

Registered Crop Cultivars Composed of Multiple Biotypes: What About “DUS” rules?

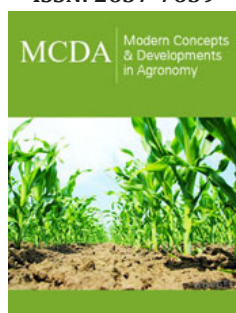
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ISSN: 2637-7659



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Submission: 📅 August 18, 2020

Published: 📅 September 01, 2020

Volume 7 - Issue 2

How to cite this article: E Metakovsky, VA Melnik, L Pascual, CW Wrigley. Registered Crop Cultivars Composed of Multiple Biotypes: What About “DUS” rules?. *Mod Concep Dev Agrono.* 7(2). MCDA. 000658. 2020. DOI: [10.31031/MCDA.2020.07.000658](https://doi.org/10.31031/MCDA.2020.07.000658)

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Background

To be officially registered and therefore to acquire the right to be called “a cultivar”, any newly bred common wheat genotype must pass a series of tests to confirm that it fits three requirements (called “DUS”-it must be genetically Distinct, Uniform and Stable). One of the more important of these requirements is that the candidate cultivar should be composed of genotypically identical homozygous individuals (seeds, plants). Thus, SW genotypic uniformity is one of the more important definitions of the officially registered cultivar [1]. The DUS procedure provides a basis for protecting the intellectual property of the breeder for a given cultivar [1-3].

History and Advances

Once any new wheat genotype has passed the tests of DUS, and is called “a registered cultivar”, it will be always treated as being composed of genotypically identical homozygous individuals and its uniformity will be accepted as a self-evident truth. However, there is a multitude of previous (“aged”) data certifying the intra-varietal non-uniformity of registered wheat cultivars, based on studies of polymorphic storage proteins of wheat grain [4-11] and of grain enzymes [12,13].

The non-uniformity of a cultivar (the concept is internally contradictory) may occur in two broad categories, authentic biotypes (genuine progeny from the original parental lines) and “foreign” seeds (originating from out-crossing or from mechanical admixture with foreign genotypes). The way to distinguish authentic biotypes from foreign seeds is the comparison of sets of alleles present in a non-uniform cultivar and in its parental cultivars. To do that, high-resolution genetic markers are needed.

In common wheat (*Triticum aestivum*), that requirement can be provided using the enormous polymorphism of the seed storage proteins, which provide multiple allelism at several gliadin-encoding (*Gli*) loci (from 16 to 44 alleles at each of the six major *Gli* loci are known). Thus, it is possible (theoretically) to distinguish more than a billion homozygous genotypes [14]. Using alleles at the *Gli* loci as genetic markers, it is possible to prove that any non-uniformity of registered cultivars is due to the presence of authentic biotypes (genotypes that originated from the initial cross, namely sister lines), but not to any type of admixture or error [15].

As a result of analyzing the gliadin genotypes of 8-10 individual seeds in each of 450 registered cultivars from 12 countries, an unexpected finding is now emerging that many (from 16% to 70% of registered varieties per country) of these cultivars are composed of multiple but authentic biotypes [16]. Equivalent findings have emerged from parallel studies

involving microsatellite markers; for example, 74% of Bulgarian cultivars were non-uniform at least at one of 19 markers used, although the origin of this non-uniformity (authentic biotypes or foreign seeds) was not analyzed [17].

Outlook

The current Plant Breeders' Rights rules have the strict demand for each cultivar to be genotypically uniform. Nevertheless, many registered cultivars have been found to be composed of multiple biotypes (although in many cases authenticity may have been demonstrated with respect to origins from the original cross). The presence of hidden (morphologically identical) biotypes, even as sister lines, may provide agronomic advantages for a cultivar, for example, improving its adaptability to the agro-ecological conditions of growth. Therefore, the demand of being "Uniform" may impose an unintended penalty on breeders, requiring yet a further hurdle in the processes of selection and registration of novel genotypes. There may thus be a need to re-evaluate relevant rules of cultivar registration for crop species in general.

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