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# Clinical and demographic features of SARS-COV-2 variants of concern (VOC): B.1.1.7 and B.1.617.2 At a tertiary care hospital in Southern Rajasthan.

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## *Abstract*

Introduction: As the global severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) pandemic expands, genomic epidemiology and whole genome sequencing are being constantly used to investigate its transmissions and evolution.
Aims and Objectives: To ensure that best use is made of the whole genome sequencing programmes for SARS-CoV-2 results, in improving public health. Analyze and establish a correlation of demographic features and vaccination status with clinical outcome of VOC's.
Material and Method: 478 samples (December 15, 2020- June 15, 2021) were shortlisted as per state government policy of sample selection criteria for genome sequencing, packed in triple layer according to standard transportation protocol and sent to the National Public Health Laboratory (NPHL) for whole genome sequencing.. The data collected by us were analyzed and correlated with the results of whole genome sequencing, shared by the NPHL to enhance public health impact of the variant identified.
Observation and Results: In our study we found 92% of B.1.617.2 (Delta) variants and 8% of B.1.1.7 (Alpha) variant. We found significantly high mortality (25%) in age group > 60 years compared to other age group (20-40years, 40-60years) with Delta variant (p value < .05). We also found that Delta variant is significantly more transmissible (p value < .05) than Alpha variant. Mortality was significantly higher among unvaccinated patients having co-morbid conditions rather than vaccinated patients having co-morbid conditions with delta variant (p value <0.05).
Conclusion: B.1.617.2 (Delta) variant has emerged as a common VOC among SARS-COV-2 patients in southern Rajasthan. Vaccination has a very high level of protective role in decreasing mortality, especially old age patients with associated co-morbidities among Delta variant.

**Keywords**:

SARS-CoV-2 variant of concern whole genome sequencing pre-existing medical condition