Mendel's seven factors: What they tell us about mutations in garden pea and perhaps other organisms with large genomes

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The molecular basis underlying the seven morphological variants Mendel studied has been gradually elucidated over the last 120 years. That for the final three mutations only was exposed in this last year in a masterful combination of classical and modern approaches. Not only did this study provide a detailed molecular understanding of all Mendel's 'factors,' but it also indicated a watershed moment for pea genetics and that for other organisms with complex genomes. The sequencing of entire genomes can now be thought of as standard practice for genetic analyses of large, segregating populations. Even for organisms, such as pea, that are difficult to transform, there exist numerous methods for providing compelling evidence of the identity between a morphological mutation and a change in DNA sequence or structure. Perhaps the most intriguing finding regarding the mutants Mendel investigated was that only two were caused by SNPs, two others by minor indels, and three by major indels (one being far upstream of the gene and flanking regulatory sequences). Textbooks on eukaryotic genetics may be inaccurate in their description of typical mutations in organisms with high fractions of repetitive DNA in their genomes.

Biography

Dr. Weeden obtained his Ph.D. in Genetics at University of California, Davis, served on the faculty at Cornell University for 18 years and then transferred to Montana State University to head the newly formed Department of Plant Sciences and Plant Pathology. He is now Professor Emeritus in that department and has published nearly 200 peer reviewed papers, chapters and books primarily on the genetics of crop plants and their wild relatives.