DENV outbreak revisions

TASK 1: Sequence NDCP samples to demonstrate representativeness of Kampong Speu

* 302 national surveillance samples collected from 9 sentinel sites (Prey Veng, Banteay Meanchey, Tbong Kmom, Kampong Speu, Kampong Chhnang, Kampong Thom, Preah Vihea, Kratie) between Nov 2021 and Jul 2023
* 65 DENV pan-serotype PCR positive (shocking!)
* 33 with PCR Ct <35, we sequenced all of these. The remainder had too little material to work with; as you can see from the next step we only recovered sufficient reads from those with Ct <=25
* Of 33 samples, we could only generate consensus genomes from 10 (the remaining samples we suspect were too degraded at time of sequencing, had extremely low read counts) metadata: NDCP-additional-genomes.csv; fastas: denseq\_11235.zip
  + 3 from Kampong Speu: all DEN2 from 2022
  + 7 from other provinces: 3 from 2021, all DEN1; 4 from 2022, all DEN2
* We also have 130 dengue+ samples from IDSEQ in 2021-2022. Would it help to add these? I haven’t shared here but we have already sequenced them, would just need to create the genomes. metadata: NIH-sequence-data-additionalgenomes.csv
  + 1 DEN1, 121 DEN2, 8 DEN4
  + 104 from Kampong Speu, 26 from elsewhere
  + 11 from adults (>18)

TASK 2: Sequence older patients from 2019-2020

* I mentioned the additional genomes from adults (>18) in 2019-2020: realize that one of them was already in the table. So we just have one more to add (109-0283) from a 29 yo man in Kampong Speu in 2020. metadata: NDCP-additional-genomes.csv; fasta: 109-0283S\_L1\_1\_109216\_MH827546.1\_consensus.fa

>> Let me know which additional samples you end up using and I can work on uploading them to Genbank to get accession numbers while you update analyses.