# Evolving VDPV2 Epidemiology - 2019

Polio Partners Group Meeting, 6 December 2019, Geneva Mark A Pallansch, Centers for Disease Control and Prevention

#### cVPDV2 in 2019

- Dramatic increase in the number of new emergences (>40 in 2019 alone), disproportionately in Central Africa
- New emergences without obvious source
  - Pakistan: Multiple VDPV2 emergences that are cVDPV2 or unclassified
    - Several genetically linked SL2 viruses with as few as 2 nt changes from Sabin 2, despite no recent OPV2 use

## cVDPV2 in Central Africa



#### **Emergence** Name

0 ANG-HUI-1 (latest: contact 5019-06-04) ANG-LNO-1 (latest: contact 2019-05-14) ANG-LNO-2 (latest: contact 2019-08-01) 0000 CAF-BAM-1 (latest: case 2019-09-07) CAF-BAM-1-ENV (latest: collection 2019-07-22) CAF-BAM-2 (latest: contact 2019-05-27) CAF-BIM-1 (latest: case 2019-09-08) CAF-BIM-1-ENV (latest: collection 2019-09-05) 8 CAF-BIM-2 (latest: contact 2019-06-28) CAF-BIM-2-ENV (latest: collection 2019-09-11) CAF-BIM-3 (latest: contact 2019-08-23) RDC-HLO-2 (latest: case 2019-09-02) RDC-KAS-1 (latest: contact 2019-03-17) RDC-KAS-2 (latest: case 2019-06-07) RDC-KAS-3 (latest: case 2019-06-30) 0 RDC-SAN-1 (latest: case 2019-08-29) 0 RDC-TPA-1 (latest: contact 2019-06-27) 0 cVDPV2 (latest: case 2019-08-15)

Dots random within LGA
Created:10/24/2019
Last case dates are onset dates.
Last contact dates are specimen dates.
Last ENV dates are collection dates.

AFP cases, Contacts, Community Contacts, and ENV Specimens

#### Changing frequency of emergences



## Investigation - Sequencing

#### Virus Genetics – Challenges of interpretation

- Because of low divergence it has been challenging to establish unambiguous genetic linkages or independence among an increasing number of events.
- However, a unique mutation in the Kasai and Angola viruses allows for a unique opportunity to analyze the question of linkage and independence.
- This is being addressed by complete genome sequencing of all VDPV2 viruses in Central Africa (DRC, ANG, CAR).
- This is being expanded to other emergences sequentially (e.g., PAK is also in progress)

#### ANG, RDC/KAS, RDC/KCE whole genome analysis

- VDPVs from ANG, RDC/ Kasai & Kasai Centrale all share 5'UTR
  - Different from RDC/HLO and RDC/TAN
- Multiple recombination partners in P2 and P3
- Suggests linkage
- Sequencing and analyses still ongoing

3. PV2-PolioSabin2_AY184220
4. 3015616137_ZZYQXBFB_RDC-KAS-KAM-19-001_5nt_2019.1068
5. 3015616138_ZZYQXBFC_RDC-KAS-KAM-19-001_5nt_2019.1068
6.3015619633_ZZYQXBO4_RDC-KAS-KAM-19-001CC3_6nt_
7.3015619631_ZZYQXBO2_RDC-KAS-KAM-19-001CC10_5nt_
8.3015619632_ZZYQXBO3_RDC-KAS-KAM-19-001CC6_7nt_
9.3015619630_ZZYQXBO1_RDC-KAS-KAM-19-001CC14_4nt_
10.3015620583_ZZYGCDVX_ANG-LNO-CAM-19-001_10nt_2019.2603
11.3015626438_ZZYGCKTS_RDC-KCE-BIL-19-001_10nt_2019.2822
12. 3015626448_ZZYGCKU2_ANG-HUI-CUV-19-002_6nt_2019.3562
13. 3015626450_ZZYGCKU4_ANG-HUI-CUV-19-002_6nt_2019.3562
14.3015626440_ZZYGCKTU_RDC-KAS-KAM-19-004_6nt_2019.2904
15. 3015627797_ZZYGCM39_RDC-KAS-KAM-19-002_6nt_2019.2548
16. 3015626455_ZZYGCKU9_ANG-LNO-CAM-19-001-C12_8nt_
17.3015619623_ZZYQXBNX_RDC-TAN-ANK-19-003_8nt_2019.1123
18.3015619624_ZZYQXBNY_RDC-HLO-MAL-19-002_8nt_2019.1123
19. 3015619625_ZZYQXBNZ_RDC-HLO-MAL-19-002_8nt_2019.1123

	1	495	986	1,483	1,983	2,483	2,983	3,475	3,975	4,475	4,975	5,475	5,975	6,475	6,975	7,43
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#### Angola, 2019



Species C 5' UTR:

97.6-100%

### Summary of genetic inference

- The viruses in Kasai/DRC and Angola are all descended from a single 'source' that is already genetically distinct (2nt different from Sabin in VP1)
- Complete genome sequencing of multiple viruses in 2019 from this geography confirm additional genetic traits (mutation and recombination) that are consistent with a single 'source' virus.
- Viruses with minimal Sabin divergence from this source have emerged in multiple geographies from February to September, which has never been observed previously
- After emergence, spread and accumulation of genetic mutations occurred just like typical of cVDPVs

#### Possible scenarios for an explanation

- 1) The 'source' is a single child whose virus spread to multiple geographies without accumulating genetic changes inconsistent with the prior 19 years experience
- 2) The 'source' is a single child whose virus was highly transmissible prior to becoming a VDPV, also never observed
- 3) The 'source' is a common source that is highly distributed in the defined geography leading to multiple independent emergences of cVDPV2 (e.g., vaccines)

#### Summary

- Changing epidemiology of VDPV2 emergence, primarily in Central Africa
- Increasing ambiguity of linkage/independence because of low divergent cVDPV2
- Common related source but divergent from Sabin as measured by unique genetic mutations and recombination may provide insight into explanation to changing epidemiology
- Immediate change to understand these 2019 emergence events will include whole genome sequencing on all emergent VDPV2
- Uncertainty whether this will be generalizable to other Central African geographies of explanations for cVDPV2 in areas without known mOPV2 use

Thank you