Recombinant analyses in dengue virus type 1 with RDP5

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1 Introduction

Viral genome recombination influences evolution and phenotypic diversity. Understanding recombination in dengue virus (DENV) is then crucial for evolutionary biology and public health. In this study, we used the **RDP5 software** to screen for recombination in DENV variants from diverse geographical locales and all four serotypes (DENV 1-4). Our goal was to characterize recombination events, emphasizing the importance of annotation prior to recombination analysis. We found 14 recombination events on DENV dataset with 800 annotated genomes. Considering all datasets, we observed **recombination between different DENV serotypes** and **NS3 and NS5 genes** as hotspots of recombination on serotypes 1, 2 and 3.

2 Methodology

We created DENV genome datasets including all serotypes in sizes 50, 100, 200, 400, and 800 to measure **RDP5 execution time**. The recombination results discussed here are based on the 800 genomes dataset. The established **recombination detection protocol** is depicted on Figure 1.

3 Preliminary Results and Discussion

3.1 Prediction and evaluation of recombination events

Our analysis using RDP5 detected fewer recombination events in genome datasets of **DENV annotated with FLAVi** compared to those without annotation, across the datasets of size 50, 100, 200 and 800. The recombination analysis of 800 DENV genomes identified 14 recombination events with **annotation-guided alignment**, compared to 23 events with whole-genome alignment. Our results demonstrate that genome recombination detection is highly sensitive to genome annotation. The positions of **recombination breakpoints** were identified (Figure 2) on annotated genomes. We detected recombination events spanning the following genes: NS3 (8), NS5 (6), E (3), NS1 (3), M (2), pr(2), and NS2 (1).

3.2 DENV recombination landscape

We identified 3 **recombination events between serotypes** (Table 1). The recombinant and parental lineages are specified by accession code and serotype. Our methodology retrieved the results from a DENV-1 genomic dataset study published by Punpapong, Vitara *et al.* (2020). Our findigs of recombination between DENV serotypes correlates with the reported by Ko *et al.* (2018), which is suggested to be related with circulation and coexistence of diverse DENV variants within specific geographical regions.

3.3 Computational time

We assessed the execution time of RDP5 for our DENV genomic datasets. The program presented a **increase in execution time** as we duplicated the genome dataset size. With this analysis, we evaluate the time constraints of RDP5 when running large datasets on personal computers (Figure 3). This analysis was conducted on a x64-based PC with an Intel(R) Core(TM) i5-8265U with 8.00GB RAM.

4 Conclusion

Our study examines genome recombination in dengue virus (DENV) across various locations and serotypes. We emphasize the importance of genome annotation in dealing with recombination detection programs sensitivity. We also assessed the computational efficiency of RDP5, noting an increase in execution time with larger datasets. These results contribute to a better understanding of the recombination landscape of DENV.

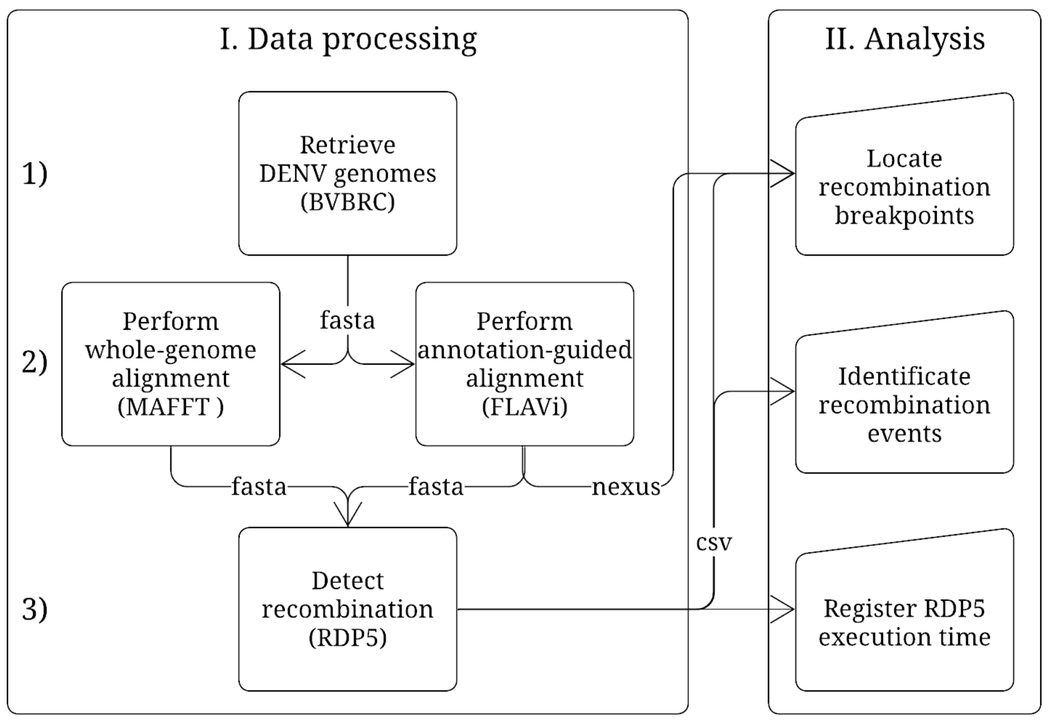

Figure 1: The process begins with (I) "Data Processing," which involves sequential steps 1, 2, and 3. The output is then used in three independent analyses in (II) "Analysis".

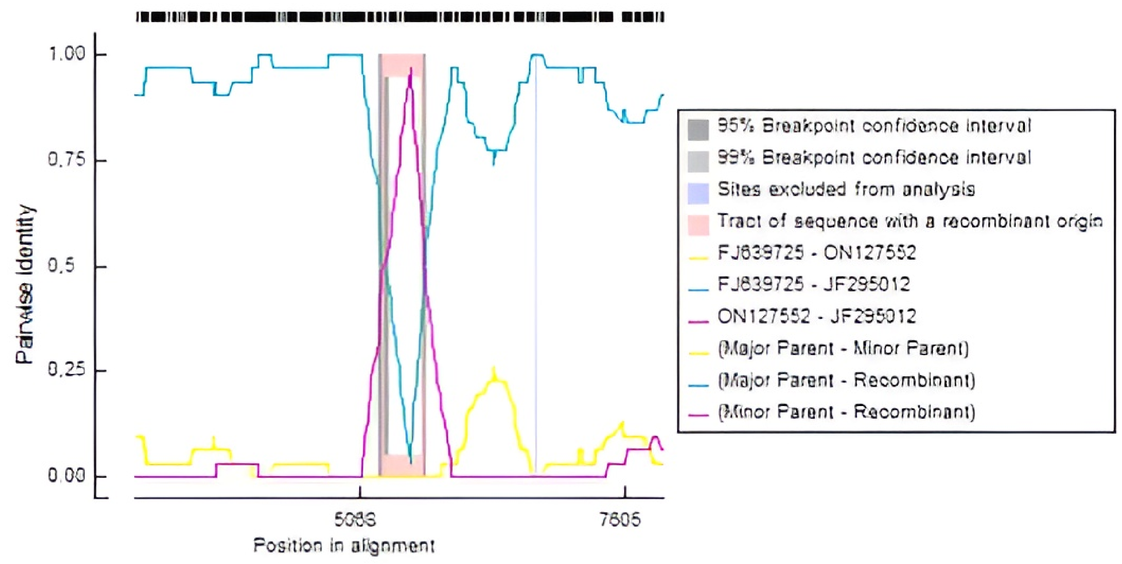

Figure 2: Recombination signal identified on DENV using the RDP5 program. The Y axis gives the percentage of identity within a sliding 100-nt window with 30-nt steps.

Recombinant	Minor Parent	Major Parent
FJ850090 (DENV-1)	EU569718 (DENV-2)	KP188567 (DENV-1)
JF295012 (DENV-3)	ON127552 (DENV-1)	FJ639725 (DENV-3)
OP895705 (DENV-3)	FJ898454 (DENV-2)	ON123658 (DENV-3)

Table 1: Description of detected DENV recombination between serotypes.

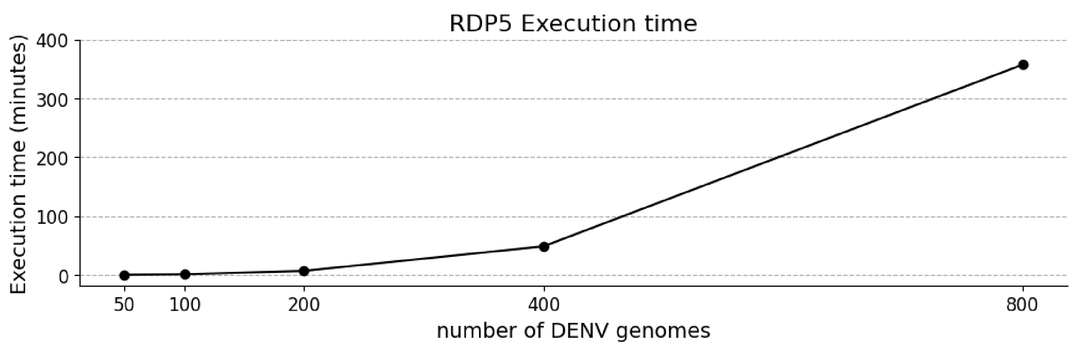

Figure 3: Execution time of RDP5 measured with the annotated DENV genome datasets.

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References

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