

“Flavivirus surveillance in Aedes mosquitoes from Albania”

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BG-Sentinel CO2-Lure trap for adult mosquito collection

**Adults’
Collection**

1. BG Sentinel + Lure + CO2 traps

2. Resting Catch - Mechanical aspirator

3. Human Landing Catches - HLC



Mosquito processing for Flavivirus detection at FLI

OBJECTIVE

In order to clarify the occurrence of mosquito-borne Flavivirus in Albania and to identify their potential as a disease causative pathogenicity, we conducted a collection of mosquitoes over a period of three years (2019-2021) along the coastal side and two central regions of Albania.

MATERIAL AND METHODS

Adult collection was performed via different adult traps, e.g. BG-Sentinel+Lure+CO₂ and light traps augmented or Not with CO₂.

We monitored 12 stations/locations that were regularly sampled every 2 weeks. Transport with dry ice to protect potentially Flavivirus-infected mosquitoes from degradation.

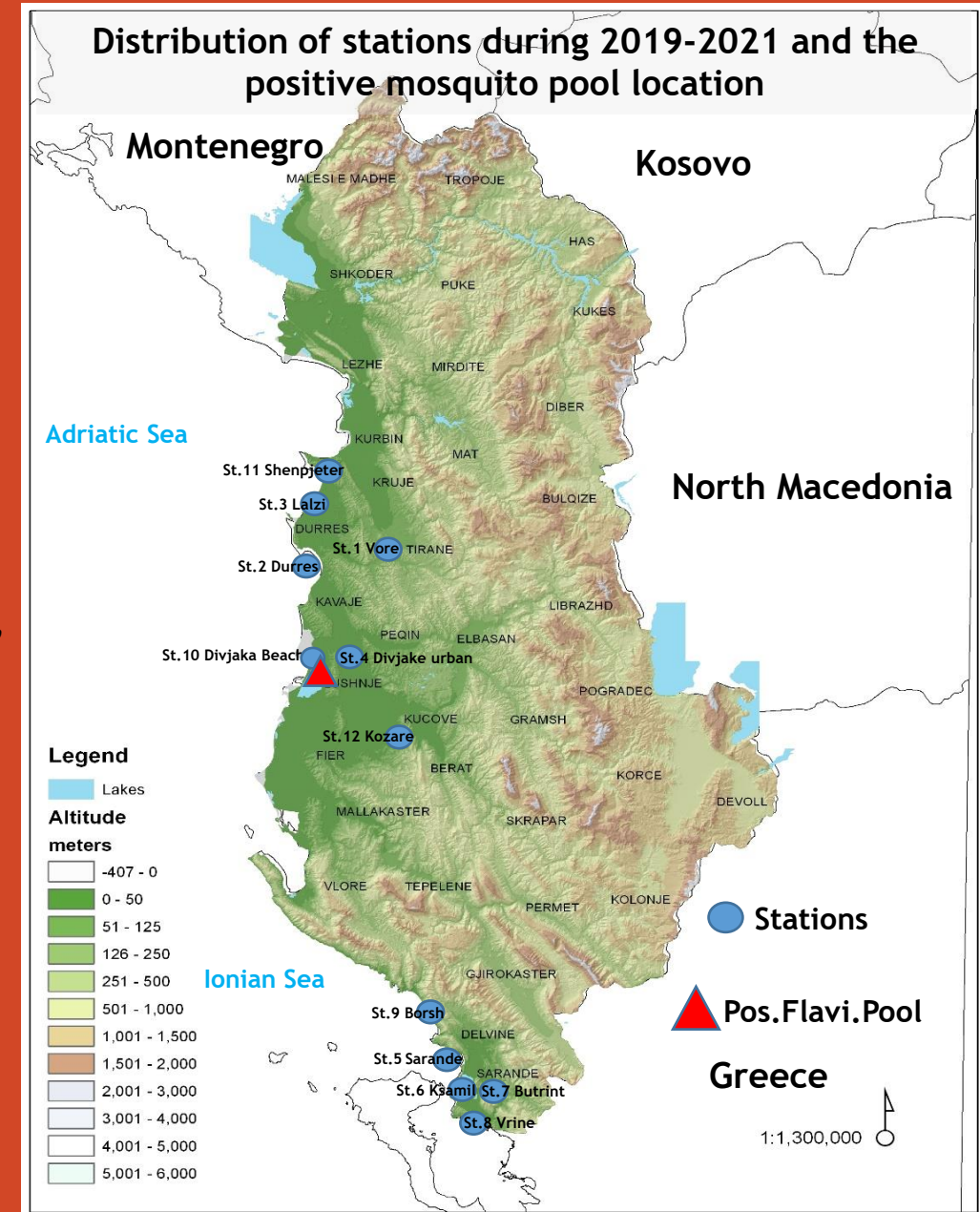
Females and males were placed separately in tubes together with two 3mm metals beads to allow for disruption and lysis of the tissue.

A volume of 500µl of media solution was added to samples containing one individual, and 750µl to pools with 2-27 individuals of adult mosquitoes.

Pan-favivirus RT-qPCR assay was applied to each pool.

Mosquito Sampling Sites

Station 1	Vore, Tirane	Station 7	Butrint
Station 2	Durres, urban area	Station 8	Vrine
Station 3	Lalzi bay	Station 9	Borsh
Station 4	Divjake urban	Station 10	Divjake Beach
Station 5	Saranda urban area	Station 11	Shenpjeter, Durres
Station 6	Ksamil	Station 12	Kozare, Kucove



RESULTS

- 17.222 mosquitoes/1068 pools of 1-27 adult females in total;
- 5 species *Aedes albopictus*, *Aedes caspius*, *Anopheles maculipennis* s.l., *Culex pipiens* and *Culex tritaeniorhynchus*;

We detected a single pool in the beach sandy area of Divjaka with a dense pine forest area, where mosquito abundance and the presence of migratory birds in high.

- The sequence has roughly 82% similarity with Flaviviruses in the NCBI GenBank database.

Next steps

1. Flavivirus isolation on cell culture.
2. Full genome sequencing of the Flavivirus detected.
3. Possibility of the Flavivirus to cause disease in human and/or animals?

The screenshot shows the NCBI Taxonomy report interface. At the top, there are tabs for 'Descriptions', 'Graphic Summary', 'Alignments', and 'Taxonomy' (which is selected). Below these are sub-tabs for 'Reports', 'Lineage', 'Organism', and 'Taxonomy' (which is selected). The main content area shows '100 sequences selected' and a table of search results. The table has five columns: 'Organism', 'Blast Name', 'Score', 'Number of Hits', and 'Description'. The results are as follows:

Organism	Blast Name	Score	Number of Hits	Description
Flavivirus	viruses		101	
• West Nile virus	viruses	171	79	West Nile virus hits
• Japanese encephalitis virus	viruses	167	2	Japanese encephalitis virus hits
• Banzi virus	viruses	163	2	Banzi virus hits
• Tyuleniy virus	viruses	143	2	Tyuleniy virus hits
• Dengue virus type 2	viruses	137	16	Dengue virus type 2 hits

CONCLUSIONS

- Our study showed the presence of a new Flavivirus species in adult *Aedes caspius* mosquitoes in coastal areas of Albania.
- Present at sites where the migratory birds are resting.
- Mosquitoes in these area continue to be a serious threat for infections disease transmission in Albania.
- Strategies of vector/mosquito control should be intense and undertaken from different bodies (public and private).

Future studies

1. Further studies to detect possible pathogen agents on adult mosquitoes in Albania are recommended.
2. Studying the vectorial capacity and competency of invasive *Aedes ssp.* for certain viruses or pathogens.
3. Harmonization of the new approaches for the improvement of the *Aedes albopictus* control in Albania.

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3. Friedrich Loeffler Institute Germany: For the great support to test a large amount of *Aedes* adult mosquitoes for Flavivirus detection, their continuous support and for future collaborations intended to be realized.