

## ***Vanilla*: a challenging genus with regards to the development of genomic resources**

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The development of enabling genomic resources for *Vanilla* would dramatically advance international efforts to improve the genetic foundation of this important global commodity for vanilla-growing countries worldwide. Currently, global production of *Vanilla planifolia* rests on a precarious genetic foundation that lacks natural resistance to disease-causing pathogens (such as *Fusarium*) and environmental fluctuations. This low genetic diversity of cultivated vanilla leaves it highly vulnerable to disease, climatic change, and other environmental stresses, placing the entire vanilla industry potentially at risk.

However, *Vanilla* is a challenging genus with regards to development of genetic resources: not only do *Vanilla* species have large genomes (approx. Cx = 2.5 Gb), but they are also characterized, like some orchids from various sections, by strict partial endoreplication (SPE) cycles, unknown in any other plant family.

We will present how we took these major constraints into account in the definition of genome sequencing strategies for this genus