

FIRST FUNGAL GENOMES FROM THE FYNBOS

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In 1989 and 1993, long before he was the director of FABI, Prof. Mike Wingfield isolated two species of ophiostomatoid fungi from *Protea* plants in the Western Cape. More than 20 years later, the full genome sequences for both species, now known as *Knoxdaviesia capensis* and *K. proteae*, are publically available. These genomes, sequenced through the DST-NRF Centre of Excellence in Tree Health Biotechnology (CTHB), are also the first fungal genomes to be sequenced from the biodiversity hotspot that is the Core Cape Subregion (CCR). These results are currently in print in the journal *Standards in Genomic Sciences*.

These fungi have fascinated mycologists and botanists alike – what are ophiostomatoid fungi,



Knoxdaviesia capensis (top) and *K. proteae* (bottom) on *Protea* flowers. Figures from Aylward et al. 2015. IMA Fungus 6: 471–476

many of which are associated with plant diseases, doing in the seed cones of our beloved *Protea* plants? Fortunately, these fungi do not seem to like our national flower, the King Protea (*Protea cynaroides* (L.)L.).

Another source of relief is that several studies failed to find any evidence that the two *Knoxdaviesia* species (or the other ophiostomatoid fungi that were later identified in this niche) cause any harm to the *Protea* plants they inhabit. Current work on whether they affect seed germination should give us more evidence for or against this assumption within

the next few years.

Since the discovery of these species in *Protea*, much work has been done to determine how they move between the *Protea* seed cones and what environmental factors influence their presence. In short, the mites that infest *Protea* flowers and seed cones get “painted” with the sticky spores of the fungus while they move around in these structures. These small mites struggle to travel over extended distances, so they use beetles and birds as taxis. The fungi, going along for the ride, get dispersed quite far in this way – some of our studies suggest as far as from Stellenbosch to Mossel Bay.



So did these fungi just see a gap in a nice-looking seed cone and decide to live there? Why are they not causing disease in their *Protea* hosts and what enables them to live in dead cones that seem to have very little nutrients? Why are some species restricted to specific proteas, while other live happily in a diversity of hosts? The genome sequences of the two *Knoxdaviesia* species are not only great

because they are the first to be produced from their family of fungi or from the CCR, but they will also provide a blue-print for us to study these and many other unanswered questions. Using these genomes, we can look at *K. capensis* and *K. proteae* from the proverbial “head to toe” and ultimately learn a little more about the amazing biodiversity of fungi.