Letter to the Editor

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It did not stop there: rapid substitution of circulating SARS-CoV-2 variant of concern B.1.1.7 (Alpha) by variant of concern B.1.617.2 (Delta) and further evolution of different Delta sublineages in Southern Saxony-Anhalt in late summer 2021

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To the Editor,

In a recently published manuscript in the *Journal of Laboratory Medicine* [1], we reported about the establishment of a regional SARS-CoV-2 surveillance program using whole genome sequencing (WGS) of SARS-CoV-2 isolates. Specimens were collected over a period of 5 months (January to May 2021) from patients suffering from COVID-19 and from outpatients without any clinical signs or symptoms. Sequence libraries were constructed from total RNA extracts using the Illumina COVIDSeq Test kit (Illumina, San Diego, US). During this time frame, the majority of the obtained sequences (252/364=69%) were assigned to the SARS-CoV-2 variant of concern (VOC) Alpha (B.1.1.7), and only very few other VOCs were found in our cohort [Beta (B.1.351, n=2); Delta (B.1.617.2, n=1)]. This situation rapidly changed throughout the sommer months of June to September 2021, in which VOC Delta (B.1.617.2 and sublineages AY.xx) rapidly became the dominant SARS-CoV-2 lineage in our study population within only one month (see Figure 1). In the months August and September 2021, a multitude of further Delta sublineages emerged (Figure 1). This spread of VOC Delta could also be observed when comparing SARS-CoV-2 genome sequences from the entire country of Germany collected in the same time period, and submitted to GISAID (gisaid.org) [2]. A similar development was reported from other European countries [3, 4]. We have created interactive websites providing up-to-date SARS-CoV-2 lineage distribution from our local area. All unfolding data determined by our surveillance program are accessible via the URL https://ngs-info.medizin.uni-halle.de/shiny/SARS_CoV2/SARS_CoV2.html. As already mentioned in our previously published manuscript [1], this fast changing situation further fosters the need for an established SARS-CoV-2 testing by WGS as an important surveillance tool for early detection of upcoming new lineages of concern [4, 5].

While in June all sequenced SARS-CoV-2 genomes from the study population were classified as B.1.1.7 (VoC Alpha), from July on only B.1.617.2 and its sublineages AY.xx (VoC Delta) were found.

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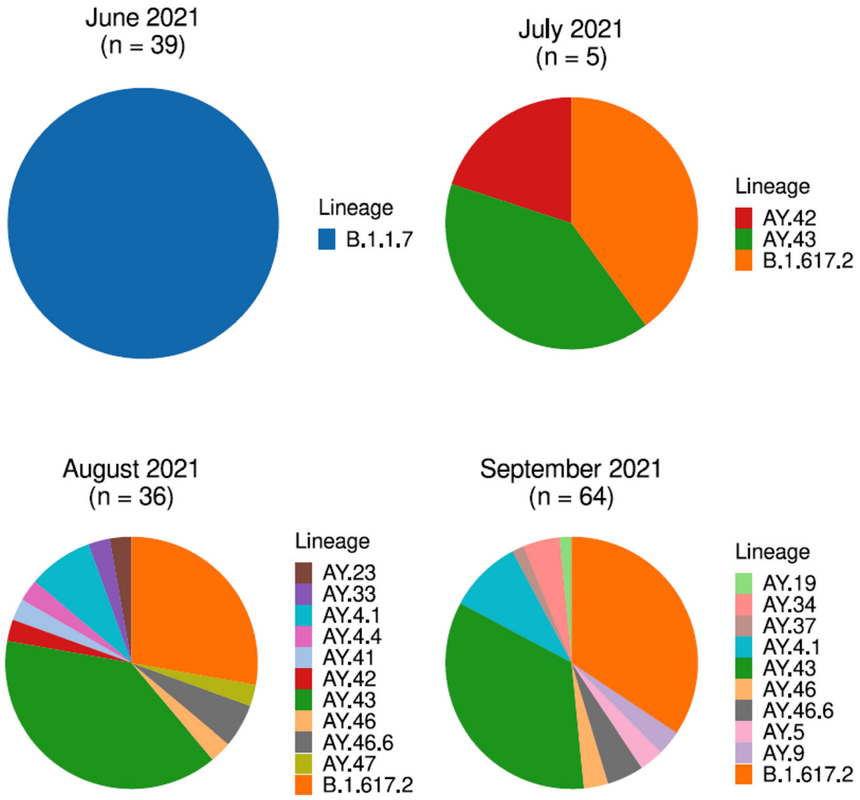

Figure 1: SARS-CoV-2 lineage distribution from June to September 2021.

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