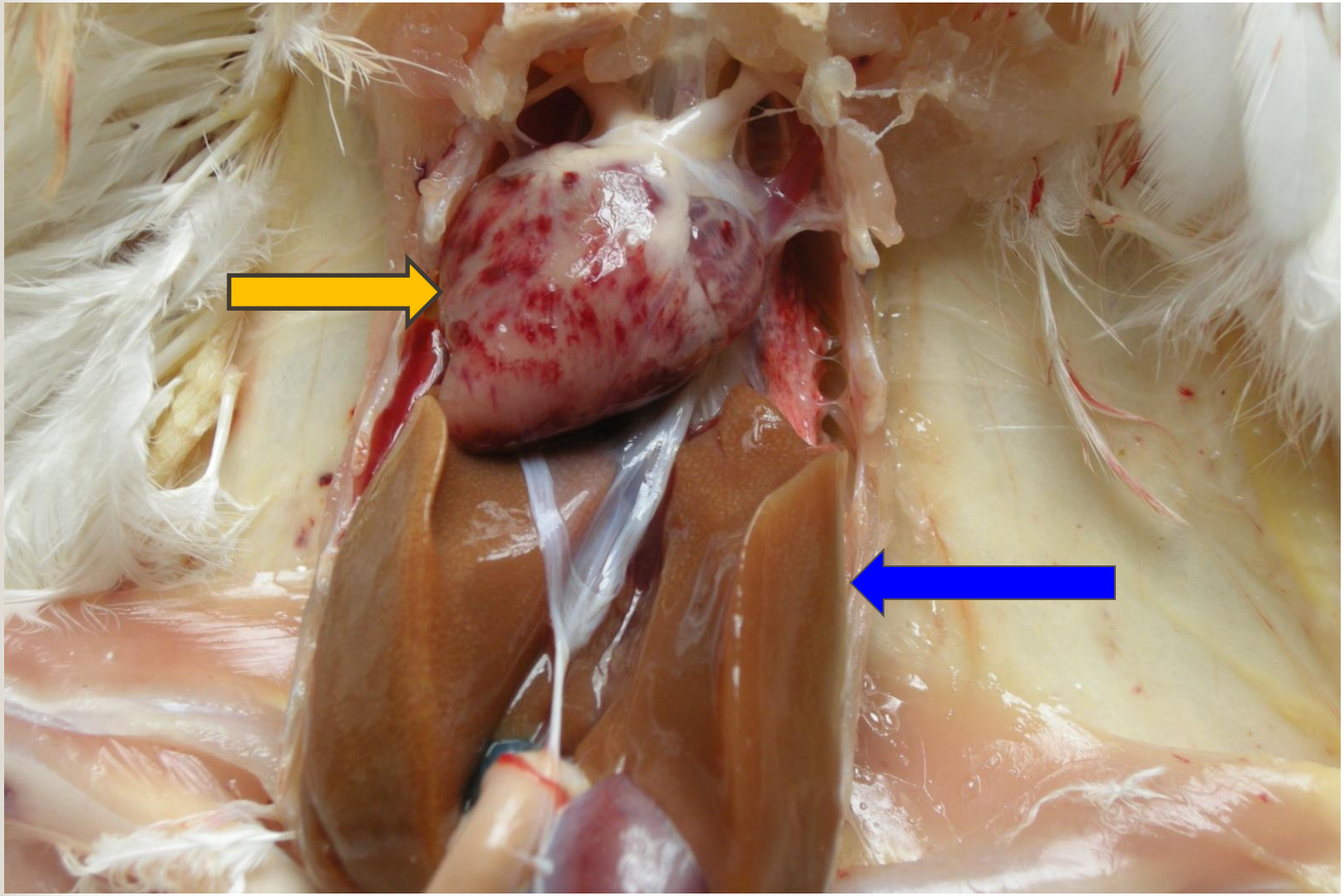
Chicken Infectious Anemia: Current Situation & Immunosupression

Dr. Muhammad Kashif Saleemi
DVM, MSc(Hons.), PhD
Associate Professor (*Tenured*)
US-NAS Fellow
Member NDCC

Department of Pathology, Faculty of Veterinary Science, University of Agriculture, Faisalabad, Pakistan

Fig. 2: Echymotic/petechial hemorrhages on heart



Clinical Signs & Lesions

Age weeks	No. of flocks	Hemorrhages				Anemic appearance	Bone marrow (pink/ yellowish)	Mortality %
		SC	Prov.	Int.org	Heart			
1-2	8	+3	+1	+3	+2	+3	+3	12.5
3-4	9	+4	+2	+2	+3	+3	+3	14
5-6	8	+4	+2	+4	+4	+4	+4	10.8
7-8	30	+4	+3	+4	+4	+3	+3	12
9-10	9	+3	+1	+2	+1	+3	+2	9.5

Hematological findings and PCR results

Farm no.	Hct.	Hb	PCR result of tissues	
			Liver	Spleen
1	11.80	5.50	-	-
2	10.90	6.00	-	-
3	12.25	5.25	+	-
4	11.00	6.16	+	+
5	11.60	6.29	+	-
6	13.20	6.50	+	-
7	17.20	6.70	+	+
8	10.85	5.70	+	-
9	12.30	6.28	+	-
10	12.00	6.00	+	-

Gross lesions

- Liver and bone marrow pale in color appearance
- Thymus atrophied
- Mortality ranged from **5-14%** on different farms
- The maximum mortality was in 5-6 week age group.
- Samples of liver and spleen from 60 farms selected on the basis of necropsy for PCR analysis
- Highly conserved VP2 coding gene using CAV1 and CAV2 primers was amplified (186-bp region) by PCR for confirmation of CIAV.
- **A total of 52 (86.66%) farms out of 60 were positive for CIA infections on PCR based results**

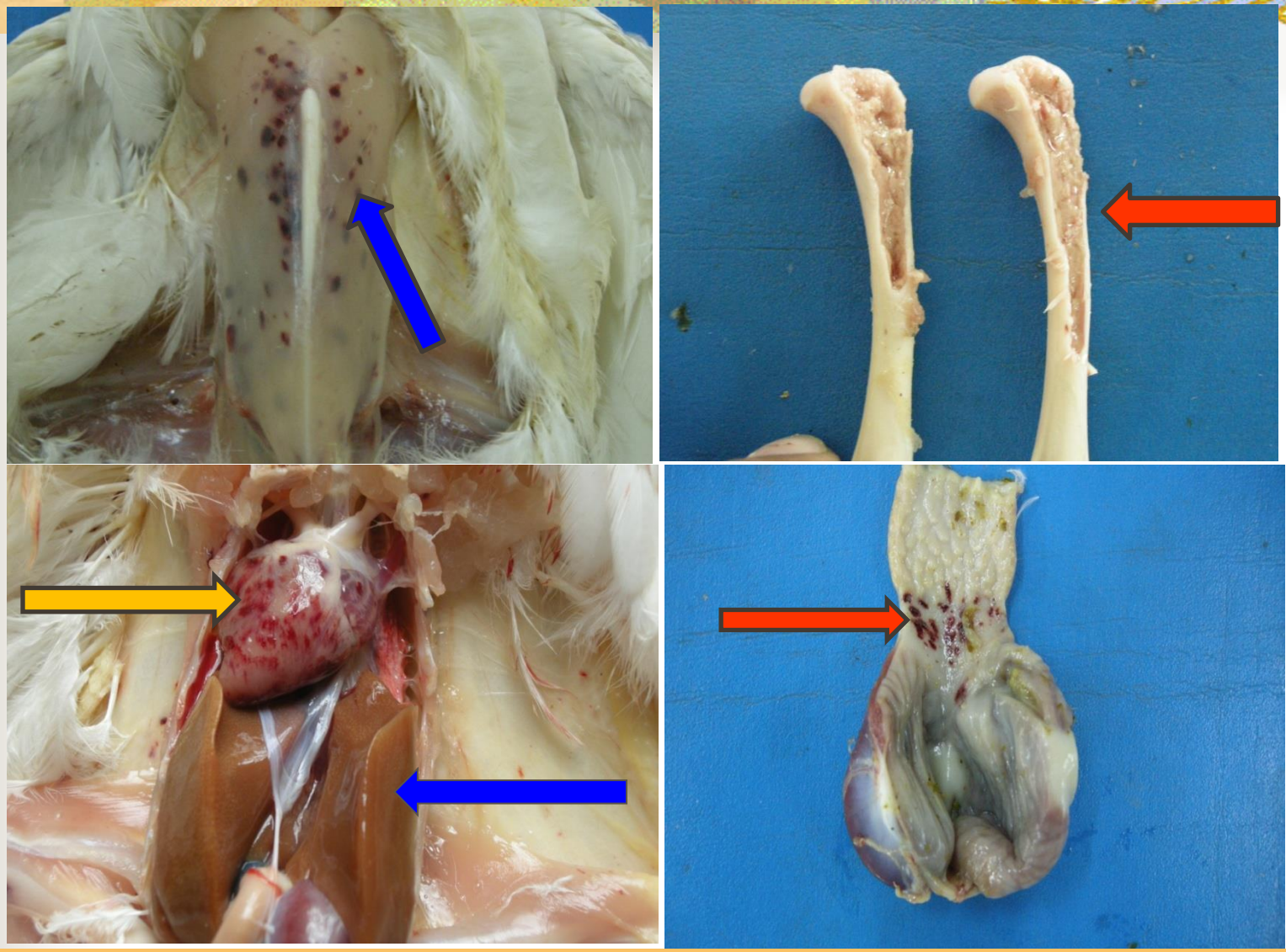


Fig. 3: Photograph of CAV infected birds indicating haemorrhages on pectoral muscles, hear, gizzard and pale/white bone marrow and anaemic liver

PCR Positive Samples

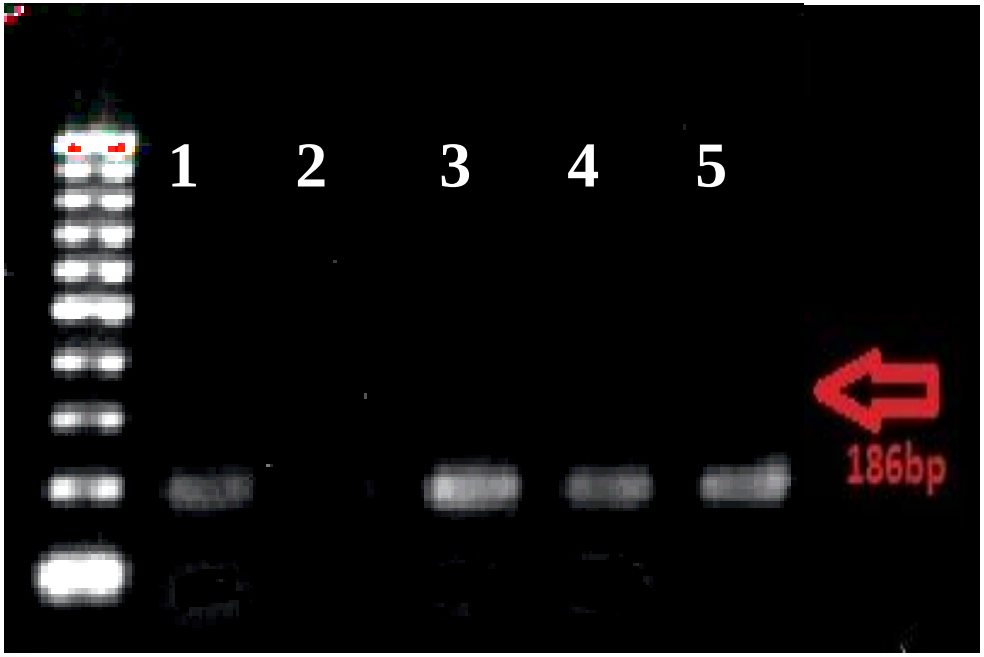


Fig. 4. Detection of CAV by PCR and amplification of highly conserved VP2 coding gene specific PCR product(186bp)
Lane 1 Positive Control, Lane 2 Negative Control and 3-5 Positive samples

Phylogenetic analysis of Recent Isolates (2018)

- Nucleotide Sequence and Phylogenetic analysis of 2018 recent cases was performed at HVRI, Harbin China
- All the 14 CAV VP2 sequences showed 99% nucleotide identity for VP2 region in GeneBank.
- All the sequences in this study were closely related.
- The result showed samples and the reference sequence has common ancestor (Figure. 5)
- The authenticity of PCR amplification of VP2 was confirmed by the nucleotide sequencing.

RESULTS: Phylogenetic Analysis

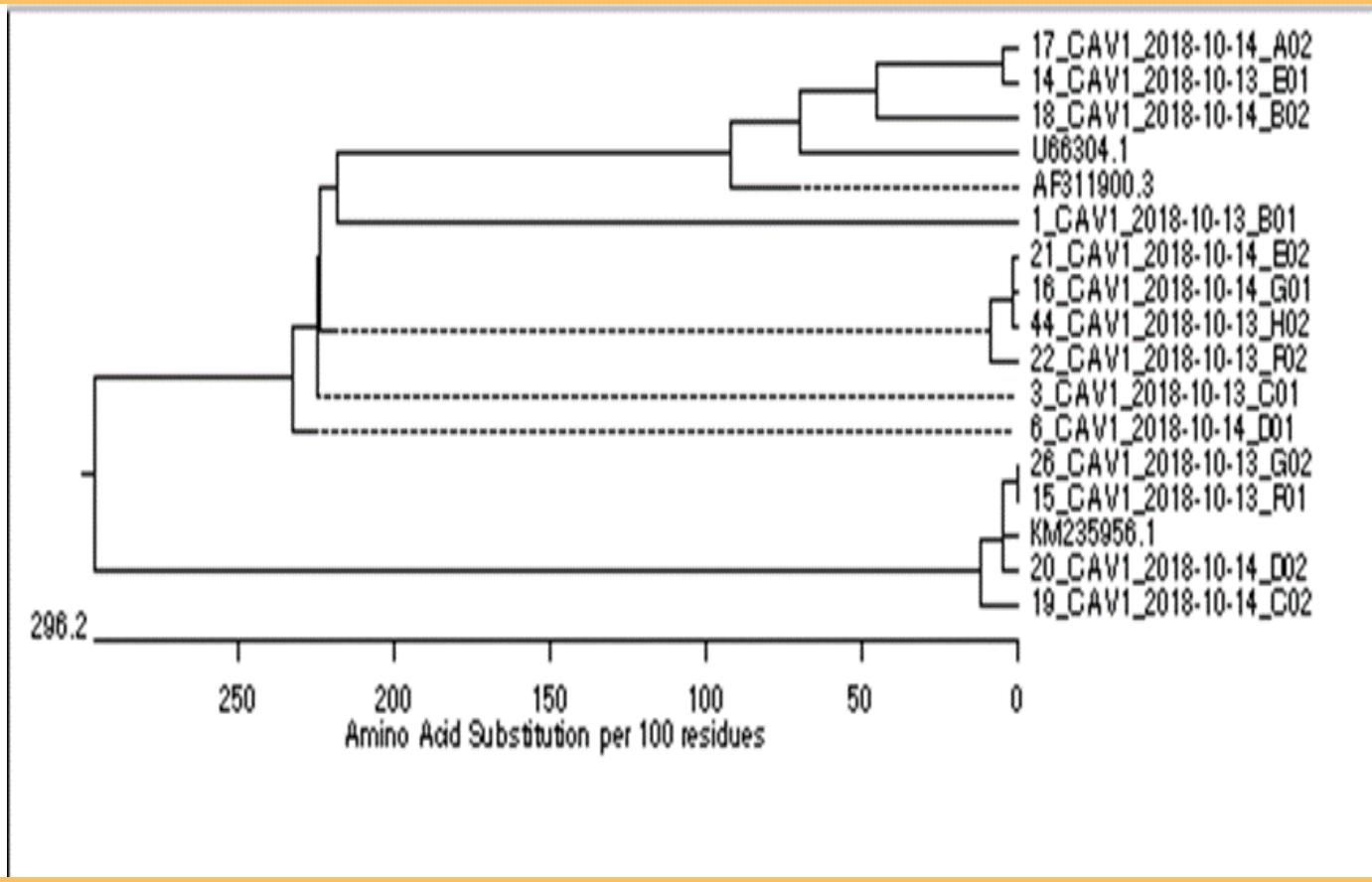


Fig. 5: Phylogenetic relationship among 14 different CAV isolates based on partial nucleotide sequences

Nucleotide Sequence and Phylogenetic analysis

- All the 14 CAV VP2 sequences showed 99% nucleotide identity for VP2 region in Genebank.
- All the sequences in this study were closely related.
- The result showed samples and the reference sequence has common ancestor (Figure 3).
- In Fig.3 sample no. 14, 17 & 18 were closely related (99%) to United kingdom (U66304) and Alabama (AF311900), USA. While sample no. 15,19,20 and 26 were closely related (99%) to Japan (KM235956).

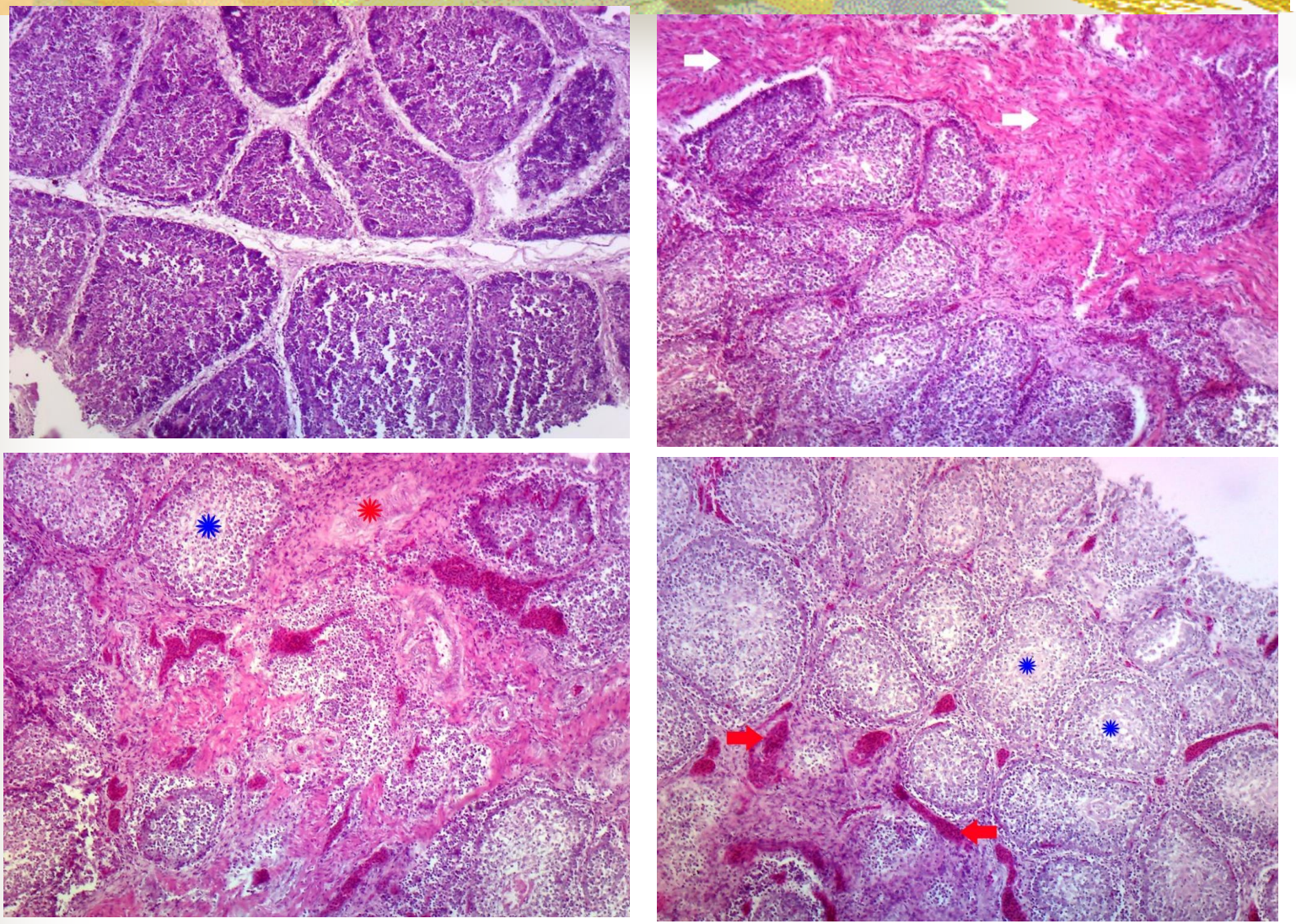


Fig. 6: Photomicrograph of control group (a) in CAV group increased interfollicular connective tissue (b & C) and lymphocytic depletion in (c & d) (H&E Staining 100X)

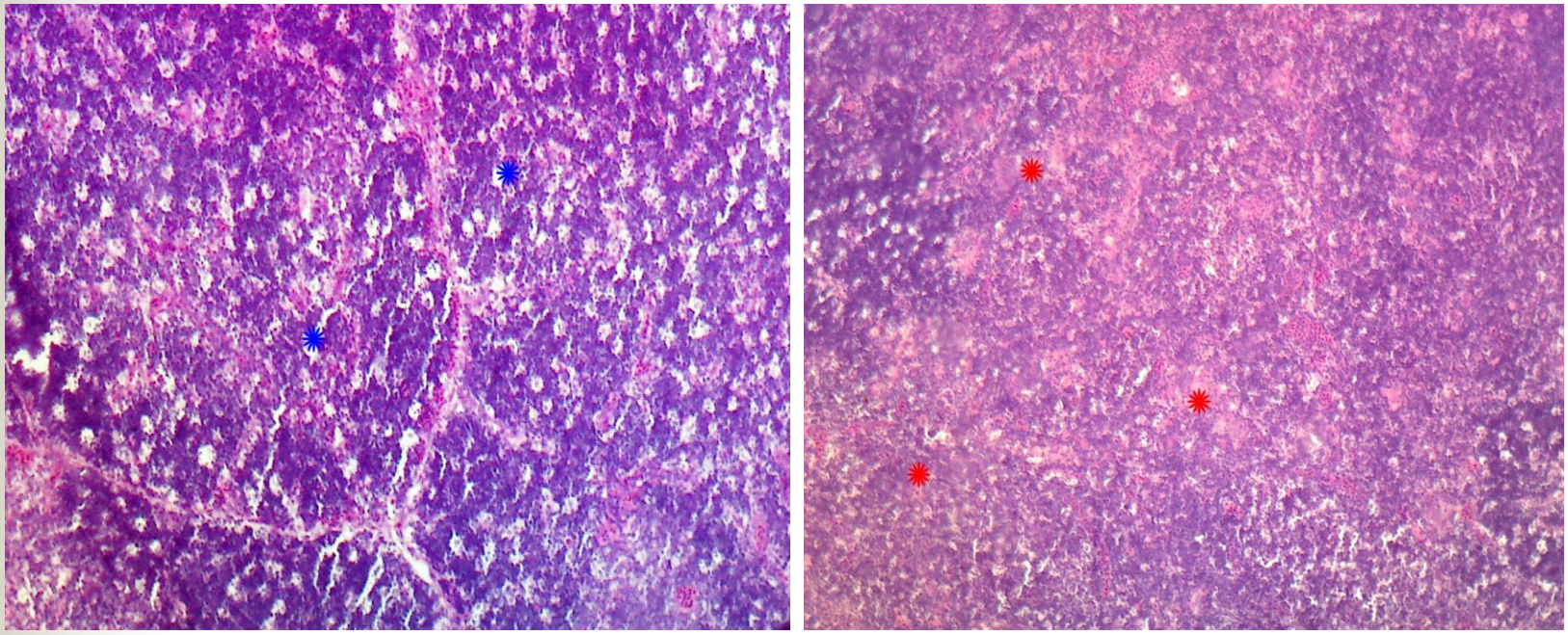


Fig. 7: Photomicrograph of thymus from CAV infected birds showing lymphocytic depletion(a) and necrotic changes(b) in the parenchyma (H& E Staining 100X)

First Outbreak Report from Pakistan by Department of Pathology, UAF (Najam-ul-Islam et al., 2013)

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RESEARCH ARTICLE

Molecular Diagnosis and Pathology of Chicken Infectious Anemia in Commercial White Leghorn Layer Flocks in Pakistan

Najm-ul-Islam[1], Muhammad Kashif Saleemi[2]*, Muhammad Zargham Khan[2], Salman Latif Butt[2], Ahrar Khan[2], Ijaz Javed[3], Faisal Saeed Awan[4]and ShahidRafique[5]

[1]Department of Livestock and Dairy Development (Poultry Production), Faisalabad; [2]Department of Pathology; [3]Department of Physiology and Pharmacology; [4]Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture, Faisalabad, Pakistan; [5]Animal Sciences Division, Pakistan Agricultural Research Council, Islamabad, Pakistan
*Corresponding author:drkashif313@yahoo.com

Data of 2013-14 Case Study: Diag. Lab data

- Total 86 Farms samples were collected from layer chicks during rearing period from Faisalabad division and Sargodha
- **More than 80% positive for CAV infection**
- Cases of 5-18 week age groups were also involved
- Severe immunosupression poor response towards other vaccine like ND, IB, IBD, AI etc.
- **In 2012-13 Disease situation was comfortable and few cases were diagnosed**

Data of 2016-17 Cases

- Total 57 farms samples were submitted to diagnostic laboratory from Faisalabad and surrounding areas and Sargodha
- **The 41 (72%) farms out of these 57 were positive for CAV infection through PCR**
- Cases of 4-16 week age groups were recorded
- All the above mentioned classical signs and lesions were observed in these birds
- **In 2015-16 situation was quiet comfortable**

Data of 2017-18 Cases

- In this year layer in rearing about 84 farms samples were collected
- Tissues samples (220) from 44 farms were processed through PCR
- **Out of these 44 farms 28 (63%) farms were positive for CAV**
- All the classical sings of CAV were observed in the birds
- Mortality is observed all age groups

Data of 2018-19 Cases

- Total no of samples: 765 Samples from 153 farms
- 95 samples out of total 765 were found positive for CIA through PCR
- Therefore 12.41 % samples were positive for CIA
- Distribution of samples among Layers and Broilers
- **Layer: 285 Samples (60 samples 21.05%)**
- **Broilers: 460 Samples (25 samples 5.43 %)**
- Broiler Breeders: 10 Samples (0 %)
- **Layer Breeder: 5 samples (5 samples 100 %)**
- Non-Descript Bird: 5 Samples (5 samples 100 %)

CAV in Broilers

(Saif et al., 2018) Department of Pathology UAF

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Full Length Article

Molecular Epidemiology and Pathology of Chicken Infectious Anemia in Day Old Broiler Chicks in Faisalabad, Pakistan

Saif-Ur-Rehman[1], Muhammad Kashif Saleemi[1], Muhammad Zargham Khan[1], Ahrar Khan[1], Asim Shahzad[1], Aisha Khatoon[1], Ahad Fayyaz[1], Bilal Aslam[2], Muhammad Sohail Sajid[3], Masood Akhtar[4] and Rao Zahid Abbas[3]
[1]*Department of Pathology, University of Agriculture, Faisalabad-38040, Pakistan*
[2]*Institute of Pharmacy, Physiology and Pharmacology, University of Agriculture, Faisalabad-38040, Pakistan*
[3]Department *of Parasitology, University of Agriculture Faisalabad-38040, Pakistan*
[4]*Faculty of Veterinary Sciences, Bahauddin Zakariya University Multan, Pakistan*
*For correspondence: drkashif313@gmail.com

Total 254 samples analyzed 38/254: 14.96 % Positive for CIA through PCR

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- Avian & Toxicologic Pathology Laboratory Team, UAF