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the Directing Council of the Pan American Health Organization in 1991 to eliminate onchocerciasis from the Americas. OEPA's objectives are to provide technical and supplemental financial assistance to the elimination programmes of the six endemic countries: Brazil, Colombia, Ecuador, Guatemala, Mexico and Venezuela (the Bolivarian Republic of). OEPA was initially supported by the River Blindness Foundation and later (in 1996) by The Carter Center. The regional initiative has been successful, and WHO has since verified the elimination of onchocerciasis transmission in 4 countries: Colombia (2013), Ecuador (2014), Mexico (2015) and Guatemala (2016). The Ministry of the Popular Ï " un

considered of high priority for 2022 MDA activities, i.e., that distribution of treatment to these communities would be scheduled first and coverage ≥85% should always be attained. Another 182 (27.8%) communities had received 11–19 effective treatment rounds and were considered a medium priority. Transmission was

Table 1 **Updated list of measles genotypes**
Tableau 1 **Liste mise à jour des génotypes de la rougeole**

Genotype – Génotype	Last detected[a] – Dernière détection[a]	Reference strain – Souche de référence	GenBank H	GenBank N
		MVi/Yaounde.CMR./12.83		
		MVi/New York.USA/0.94		
			AY047365	AY043459

Between 2018 and 2021, 97% of the 17 534 sequences reported to MeaNS were genotype D8 (67%) or genotype B3 (30%) (*Table 2*).

The standard genotyping protocol used in the GMRLN consists of analysis of the extent of sequence diversity in N-450, a highly variable region of the genome. MeVs with different genotype designations clearly represent separate chains of transmission; however, as a genotype contains multiple chains of viral transmission, analysis of genetic diversity within genotypes is also required for identification of transmission pathways, despite the reduction in the number of circulating genotypes. To label sequences within a genotype, each unique N-450 sequence submitted to the MeaNS database is assigned a distinct sequence identifier (DSId), in addition to the unique identifier assigned to each submission. DSIds allow identification of submissions with identical N-450 sequences. Although GMRLN has not established a formal definition of a lineage of MeV, the term has often been used to describe recently diverged groups that may represent a single outbreak or one or more transmis-

sion chains. Therefore, the current concept of a lineage would include one or more DSIds.

As the MeV sequences currently reported belong to only 2 genotypes, genetic diversity within a genotype is

sequences reported to MeaNS. Overall, in 2018–2021, the 10 most frequently detected named strains accounted for approximately 71% of all N-450 sequences reported to MeaNS (*Table 2*).

Because of the limited number of genotypes and widespread distribution of a limited number of contemporaneously circulating DSIds and named strains, tracking transmission chains by analysing N-450 has become less useful, as it may be diffcult to distinguish between continuous transmission of MeVs with the same DSId and repeated importations of MeVs with the same DSId. While such uncertainty can often be resolved by careful analysis of the epidemiological data, the resolution of genetic analysis can be improved by extending sequencing windows of the MeV genome, such as the non-coding region between the coding regions of the matrix and fusion proteins (MF-NCR) or by obtaining the whole genome sequence (WGS).[7] MeVs with the same DSId may be found to represent different lineages after extended sequencing windows are analysed. GMRLN recommends that N-450 sequences from as many chains of transmission as possi o e γ e smiss ← fquûM flineins

Members of these groups have co-circulated and have direct ancestral relations, indicating that N-450 sequences do not always provide adequate resolution of the chains of transmission. Acquisition of additional MeV sequence content (MF-NCR, WGS) and the usefulness of such data for phylogenetic inference are areas of intense research in GRMLN laboratories.

While ancestral relations among viral sequences are determined by phylogenetic analysis, the United Kingdom Health Security Agency has developed a prototype tool to aid GMLRN laboratories in determining the probability of sequence relatedness given a plausible nucleotide substitution rate. The tool does not require the computational resources necessary to perform advanced phylogenetic analysis[8] and allows informed but rapid decisions on the probability of relatedness among sequences (N-450, MF-NCR and WGS) obtained from measles cases within a defned time. Although the probability tool will provide answers rapidly, the methods, especially input substitution rates, will have to be standardized by GMRLN and the results confrmed by standard phylogenetic analysis.

Countries are required to report genotype data to regional verifcation commissions through their national verifcation committees. GMRLN recommendations for analysis of measles sequencing based on N-450 are as follows:

Countries should link sequences from currently detected wild-type viruses to DSIds and named strains in MeaNS.

Data for different genotypes should be displayed separately.

When possible, countries should use phylogenetic analysis to defne the relations between the sequences of contemporary cases. Regional Reference or Global Specialized Laboratories of GMRLN could provide assistance.

For countries that have achie F

examples of display of DSIds and named strains for measles virus.

While this report provides recommendations for interpreting N-450 sequences, extended window and WGS capacity in GMRLN laboratories should be increased. The Next Generation and Extended Sequencing Working Group (NEW) of GMRLN is developing a strategy to standardize laboratory methods and increase sequencing capacity in the network. NEW will also develop quality control standards for WGS to complement those in the existing molecular external quality control programme. GMRLN is updating the procedures for accession of sequences into the MeaNS database and guidance for use of DSIds and named strain designations. GMRLN is also developing a procedure to define and display lineages of currently circulating wild-type viruses. GMRLN has established a working group to update the nomenclature for the genetic characteristics of wild-type measles viruses to reflect the phylogenetic relations among sequences with use of extended sequencing windows.

Use of molecular epidemiological tools to monitor transmission of MeV requires a robust surveillance system. The COVID-19 pandemic has reduced the sensitivity of surveillance because of substantial decreases in the number of submissions to MeaNS in 2020 and 2021 (*Table 2*). In addition, baseline virological surveillance is inadequate in many countries. Restoring]ъ ı ӯ M]ъ ı ӯ M im rP Ấ ạ o ! † ! iṙ

Figure 2 **Phylogenetic tree based on sequence information displayed in *Figure 1* indicated by colour**
Figure 2 **Arbre phylogénétique fondé sur les informations de séquence présentées dans la *Figure 1* et indiquées par couleur**