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## HARNESSING MOLECULAR DATA TO SUPPORT DUS TESTING IN ORNAMENTALS: A CASE-STUDY ON *HYDRANGEA*

*Document prepared by experts from France*

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### HARNESSING GENOTYPING-BY-SEQUENCING TECHNOLOGIES TO SUPPORT DUS TESTING IN ORNAMENTALS: A CASE STUDY ON *HYDRANGEA*

1. Hydrangeas are one of the world's most popular ornamental flowers and one of the most economically important ornamental plants in France. Plant breeding for this genus is very dynamic. Over the last 10 years, between 40 and 70 new varieties per year have been registered for variety protection in Europe.
2. In 2022-2024, GEVES (France), in partnership with the Bundessortenamt (Germany), led a project co-financed by the Community Plant Variety Office of the European Union (CPVO) to explore the use of molecular markers to optimize DUS testing in ornamental species, using Hydrangeas as a case study. Relying on new high throughput genotyping-by-sequencing technologies, this pilot project tested a new approach combining neutral markers and markers linked to traits of agronomic and ornamental interest to characterize no fewer than 1,100 varieties from the French national reference collection of Hydrangeas.
3. The initial aim of this project was (1) to develop a molecular toolset from describing the Hydrangea collection and (2) to build a comprehensive reference library of molecular profiles which can be used (a) to secure DUS trials by checking the varietal identity of reference varieties and (b) to reduce the size of the trials by guiding the selection of similar varieties to be put side by side with the candidate varieties.
4. New sets of neutral markers were developed, and several markers potentially linked to traits of agronomic and ornamental interest were also tested. Molecular data were then used in combination with morphological data to test different approaches to secure and optimize DUS trials. Analyses are underway to design an optimal approach to integrating molecular analyses in routine DUS examinations.
5. This project demonstrated the cost-effectiveness of opting for high-throughput sequencing to describe an entire reference collection with a high number of molecular markers in a single experiment. It may pave the way for similar projects to support DUS testing in other ornamental species for which genomic resources are not available or maintaining a living collection is difficult and in silico reference library of molecular profiles may be an attractive alternative.

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