



Architectural and genetic characterization of *Hydrangea aspera* subsp. *aspera* Kawakami group, *H. aspera* subsp. *sargentiana* and their hybrids

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Résumé en anglais	<p>Hydrangea macrophylla (Thunb.) Ser. and H. paniculata Sieb. are the two most economically important species within the genus Hydrangea, and have been used as ornamental garden plants for a long time. However, other species such as H. aspera D. Don are of horticultural interest, particularly for the color of their inflorescences and plant shape. This species is composed of four sub-species and has previously been characterized both genetically and morphologically. The previous morphological characterization was qualitative, but was based mainly on leaf and inflorescence parameters outlined by UPOV, and provided little information about plant shape. To better characterize the shape of H. aspera, an architectural analysis was applied to the two most distantly related sub-species at the cytogenetic level: subsp. sargentiana (Redher) E.M. McClint. (clone 188) and subsp. aspera Kawakami group (clone 352). This method made it possible to reveal significant differences between these clones, both at the axis and the growth unit (GU) scale, in agreement with the high level of genetic differentiation (Jaccard dissimilarity index equal to 0.97) revealed between the two clones by Inter simple sequence repeats markers. Because this method is difficult to apply to a large population of individuals, a qualitative architectural characterization was tested on ten progenies derived from hybridization of the two clones, on the basis of their most discriminating architectural components. The hybrid nature of the progeny was confirmed by the architectural analysis. The architectural components of the hybrids are therefore a combination of those of the parents, with a predominance of clone 352, the female parent. Architectural differences between hybrids were clearly revealed by the length of the first vegetative GU (VGU1), the presence or the absence of VGU2 and the length of the floral GU of the A2 axis, and GU branching, allowing us to define five architectural profiles. These differences are supported by the average Jaccard dissimilarity index (0.33). This method, based on a qualitative description of the main architectural components of the plant, proved to be useful for characterizing the shape of H. aspera subsp. sargentiana, and subsp. aspera Kawakami group, and their hybrids. It could be extended to other sub-species of H. aspera and to their respective hybrids, providing an efficient tool for better characterizing genetic resources of H. aspera.</p>
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