

Identification of viruses infecting indigenous ornamental bulbous plants in South Africa using NGS

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There are critical gaps in the knowledge of new and existing virus diversity in indigenous ornamental bulbous plants in South Africa. This project aims to determine the viromes of unknown viruses and local genetic variants of known viruses of indigenous ornamental bulbous plants in South Africa. Four related species (*Ornithogalum*, *Lachenalia*, *Eucomis* and *Veltheimia*) will be investigated.

Classical virus detection and identification are biased in that they all rely on prior knowledge of possible viruses present. Next generation sequencing (NGS) provides an efficient method to determine the entire virus population (virome) of plant organs, whole plants or even entire fields in an unbiased way. The technology has the ability to discover new viruses and to identify new genetic variants of existing viruses. Viral genome sequence information will allow the development of rapid and sensitive sequence-specific molecular diagnostic tools by crop protection specialists.