



## PE1164: Sequencing of *Vellozia* Spp. Genomes to Understand Drought Tolerance and Phosphorus Acquisition in Angiosperms

*Velloziaceae* are an angiosperm family that contains the most desiccation-tolerant species (approximately 200 out of 270 species). These species are distributed among five genera: *Acanthochlamys*, *Xerophyta*, *Barbacenia*, *Barbaceniopsis* and *Vellozia*. More than 80% of the *Velloziaceae* species occur in South America, where the greatest morphological diversity is also found. The genus *Vellozia* comprises both desiccation-tolerant and non-desiccation-tolerant species, offering an excellent model for studying the evolution of desiccation- and drought-tolerance traits on plant genomes. Desiccation-tolerant *Vellozia nivea* and evergreen *Vellozia intermedia* are both drought-tolerant, endemic to the Brazilian *campos rupestres* (rupestrian grasslands) and highly adapted to their extreme conditions. These are characterized by an extended dry season from May to September, high solar radiation and rocky, shallow, nutrient-poor soils with particularly very low phosphorus (P) availability. Unlike most model plants that come from environments where nitrogen (N) is the major limiting nutrient, *Vellozia* spp. have evolved in an environment where P is the key limiting nutrient, becoming a valuable model for crops cultivated in tropical soils.

Here we report the genome assemblies of the two *Vellozia* using a PacBio based, single-molecule real-time (SMRT) sequencing approach. We generated over 50 Gb of long reads for each species, representing ~100x coverage. We have also generated Illumina short reads at a depth of 60x. The genome size was determined by flow cytometry, resulting in 510 Mb for *V. intermedia* and 477 Mb for *V. nivea*. PacBio reads were assembled using Canu, and Illumina short reads were only used to polish the assemblies with Pilon. Construction of primary haploid assemblies were performed using HaploMerger2. The *V. intermedia* assembly spanned 452.7Mb across 1541 contigs with a contig N50 of 756.4 kb. The *V. nivea* assembly is smaller, at 323.9 Mb with 1521 contigs and an N50 of 671.7 kb.

*Vellozia* species are self-incompatible, and their genomes are highly polymorphic. The availability of high-quality genomes are crucial to allow the comparative analysis of specific genes and genes families encoding proteins characteristically involved with several molecular processes underlying responses to stresses. In order to achieve high-quality genomes, Chicago and Hi-C libraries preparation and sequencing are underway.

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