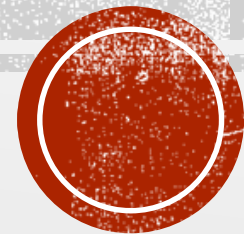


CHARACTERIZATION OF NOVEL LCMV STRAINS IN SOUTHERN IRAQ

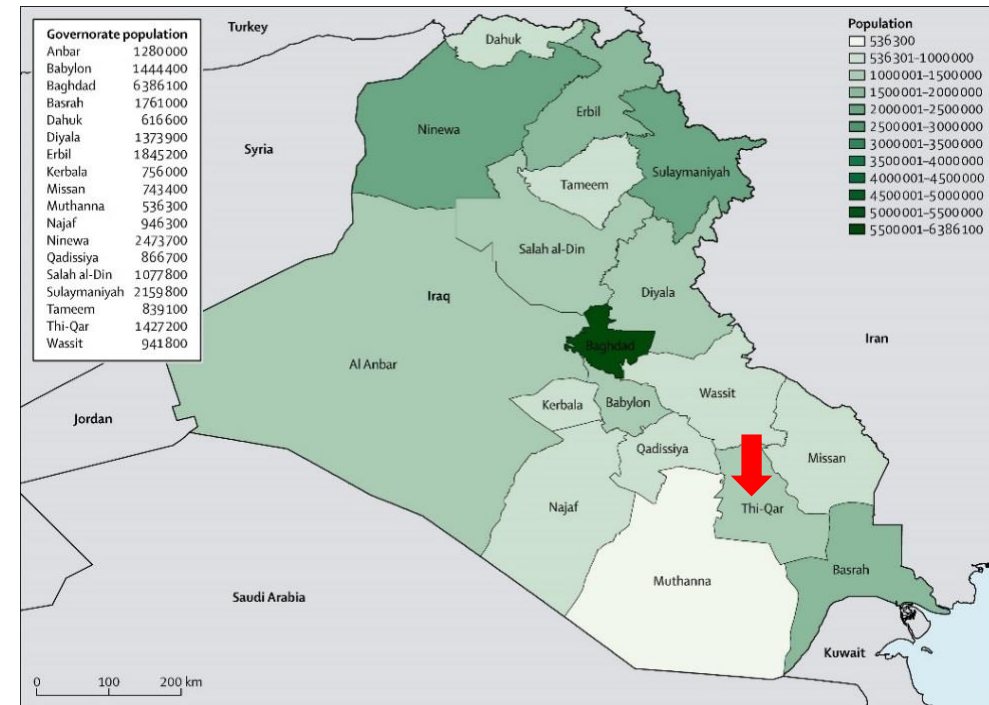
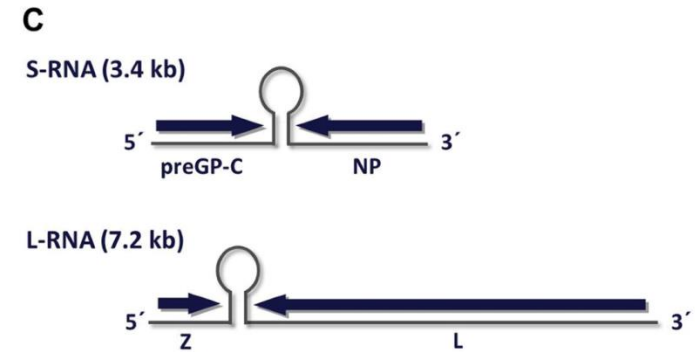
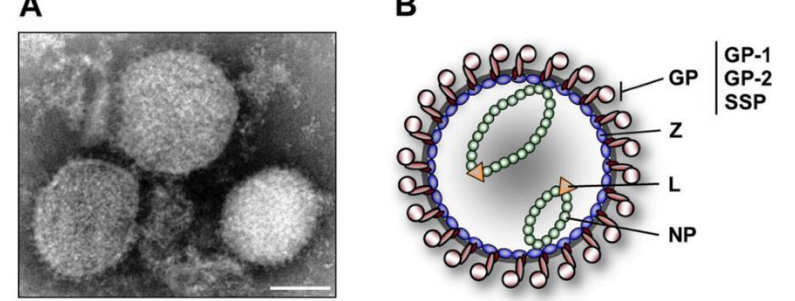
ESCV Workshop in Emerging Virus Infections 2020 23rd – 24th January 2020 Vienna, Austria

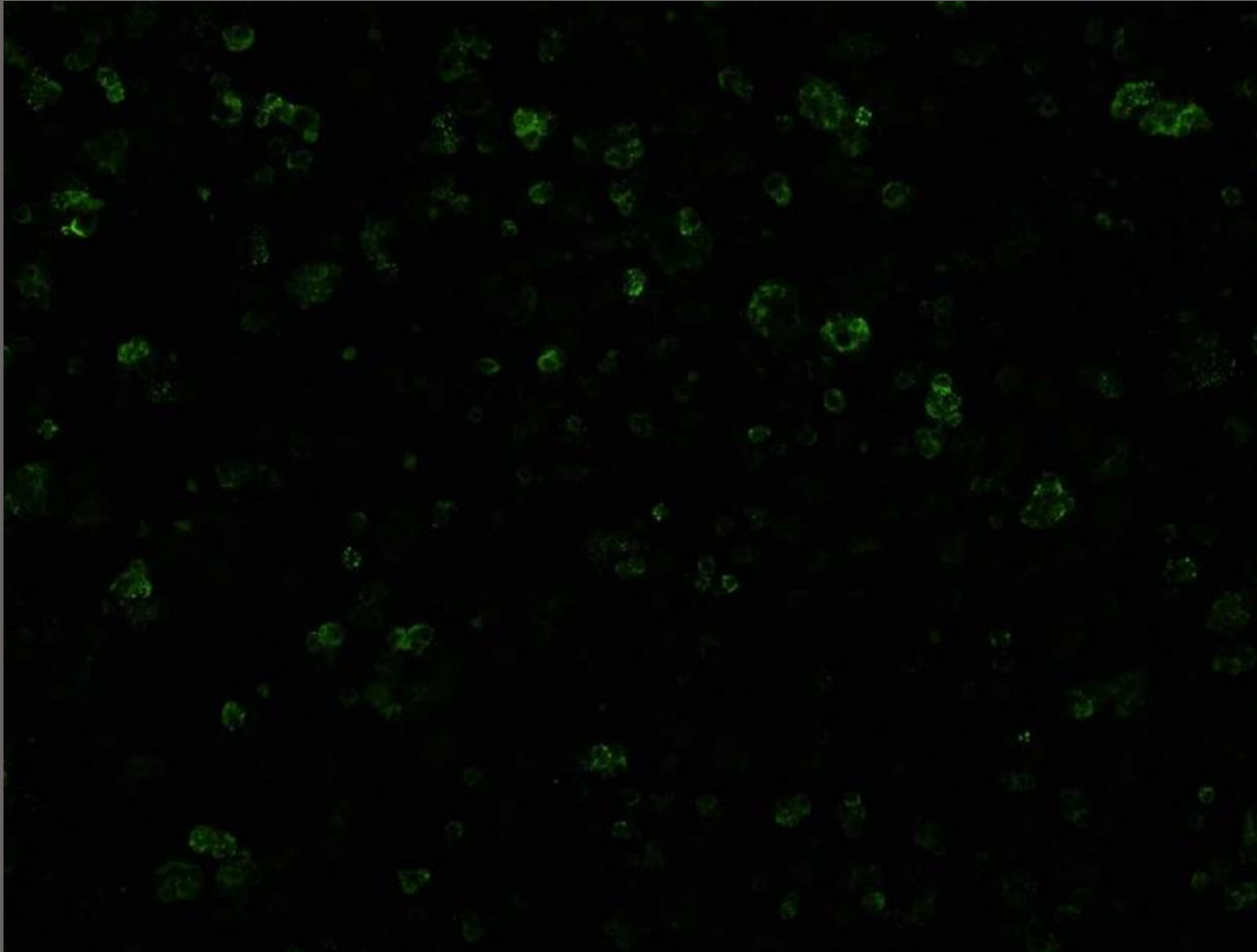


Hussein Alburkat
University of Helsinki

BACKGROUND

- LCMV prototype arenavirus
- Its main reservoir house mouse (*Mus musculus*)
- LCMV causes aseptic meningitis
- Common-cold like symptoms/Asymptomatic
- Investigate the prevalence of LCMV in Southern Iraq
- No available studies were performed in Iraq generally and in Southern Iraq specifically





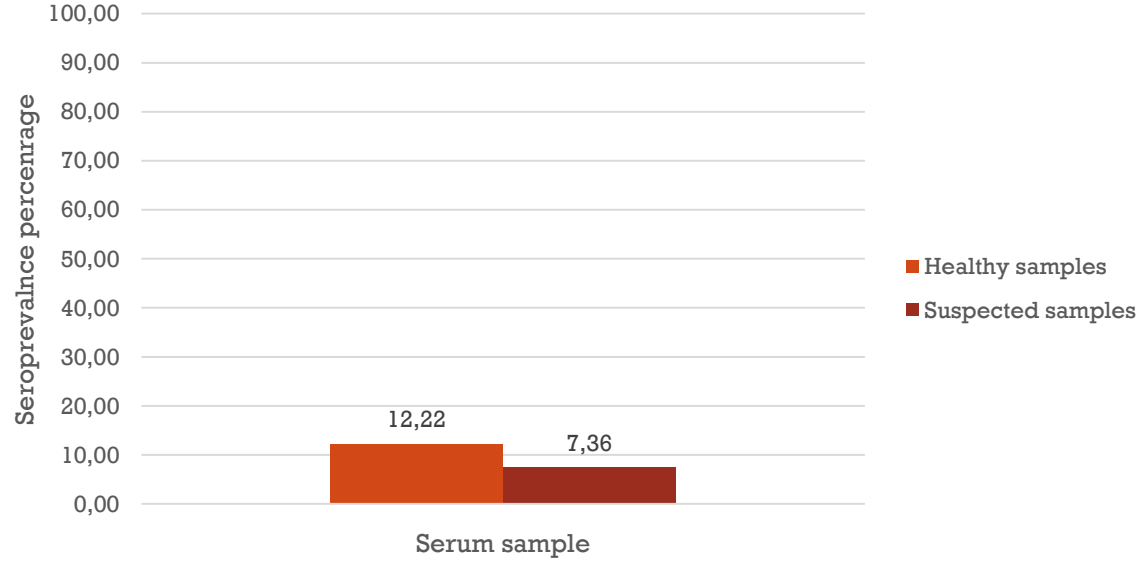
Immunofluorescence assay (IFA)

- 281 sample comprehensive number
- Healthy group includes 90 samples
- Suspected samples are 191
- Samples were screened for both IgG and IgM
- Eight CSF samples were collected as well but not screened by IFA.

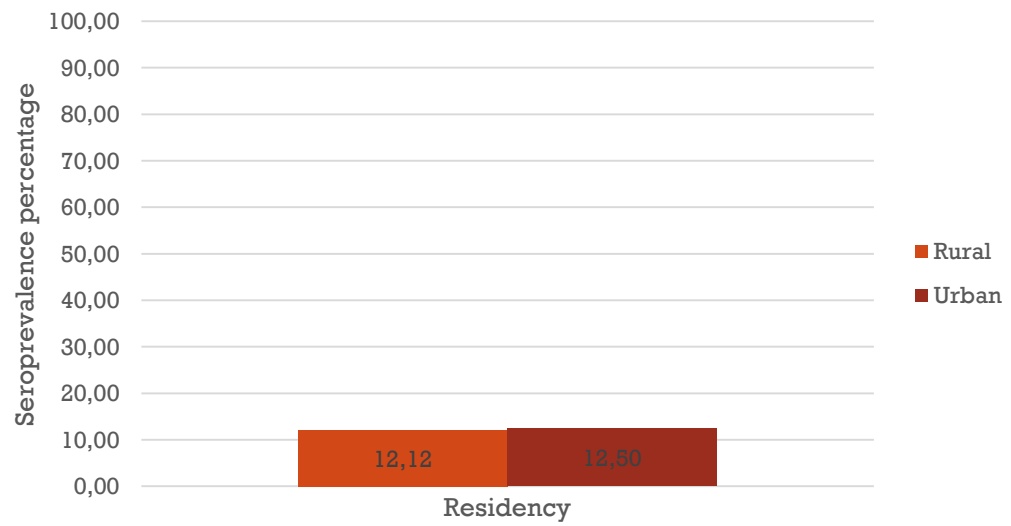
IFA slide under fluorescence microscope illustrates positive IgG.



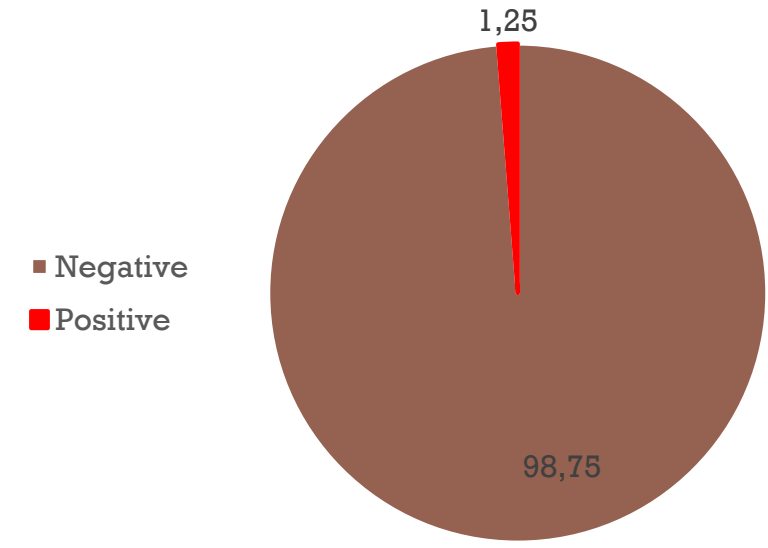
IgG seroprevalnce among the sreum samples



IgG seroprevalence among residency

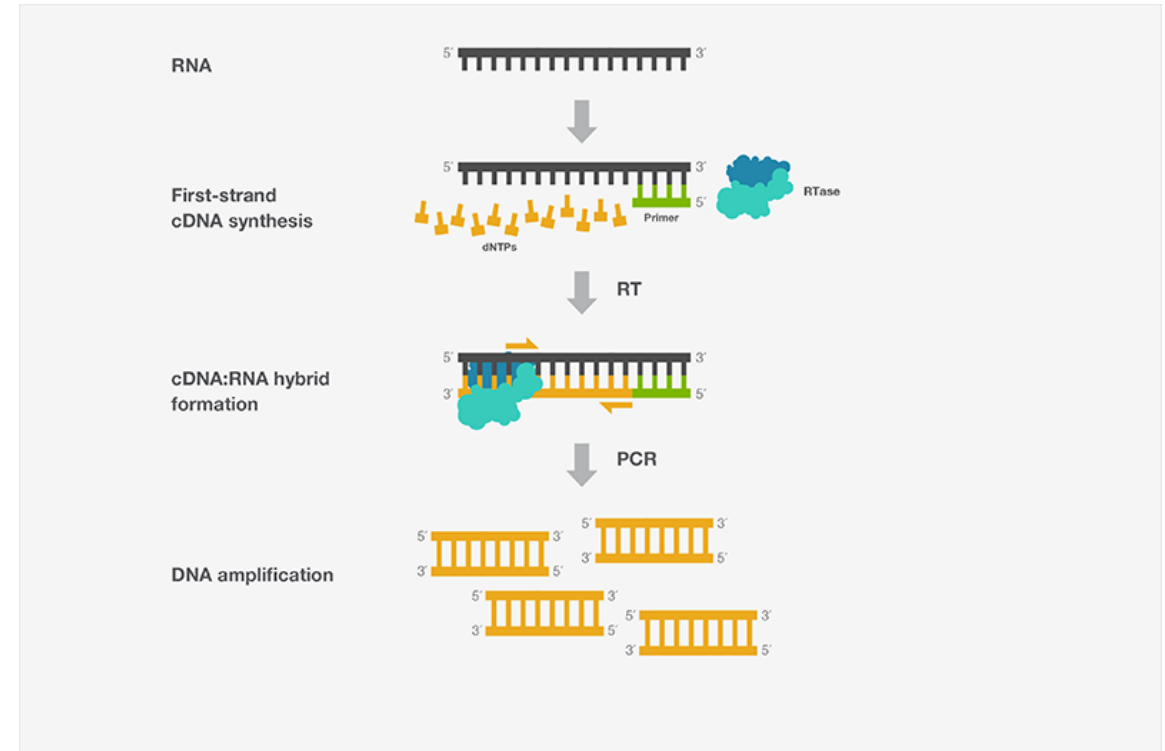


IgM seroprevalence among the serum samples



RT-PCR

- Using random reverse and forward primers.
- PCR products were validated in agarose gel-electrophoresis 2% including an ethidium bromide.
- Two CSF samples were positive in the RT-PCR

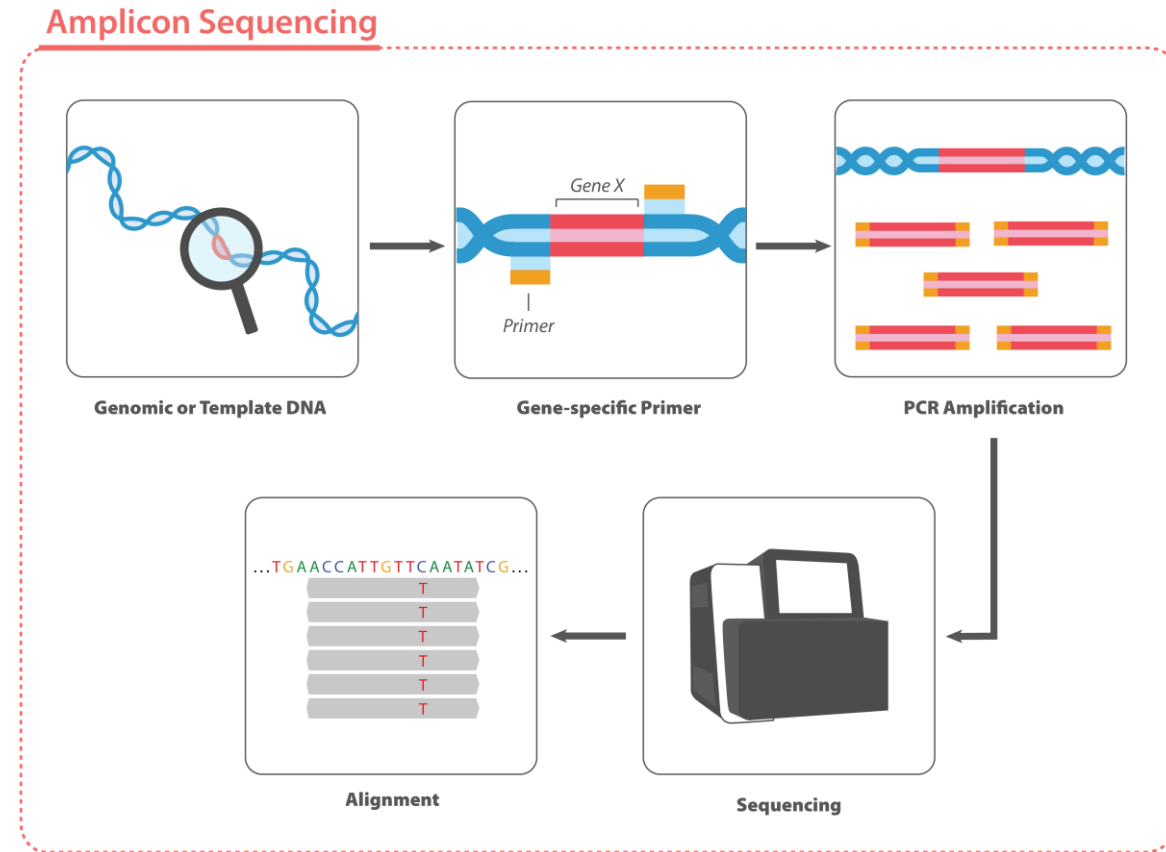


RT-PCR	Positive	Negative
	22	94



Amplicon PCR and Sanger sequencing

- Specific primers targeting OW arenavirus L-segment were used.
- The primers were overhanged with adapters to facilitate the compatibility with the illumina indices.
- The resulted amplicon composed of 400 bp as maximum.



www.abmgood.com/Amplicon-Sequencing-Service.html

Results of Amplicon PCR

Positive	Negative
22	0

Results of Miseq

Positive LCMV	12 out of 22 samples
---------------	----------------------



Partial genome sequencing

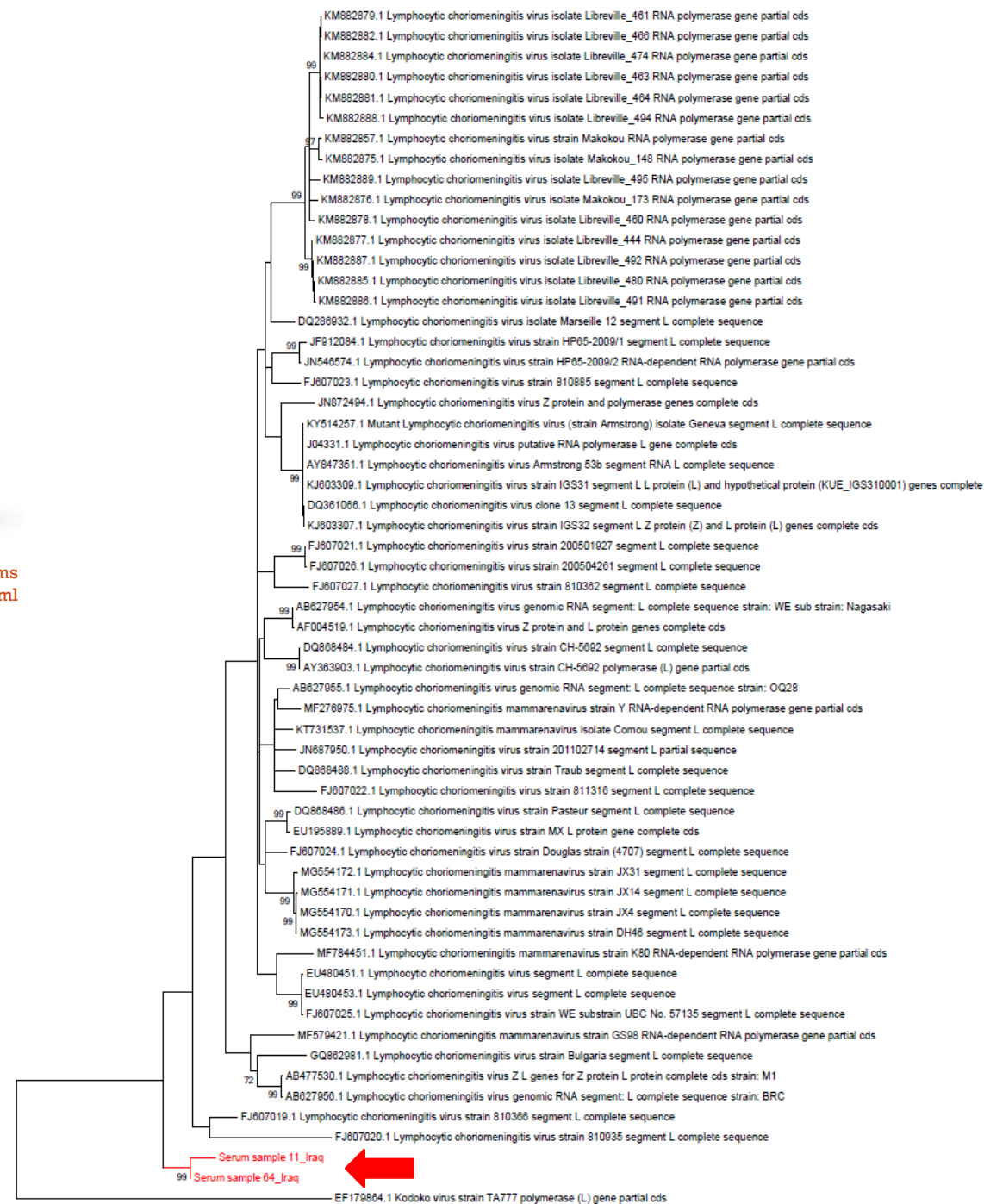
- Started with the enrichment of viromes to sequencing on the Illumina® MiSeq® system.



<https://www.illumina.com/systems/sequencing-platforms/miseq.html>

Phylogenetic tree

- Phylogenetic tree was constructed using MEGA7 and multiple sequence alignments were performed using Clustal W.
- The best model to estimate the number of nucleotide substitutions was Tamura-Nei (TrN) T92+G+I with pairwise gap deletion.



CONCLUSION

- This is the first study of LCMV in Southern Iraq
- The seroprevalence of LCMV was detected
- Two new strains of LCMV were detected
- Improving specific primers of LCMV is needed
- Collecting of rodent samples is needed too to study LCMV infections in rodents as well.
- Further studies are needed to investigate the viral infections in Asia such as: Iran, Gulf countries, Jordan, Syria ..etc.



ACKNOWLEDGEMENT

Professor Olli Vapalahti

Dr. Haider Al-hello

Dr. Teemu Smura

Special thank for all members of the
viral zoonosis group

Thank You

