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A proposed revision of the IBPGR barley descriptor list*

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Summary. The International Board for Plant Genetic Resources (IBPGR) promote a set of morphological characters considered to be the minimum number for the description of crop germ plasm collections. The format and style of these IBPGR minimum descriptors are typical across numerous crop and species genera. However, no research publications have reviewed the relative usefulness of individual descriptors, nor indeed if additional descriptors should be included into the "minimum descriptor list".

A diverse collection of 1,379 spring sown barleys were evaluated for the 12 IBPGR "minimum" descriptors, an "additional" 9 morphological descriptors of similar type of the minimum descriptors, and a contrasting group of 3 hordein and 3 leaf esterase biochemical markers. Multivariate analyses were performed on combinations of the "minimum", "additional" and biochemical markers to reveal detailed associations amongst these various descriptors. The IBPGR minimum descriptor list for barley was shown to be inadequate in descriminating between accessions, and a revised list is proposed.

Key words: Germ plasm collections – IBPGR – Morphological descriptors – Barley

Introduction

Conservation of ex situ seed crop species has gained increasing popularity in the last few decades. From a modest effort of only five genebanks worldwide available for the good storage of seeds in 1974 (Williams 1984), the number of genebanks has expanded to at least 72 in 1985 (Plucknett et al. 1987). The total number of seedlines conserved in ex situ genebanks is estimated at 1.4–1.8 million individual accessions (Lyman 1984; Plucknett et al. 1987; Adham and van Sloten 1990). However, much material within genebanks remains poorly documented and accession characteristics largely unknown, and the problem of poor documentations has been a continuing problem (Shevchuk 1973; Frankel and Hawkes 1975; Erskine and Williams 1980; Lyman 1984).

In an effort to promote the evaluation and screening of germ plasm collections, the International Board for Plant Genetic Resources (IBPGR) produce a series of "descriptor lists" that encourage a unified documentation system thereby enabling through a standardised format, easier exchange of information between researchers and curator collections. Typically, descriptor lists comprise four sections (Chapman 1989; Cross 1990): passport, characterisation, preliminary evaluation and further characterisation and evaluation. In the preface section of each crop specific descriptor list there is a strong recommendation that curators collect information on the first three of these four sections.

Numerous studies highlight the significance of geographical origin as a major determinant in identifying areas of significant genetic variation (eg. Vavilov 1949–50), and geographical origin is the major collecting determinant of the IBPGR (Williams 1988). However, once a specific geographical grouping has been found, there may be significant numbers of genebank accessions that are duplicates or "near duplicates". Of the total ex situ world genebank resource of 1.8 million individual accessions (Plucknett et al. 1987), about 35–50% are considered indiscriminate duplicates (Lyman 1984; Plucknett et al. 1987; Perret 1989; Adham and van Sloten 1990). These indiscriminant duplicates represent cost inefficien-

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cies and contribute to an unnecessarily large number of accessions within world collections.

To rationalise the size of world collections to a smaller, yet comprehensive set of accessions, a highly discriminative method of comparing individuals needs to be developed. Such a discriminative method could then be applied to pre-determined (eco)geographical groupings to detect similar individuals, thereby enabling the rejection of duplicates and "near duplicates". Because the IBPGR has already developed a descriptor list infrastructure for most of the agriculturally/horticulturally important crop species, it could make an excellent vehicle for the elimination of indiscriminate duplicates within collections. The only modification would be to ensure that the preliminary characterisation and evaluation sections contain descriptors capable of high resolution between individual phenotypes. This paper addresses the discriminating power of descriptors "within the preliminary characterisation and evaluation" sections of the IBPGR descriptor list for cultivated barley.

Materials and methods

The plant material used in this study was the entire barley (*Hordeum vulgare* L.) collection of 1,379 pure line varieties maintained by the author at the DSIR Crop Research germplasm repository. These varieties were evaluated for the 21 morphological descriptors listed in Table 1 and 6 biochemical descriptors listed in Table 2. The field experiment was conducted in 1987–1988 under high-yielding conditions of applied fertiliser (300 kg/ha diammonium phosphate just prior to sowing), fungicide (0.5 l/ha "Cereous" just prior to ear emergence) and supplementary irrigation (two irrigations each of 25 mm: prior to ear emergence and at the soft dough stage). Height, maturity and physical grain measurements were scored on a single whole plot (6 rows × 2 m). Three spikes were sampled from the middle of the plot for subsequent laboratory examination. Foliar disease reaction to natural infections of brown rust (*Puccinia hordei*) was scored on single 2-m row plots in a nearby field, with similarly applied fertiliser and irrigation but with no applied fungicide. Biochemical evaluations were of seed storage proteins and leaf esterases. Hordein loci were determined electrophoretically by SDS-PAGE using the recommended procedure of Nielsen and Johansen (1986) with a small modification to the buffering potential of the gel matrix. Nomenclature of gene and allelic symbols were as described in Johansen and Shewry (1986) for *Hor 1* and *Hor 2* and in Shewry et al. (1983) for *Hor 3*. Esterase loci were determined electrophoretically by the native-PAGE method of Davis (1964) using allelic designations and the standard cultivars recommended by Nielsen and Johansen (1986) and Hvid and Nielsen (1977). Multivariate Principal Components Analysis (PCA) was based on Ward's method in the SAS® software package (SAS 1985). Further experimental details and discussion may be found in Cross (1990).

Results

Table 1 lists the 12 IBPGR "minimum" (1.1–1.12) and 9 "additional (2.1–2.9) morphological/agronomic descriptors. The number and frequency of descriptor states within each of the 21 descriptors are also given in Table 1. All characters states within each description were unequally represented with statistically significant chi-square deviation from equal representation. Allelic forms and their percentage frequency of the six biochemical descriptors are shown in Table 2.

Level of discrimination

Identical pairs of accessions were identified by an "exact match" of character states for each combination of morphological descriptors. For the IBPGR minimum sets of descriptors, 44% were identified as unique phenotypes whereas for the IBPGR minimum plus 9 additional descriptors, 96% of the DSIR collection could be uniquely identified. With the 6 biochemical descriptors detailed in Table 2, 46% of the DSIR collection could be uniquely identified. The combined discriminating power of the IBPGR minimum, additional and biochemical markers ($n=27$) identified 99.6% unique phenotypes within the DSIR collection of 1,379 barley cultivars. Biochemical evaluation requires specialist knowledge, equipment and laboratory space. Because these factors are not always available to curators of collections, and because field observation is a logical extension during seed rejuvenation, the characterisation of accessions by agronomic phenotype is therefore preferred as the preliminary/characterisation step. For most custodial purposes, therefore, the IBPGR minimum plus 9 additional morphological descriptors alone were sufficient for a detailed descrimination between accessions. With regard to the development of a practical but effective IBPGR minimum descriptor list, the biochemical descriptors were therefore omitted from further consideration.

Comparison with other morphological studies

There have been two major studies of worldwide morphological variation in the cultivated barley species: One with the USDA collection (Tobert et al. 1979); the other, the ICARDA collection (Somaroo et al. 1986). The descriptors in common between these and the current study are summarised in Cross (1990): within broad limits, the overall proportions of character states for the descriptors in common were generally not too dissimilar, with the exception of grain colour, growth habit and stem colour. For grain colour, Somaroo et al. (1986) reported a 50% proportion of the character state of "other", and similarly for stem colour a 99% proportion "other" within the ICARDA collection. Unfortunately, these authors did not elaborate what comprised "other". The ICARDA collection had a much higher proportion of intermediate and prostrate character states for growth class, reflecting a slightly higher proportion of accessions with winter habit.

Table 1. Summary statistics of "IBPGR minimum" (1.1–1.12) and other "additional" (2.1–2.9) morphological/agronomic descriptor states[a]. χ^2 values are deviations from equal distributions

Descriptor and character state	Number of Accessions	Frequency (%)
*1.1 Growth class† ($\chi^2 = 1{,}649$***)*		
1 Winter	8	0.6
2 Facultative	210	15.2
3 Spring	1,161	84.2
*1.2 Plant Height† ($\chi^2 = 211$**)*		
1 < 75 cm, (< −1 σ), short	232	16.5
2 75–85 (±1 σ), medium	673	47.8
3 > 85 (> +1 σ), tall	502	35.7
*1.3 Heading† ($\chi^2 = 472$***)*		
1 <70 days, early	626	45.4
2 70–80 mid-season lateral florets	673	48.8
3 >80 (> +1 σ), late	80	5.8
*1.4 Row number † ($\chi^2 = 467$***)*		
1 Six row	747	54.2
2 Two row + large	529	38.4
3 Two row with small sterile lateral florets	103	7.4
*1.5 Spike density † ($\chi^2 = 233$***)*		
1 Lax rachis internode	299	21.7
2 Intermediate	725	52.6
3 Dense	355	25.7
*1.6 Spikelet number† ($\chi^2 = 214$***)*		
1 < 20 (−1 σ), few	432	31.3
2 20–30 (±1 σ), average	725	50.3
3 >30 (+1 σ), many	355	18.4
*1.7 Hooded/awned† ($\chi^2 = 4{,}821$***)*		
1 Sessile hoods		
2 Elevated hoods	37	2.7
3 Awnless	14	1.0
4 Awned	17	1.2
5 Awned on central fertile now only	1,307	94.8
	4	0.3
*1.8 Awn roughness † ($\chi^2 = 759$***)*		
1 Smooth	178	12.9
2 Rough	1,201	87.1
*1.9 Rachilla hairs † ($\chi^2 = 439$***)*		
1 Short	813	59.0
2 Long	566	41.0
*1.10 Kernel covering † ($\chi^2 = 771$***)*		
1 Naked	174	12.6
2 Covered	1,205	87.4
*1.10 Lemma colour † ($\chi^2 = 623$***)*		
1 White/brown	1,153	83.6
2 Purple/black	226	16.4
*1.12 Grain colour † ($\chi^2 = 336$***)*		
1 White	576	41.8
2 Blue	660	47.9
3 Black	142	10.3
*2.1 Growth habit † ($\chi^2 = 2{,}348$***)*		
1 Erect	1,307	94.8
2 Intermediate	72	5.2
3 Prostrate	0	0.0
*2.2 Awn colour † ($\chi^2 = 1{,}558$***)*		
1 White	307	22.3
3 Yellow	822	59.6
5 Brown	192	13.9
7 Peddish	1	0.1
9 Black	57	4.1
*2.3 Glume colour † ($\chi^2 = 322$***)*		
1 White	322	23.4
3 Yellow	435	31.5
5 Brown	535	38.8
7 Black	87	6.3
*2.4 Stem colour † ($\chi^2 = 954$***)*		
1 Green	1,263	91.6
4 Purple	116	8.4
*2.5 Head shape ($\chi^2 = 575$***)*		
1 Parallel	1,135	82.4
2 Tapering	116	17.6
*2.6 1,000 Seed weight † ($\chi^2 = 253$***)*		
1 ≤35.4 mg, (−2 σ), small	248	18.0
2 35.5–40.4 (−2 to −1 σ), moderately small	117	8.5
3 40.5–45.4 (±1 σ), medium	200	14.5
4 45.5–50.4 (+1 to +2 σ), moderately large	365	26.4
5 ≥50.5 (> +σ), large	449	32.5
*2.7 Test weight † ($\chi^2 = 302$***)*		
1 ≤50 kg/hl, (< −1 σ), light	495	35.9
2 51–60 moderately	324	23.4
3 61–70 moderately heavy medium	471	34.2
4 ≥70 (> +1 σ), heavy	89	6.5
*2.8 Brown rust †[b] ($\chi^2 = 869$***)*		
1 Resistant (R)	140	10.2
2 Moderately resistant (MR)	401	29.0
3 Moderately susceptible (MS)	768	55.7
4 Susceptible (S)	70	5.1
*2.9 Purple auricle † ($\chi^2 = 90$***)*		
0 Absent	613	44.4
1 Slight pigment	328	23.8
2 Heavy pigment	438	31.8

*** $P < 0.001$

[a] Descriptors for the proposed revision are marked with a dagger (†), with quantitative character states expressed as standard deviation (σ) points about the ground trial mean

[b] Predominant brown rust race (avirulent/virulent) = Pa3, Pa5, Pa7/Pa, Pa2, Pa4, Pa6, Pa8, Pa9, Triumph

Table 2. Percentage frequency of allelic forms of 6 biochemical descriptors within the DSIR Crop Research world barley collection of 1,379 varieties

Hordein storage protein						Leaf esterases					
Hor 1		*Hor 2*		*Hor 3*		*Est 2*		*Est 4*		*Est 5*	
Al	5.1	An	6.9	Cb	78.0	Dr	40.2	At	69.0	Me	8.8
Ar	6.0	Ar	15.8	Ni	22.0	Fr	41.3	Su	31.0	Mi	6.0
Br	1.5	Ca	10.5			Pn	11.5			Pi	85.2
Cl	3.0	Cr	4.1			Un	7.0				
Fo	3.5	Gl	5.8								
Fr	8.1	Gn	2.6								
Gu	1.0	Go	0.6								
Ha	8.6	Hn	0.2								
Ju	2.3	Je	1.8								
Kw	3.1	Jo	1.5								
Ma	0.8	Ju	0.7								
Ni	1.4	La	13.9								
Pr	55.1	Ni	1.8								
Ta	0.4	Om	2.8								
		Pr	9.0								
		Rf	6.5								
		Ro	3.0								
		So	3.3								
		Wk	9.2								
Total											
14	100	19	100	2	100	4	100	2	100	3	100

Table 3. Simple correlation coefficients among 21 morphological descriptors whose values are statistically significant ($P = 0.001$) and large ($r \geq 0.4$)

1st component	2nd component	*r*
Heading	Growth habit	0.55
Lemma colour	Grain colour	0.58
Test weight	Row number	0.69
	Purple auricle	0.43
Number of spikelets	Row number	0.58
	Test weight	0.54
	Purple auricle	0.49
Awn colour	Glume colour	0.46
	Stem colour	0.49

Relationship between the morphological descriptors

Both simple correlations and PCA revealed the level of association between the various descriptors. Simple correlations among the 21 descriptors that were statistically significant ($P < 0.001$) and reasonably large in value ($r > 0.4$) are shown in Table 3. Based on the results of simple correlations, there were nine pairs of correlations (Table 3) whose values were statistically significant and greater than $r = 0.4$. However, no correlations were greater than $r = 0.7$. More detailed relationships were revealed by principal component analysis. With regard to the multivariate analysis, the first three principal components of the PCA explained 46.5% and 39.1% of the IBPGR minimum and IBPGR minimum plus additional datasets, respectively (Table 4). The magnitude of the individual descriptors indices within each eigenvector (Table 4) indicated the relative importance of each descriptor in explaining the variation within the first three principal components. These data are shown pictorially in Figs. 1 and 2 for the IBPGR minimum, and IBPGR minimum plus 9 additional descriptors, respectively. Spike density was the least useful descriptor in discriminating pattern within both the IBPGR minimum and IBPGR minimum plus 9 additional descriptor datasets. Head shape was a similarly poor descriptor within the IBPGR minimum plus 9 additional descriptor dataset. The magnitude of indices for hoodedness, awn roughness and kernel cover was reduced when the 9 additional descriptors were included in the PCA. On the basis of these statistical data the proposed revision of the IBPGR minimum descriptor list is given in Table 1.

Discussion

With respect to the 27 descriptors detailed in Tables 1 and 2, the DSIR Crop Research world barley collection encompassed a diverse range of germ plasm. However, if the uneven proportion of individuals within each character state is considered, the collection was not comprehensive. The DSIR collection did not have any accessions with prostrate growth habit and was poorly represented in several other character states; in particular, reddish awn colour (0.1%), winter growth class (0.6%), awnless varieties (1.2%) and varieties with elevated hoods (1.1%). However, in comparison with the world barley collections of the USDA (17,169 accessions; Tolbert et al. 1979) and ICARDA (8,000 accessions; Somaroo et al. 1986) the overall proportions of character states for the descriptors in common were generally not too dissimilar. Details of these comparisons are given in Cross (1990). This commonality may be a reflection of mutual exchange between these groups, either consciously (as with a substantial part of the USDA-ICARDA collections; Somaroo et al. 1986) or unconsciously, or it may be a reflection of the proportions of character states of the in situ-cultivated barley species. Since there was similarity of distribution of character states between the DSIR collection and that of larger collections, then number of samples alone cannot be used to form comprehensive germ plasm collections.

The level of discrimination afforded by an "exact match" of character states amongst the various descriptors showed that a "duplicate" was a function of the descriptors used. The IBPGR minimum descriptor list (12 descriptors) identified only 44% of the DSIR collection as unique phenotypes, which contrasted with a high level of descrimination (96%) when the additional 9 phenotypic/agronomic descriptors were included in the pair-

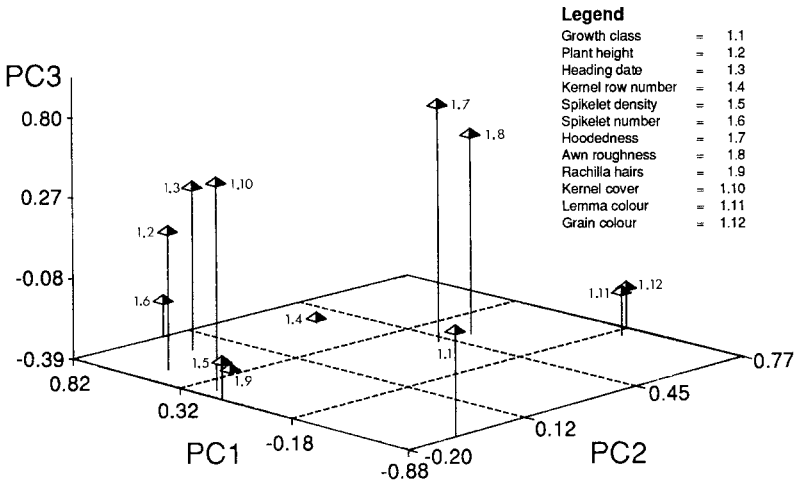

Fig. 1. Associations among the 12 IBPGR minimum descriptors revealed by PCA

Table 4. Eigenvalues, cumulative contribution percentages and eigenvectors of the first three principal components, of IBPGR minimum, and IBPGR minimum plus additional descriptors among the DSIR Crop Research world barley collection of 1,379 accessions

Principal component	IBPGR minimum descriptors			IBPGR minimum + additional descriptors		
	1	2	3	1	2	3
Eigenvalue:	2.48	1.74	1.35	3.49	2.81	1.91
Cumulative contribution (%):	20.70	35.20	46.50	16.60	30.00	39.10
Descriptor	Eigenvector					
1.1 Growth class	−0.68	−0.07	0.03	−0.55	0.24	−0.24
1.2 Height	0.51	−0.12	0.18	0.25	−0.40	0.36
1.3 Heading	0.63	0.02	0.29	0.24	−0.52	0.68
1.4 Row number	0.59	0.35	−0.36	0.82	0.11	−0.11
1.5 Spike density	0.13	−0.20	−0.23	0.06	−0.15	−0.04
1.6 Spikelet groups	0.82	0.05	−0.23	0.76	−0.34	0.08
1.7 Hoodedness	0.14	0.42	0.60	0.13	−0.04	0.12
1.8 Awn roughness	0.13	0.51	0.45	0.13	0.10	0.18
1.9 Rachilla hair	0.39	−0.02	−0.39	0.41	−0.12	−0.13
1.10 Kernel cover	0.22	−0.16	0.45	−0.05	−0.23	0.22
1.11 Lemma colour	−0.23	0.72	−0.20	0.00	0.65	0.47
1.12 Grain colour	−0.18	0.77	−0.21	0.09	0.65	0.36
2.1 Growth habit	–	–	–	−0.13	−0.30	0.65
2.2 Awn colour	–	–	–	0.48	0.60	0.18
2.3 Glume colour	–	–	–	0.14	0.52	0.25
2.4 Stem colour	–	–	–	0.36	0.51	0.21
2.5 Head shape	–	–	–	−0.12	−0.12	0.03
2.6 Seed weight	–	–	–	0.27	0.28	−0.42
2.7 Test weight	–	–	–	0.79	−0.02	−0.29
2.8 Brown rust	–	–	–	0.40	−0.04	−0.15
2.9 Purple auricle	–	–	–	0.61	−0.29	−0.12

wise comparisons. As a minimum objective, therefore, the currently recommended IBPGR minimum descriptor list for cultivated barley is, at best, modest in discriminating between phenotypes and may be described only as a book-keeping exercise.

If the overall objective is the ability to distinguish effectively between individual phenotypes, then the IBPGR barley descriptor list needs to be revised. The nine additional phenotypic/agronomic descriptors described in this paper yield an effective level of discrimination, and the principal component analyses suggest that 2 descriptors (i.e. spike density, head shape) could be safely omitted from the revised listing without loss of discriminating power. Although the indices for the eigenvectors for "awn roughness" and "hoodedness" were also small, the author reserves judgement on their dis-

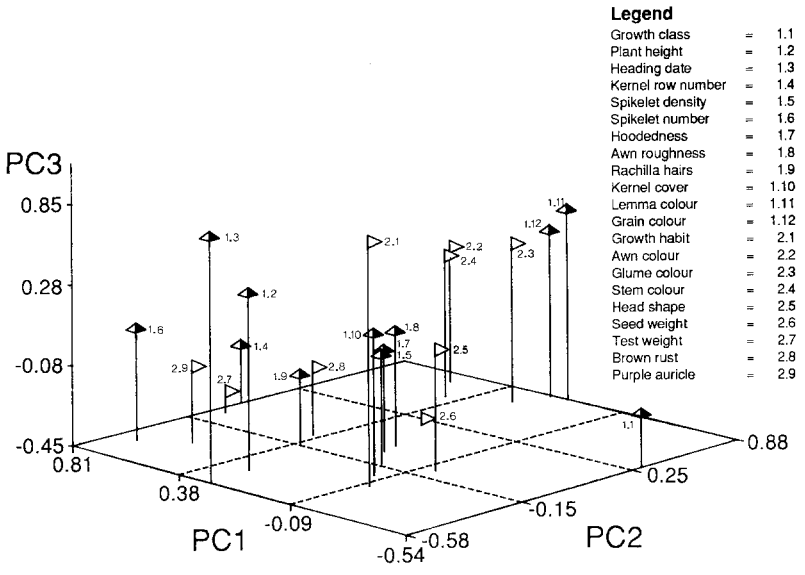

Fig. 2. Associations among 21 morphological descriptors revealed by PCA of IBPGR minimum (1.1–1.12, *pyramid*) and additional (2.1–2.9, *flag*) descriptors

criminating power because of the low number of accessions within the collection expressing these characters.

Within cultivated barley, there are numerous descriptors available for taxonomic description (e.g. Reid and Weibe 1979). Although the actual choice of descriptions recommended for inclusion in each IBPGR crop specific descriptor list is likely to be subjective, the have been chosen in consultation with groups of experts for each crop (Chapman 1989). The present study therefore utilised the 12 currently recommended descriptors as a starting point for the discrimination between phenotypes. Choice of the 9 additional descriptors was made with reference to and compromise between ease of scoring, relevance for other usage and general taxonomic value.

The revised IBPGR descriptor list as proposed in Table 1 lists several descripors that are, to varying degrees, complexly inherited. As such, these complexly inherited phenotypic traits (plant height, heading date, spikelet number per spike, 1,000 seed weight, test weight) are subject to genotype-environmental interaction influences and therefore liable to differing phenotype response in different environments. In such circumstances, as a method of reducing the experimental error of actual phenotypic response, a range of categorical character states is proposed, with each class expressed as a fraction of standard deviation points about the grand trial mean. A problem remains with continuous data being transformed into discrete categorical classes whereby phenotype observations that are close to the partition point between adjacent categorical classes may, by chance, be placed in either category. This potential for false declaration as "different" would only apply to observations close to the limits of each categorical class and in practice represent in minor proportion of observations. Despite the problem of "borderline observation" within/between categorical classes sometimes by chance describing a similar phenotype as "different", most of a curator's collection could be inspected for indiscriminate duplicates and rationalised to fewer accessions.

As a cautionary note, however, a "duplicate" is viewed by phenotypic markers used to describe an individual accession. Higher levels of precision in identifying duplicates require more points within the genome to be evaluated, and not until the majority of the genome is described can a true genotypic duplicate be identified. In terms of practice in custodial maintenance of germ plasm collections, the author suggests a compromise with the use of a set of quickly identified, highly discriminate and reasonably reliable phenotypic markers as a practical solution toward the elimination of very similar ("duplicate") accessions from germ plasm collections.

Plucknett et al. (1987) list the world holdings of cultivated barley at 280,000 individual accessions, of which 55,000 only are likely to be distinct samples. If these estimates of indiscriminate duplicates are correct then, at an annual cost of US $ 20 per accession (Plucknett et al. 1987) the rationalisation of the world-cultivated barley to "distinct" types would represent an annual savings of US $ 4.5 million. Emotive issues would probably emerge if "duplicates" were permanently removed from resource collections. Perhaps a satisfactory compromise would be to place all duplicates in cryogenic storage and to optimise the size of working collections and through their comprehensiveness, encourage their efficient and full evaluation.

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