Scientists crack the genome of Singapore's national flower
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Ple. Miss Joaquim 'Agnes'. a The flower of Ple. Miss Joaquim 'Agnes' in front view with a dorsal sepal (ds), two lateral petals (lp), labellum (la), a modified petal, two lateral sepals (ls) and the gynostemium (gy), which is enlarged in the white-bordered inset image. b Terete leaves of Ple. hookeriana (PH), Ple. Teres (PT) and the hybrid Ple. Miss Joaquim 'Agnes' (PMJ), from left to right. Credit: Communications Biology (2022). DOI: 10.1038/s42003-022-03940-6

A collaboration between A*STAR's Genome Institute of Singapore (GIS) and SingHealth Duke-NUS Institute of Biodiversity Medicine (BD-MED) has decoded the entire genetic blueprint of Singapore's National Flower, Papilionanthe Miss Joaquim, also commonly known as Vanda Miss Joaquim, has revealed a total of 19 chromosomes spanning 2.4 billion nucleic acid base pairs with approximately 32,000 genes. These genes influence the production of proteins which impact the orchid's traits and cellular processes, and demonstrated the presence of natural products in our national flower responsible for its distinctive color pigmentation, smell, and other natural bioactive compounds.

Knowledge of the VMJ genome enables the team to perform chemical profiling to uncover VMJ's antioxidant properties and distinctive color pattern—flavonols and anthocyanins. The orchid was also found to contain vandaterosides, a bioactive compound capable of slowing the skin-aging process which was previously discovered in Papilionanthe Teres, the seed parent of VMJ.

Prof. Teh Bin Tean, Director of SingHealth Duke-NUS BD-MED, and Senior Group Leader of the Laboratory of Biodiversity Genomics at A*STAR's GIS, said, "We are heartened to be able to construct and decipher the genetic blueprint of our national flower, and hope that this achievement will be a significant contribution to our national heritage. VMJ is an orchid hybrid with magnificent blooms, and it is widely used as a breeding stalk for over 400 various orchid hybrids."

"Findings on its genomic makeup could help us better understand how to enhance genomic resources and pave the way for future research in gene and metabolite engineering. Deciphering the genetic code of flora species such as the VMJ also allows us to uncover naturally occurring bioactive compounds, which could be used for healthcare purposes and to understand, prevent and fight diseases."

Prof. Patrick Tan, Executive Director of GIS, said, "Singapore's biodiversity is well represented, with
over 4,000 species of native flora which are threatened in the face of global climate irregularities and issues. Thanks to advancing sequencing technology, we are able to conserve the genomes of flora by preserving the genetic code through sequencing. We are tremendously honored to start our journey studying Singapore's plant biodiversity with our national flower."

**More information:** Abner Herbert Lim et al, Genome assembly and chemogenomic profiling of National Flower of Singapore Papilionanthe Miss Joaquim 'Agnes' reveals metabolic pathways regulating floral traits, *Communications Biology* (2022). [DOI: 10.1038/s42003-022-03940-6](https://doi.org/10.1038/s42003-022-03940-6)

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