

Back to the measles – first evidence of viral circulation in Liguria, Northern Italy, 2024

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Introduction

- After a prolonged period characterized by substantial absence of viral detection, during the COVID-19 pandemic in 2020–2022, measles activity began to increase in 2023 with sporadic cases and local-regional outbreaks in several WHO European regions.

Study Design

- In Italy the surveillance network MoRoNet reported 64 measles cases in January and February 2024, 40% of which classified as imported; confirmed cases were mostly unvaccinated, with a median age of 35 years, and at least one third of patients reported a complication.

Material and Methods

- As a Subnational Reference Laboratory of MoRoNet for Liguria region, Northern Italy (about 1.5 million inhabitants), we currently perform serologic and molecular assays (extraction by ELITE InGenius®, ELITech Group Empowering IV).
- Amplification by Real-Cycler Chic-Out Measles virus, Progenie Molecular) to confirm suspected measles cases and Sanger sequencing (SS) of the 450 nt region in the C-terminal of the N gene (N-450), which is recommended for routine genotyping by the World Health Organization.
- Basic Local Alignment Search Tool (BLAST) was used for genotype identification, confirmed by phylogenetic analysis inferred with Neighbour Joining method. Sequences will be uploaded on the GenBank database.

Results

- Since February 2024, 8 measles cases were detected in the surveyed area, from 3 of the 5 local health units in Liguria: patients had an average age of 31 years (15.7), a median age of 34,5 years (min 7, max 50, IQR 25-39) and 75% were male. Patients' year of birth is shown in Figure 1.
- All cases reported at least one complication (diarrhea, pneumonia, thrombocytopenia, hepatitis) and all but one required hospitalization or access to Emergency Department.

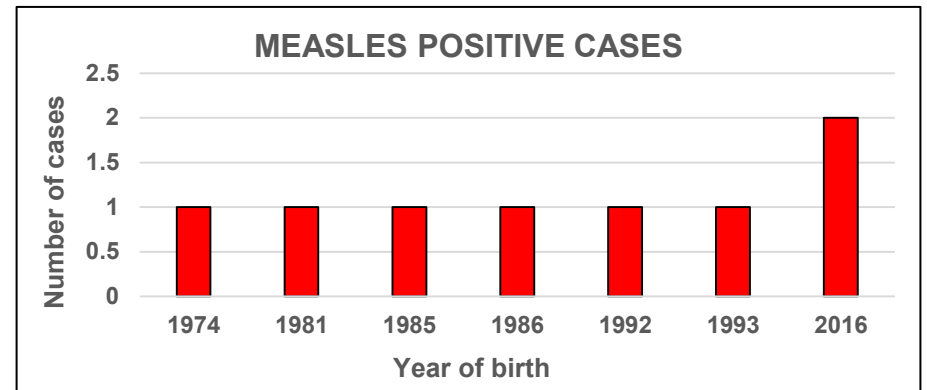


Figure 1. Years of birth for each positive Measles case

- There were no clear epidemiological links between cases; 2 were classified as imported (recent history of travel); 7 patients were unvaccinated, 1 patient reported one dose of a measles containing vaccine.
- All cases were confirmed by real-time RT-PCR assay performed on urine and/or oropharyngeal swabs. Seven samples were genotyped by SS: 6 belonged to genotype D8 (99.9% identity between strains, 100% BLAST identity with strains identified in Moscow – Russia in 2023), 1 sample collected from one of the two imported cases belonged to genotype B3 (BLAST 99.7% identity with strains identified in Florida – USA in 2016) (Figure 2).

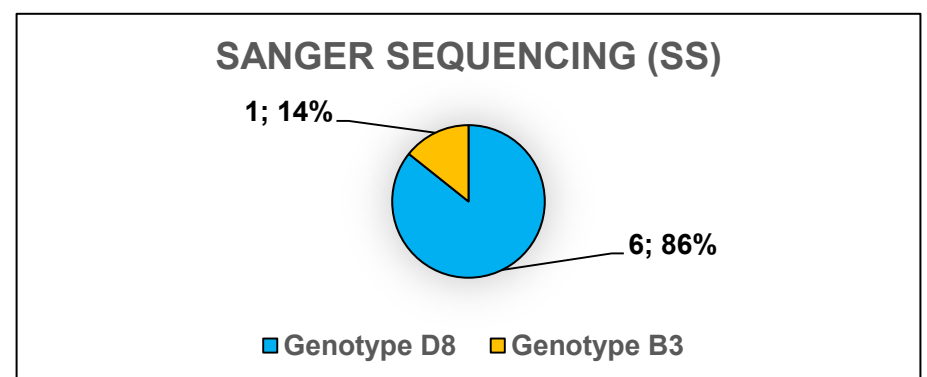


Figure 2. Percentage of Measles genotypes by Sanger Sequencing (SS)

- Noteworthy, none of the genotyped measles strains possessed the mutations previously identified as a possible issue for molecular diagnostics failure.

Conclusion

- Our results represent the first evidence of measles circulation in Liguria, after a period of low or no activity, and support the hypothesis of a sustained spread on the territory, with the possibility of a certain degree of underreporting.
- Measles molecular surveillance is a fundamental tool to track viral variants, transmission routes and outbreak evolution, allowing an accurate identification of imported cases.

References

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