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Genome size estimation of *P. peltatum* using flow cytometry

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Podophyllotoxin is an active cytotoxic natural product that is precursor to important anti-cancer drugs. My laboratory has a fungal endophyte, PPE7 derived from the *Podophyllum peltatum* plant, both sources of the compound. Multiple locations of *P. peltatum* colonies have been mapped throughout the south eastern portion of Pennsylvania, some with slightly different phenotypic representations. Preliminary data suggests aneuploidy in the plant genome. Research has begun to confirm the aneuploid state and determine the implications for podophyllotoxin production. Plant nuclei were isolated and treated as single cells in flow analysis. I have perfected this protocol using both *Vicia faba* as an internal standard (Fava bean) and *Podophyllum peltatum* (American Mayapple). The nuclear isolation buffer, buffer volume and plant biomass amount have been optimized to produce an appropriate number of nuclei in a volume suitable for analysis. By these methods, I have determined the genome size of *Podophyllum peltatum* to be approximately 52.6327 ± 0.5877 Gbp (mean \pm SD, n=6). With these findings I will next determine if aneuploidy is prevalent throughout all mapped colonies and the podophyllotoxin production implications.

Biography

Lauren J Brown has completed her Master degree at the age of 22 at Thomas Jefferson University. From there she went on to work at Thomas Jefferson University Hospital in the Clinical Pathology Department. She is currently a 4th year PhD Graduate student at University of the Sciences in Philadelphia where she is studying natural products research with a focus on plant and fungal metabolites.

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