**The OWB populations – how big are they?**

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*August, 2010*

*Updated December, 2018 by PMH*

The original set of OWB lines, used for construction of a linkage map by Costa et al. 2001, consists of 94 doubled haploid (DH) lines. The DH lines are numbered consecutively 1 – 94.

The OWB mapping population used by Szucs et al. (2009) and Close et al. (2009) consists of 93 DH lines due to a DNA quality and quantity issue leading to the removal of DH # 12 . In the n = 93 map data file on GrainGenes (<http://wheat.pw.usda.gov/ggpages/maps/OWB/> - “OWB OPA 2008 mapdata”), DH # 12 is missing and the DH lines are numbered 1 - 11 and 13 - 94.

The OWB mapping population used by Chutimanitsakun et al. (2011) consists of 82 DH lines. Eleven lines were dropped because we identified nine sets of identical lines. Specifically, the following sets of lines are identical: set 1 = DH 1, 4, 27, 62; set 2 = DH 16, 71; set 3 = DH 5, 18; set 4 = DH 31, 58; set 5 = 35, 50; set 6 = DH 15, 47; set 7 = DH 61, 88; set 8 = DH 22, 70; set 9 = DH 80, 77. One representative was kept from each set and DH #1, 5, 15, 22, 27, 50, 58, 62, 71, 80 and 88 were removed. Removing these lines, along with DH 12, leads to a population size of n = 82.

The members of each set were not identified as identical in previous iterations of the map (e.g. Costa et al. , 2001) because they were different from one another at multiple loci. These loci have been progressively removed from the data set based on quality control criteria. In other words, the lines were thought to be similar but not identical but the differences were due to scoring errors. The lines within each set are identical for all the Illumina SNPs and other loci included in the Szűcs et al. (2009) map. The lines within each set are also identical for all RAD loci reported by Chutimanitsakun et al. (2011). The most likely explanation for the presence of these identical sets of lines is that multiple haploids were inadvertently advanced from callus regenerated from a single embryo. These haploids were successfully doubled and advanced.

Using the 2383 locus data set, we empirically determined the effects of the duplicated lines on map construction by comparing results of analyses based on n = 82 and n = 93. As shown in Table 1, map lengths with the n = 82 and n = 93 populations are comparable. There were no changes in locus order between maps.

Henceforth, we will distribute the set of 82 lines, and the two parents. For future reference, this set of lines will be referred to as OWB\_Hb\_82. H.b. refers to the *Hordeum bulbosum* – the method of doubled haploid production. This nomenclature involving method of doubled haploid production is necessary due to the development of additional set of 93 DH lines by anther culture.

Cistue et al. (2011) reported the development and mapping of an additional 93 OWB DH lines. These lines, developed by anther culture (A.C.), are numbered starting with 801 and ending with 914. The numbering is non-consecutive, due to removal of numbered plants due to sterility, poor seed production, and/or insufficient DNA for genotyping. For future reference, this set of lines will be referred to as OWB\_A.C. \_93. As reported by Cistue et al. (2011) the H.b. and A.C. linkage maps (built with BOPA 1 and 2 SNPs only) are quite similar, and the two data sets can be seamlessly integrated. There are no duplicate lines in the A.C. data set.

 Therefore, we are confident that the presence of the duplicated lines in the H.b. lines has not compromised prior analyses, and we are pleased to offer the research community an additional 93 genotyped lines.

Seed sets of the OWB\_A.C.\_93 and OWB\_H.b.\_82 will be available from: Oregon State University (Corvallis, Oregon, USA), the Leibniz Institute of Plant Genetics and Crop Plant Research (*IPK***)** (Gatersleben, Germany), and the Barley Germplasm Center, Resource Institute <https://barleyworld.org/main/plant-material> for ordering procedures. When ordering, please be sure to specify which seed sets are desired (e.g. OWB\_H.b.\_82, OWB\_A.C.\_93, or and OWB\_H.b.\_82 + OWB\_A.C.\_93).

Genotype and phenotype data sets are available for the H.b and A.C. “subpopulations”, and the full population, on the [OWB data page](https://barleyworld.org/owb/data) and are archived at GrainGenes (<http://wheat.pw.usda.gov/ggpages/maps/OWB/>).

Table 1. Comparison of chromosome lengths (Haldane cM) in the OWB-2383+RAD map based on population sizes of n = 82 and n = 93. For details on genotyping and map construction please see Chutimanitsakun et al. (2010).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Number of | Chromosome | | | | | | |  | Total |
| individuals | 1H | 2H | 3H | 4H | 5H | 6H | 7H |  |  |
| n=93 | 156 | 190 | 208 | 125 | 241 | 163 | 195 |  | 1278 |
| n=82 | 158 | 188 | 208 | 127 | 238 | 163 | 204 |  | 1286 |

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