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BOOK OF ABSTRACTS

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Flow cytometry measurements contribute to *Pisum* taxonomy

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Pea (*Pisum sativum* L.) has been widely used in early hybridization studies, as model for experimental morphology and physiology, and was Mendel's model species to untangle the laws of inheritance, which puts it at the foundation of modern genetics. Its large genome size (4775 Mbp as assessed by Feulgen method in 1976) slowed down progress in pea genomics compared with other plant species, but the recent availability of genome sequences of various legume species now permits genome wide comparison and allows to identify genes underlying agronomically important traits by combining candidate gene and synteny approaches. The efficient use of existing genomic resources is a key to success in these goals and several types of molecular marker sets as well as both transcriptome and proteome datasets exist. Despite this impressive background, and the fact that *P. sativum* is one of the most frequently used internal standards for flow cytometry studies with other species, there is still a need to further clarify the taxonomy within species of the genus *Pisum*. Thus, we have analysed by flow cytometry 42 accessions from a range of geographic origins and belonging to two wild species: *P. sativum* subsp*. elatius (e.g.* including former *P. elatius* and *P. humile/syriacum)*, *P. fulvum* and cultivated: *P. abyssinicum, P. sativum* as well as some primitive *P. sativum* cultigens (such as subsp. *transcaucassicum, asiaticum*), where some of them had been identified differently or tentatively in the past based on botanical characteristics. In these studies, all materials were analysed simultaneously with *Medicago truncatula* as the internal standard, and with various fluorochromes (DAPI, Propidium Iodide, Chromomycine A3) to assess the relative nuclear DNA content, genome size and AT/GC ratio. For some of the species studied this is the first report on these traits.

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