Computer-Aided Analysis of Gliadin Electrophoregrams. II. Wheat Cultivar Identification and Class Comparisons[1]

H. D. SAPIRSTEIN and W. BUSHUK[2]

ABSTRACT

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A computer-based methodology is described that facilitates identification and comparison of wheat cultivars based on gliadin electrophoregram relative mobility and band density data. The basic programmed task compares a numerically encoded unknown or test polyacrylamide gel electrophoretic (PAGE) pattern with all reference PAGE patterns in the data base. For each comparison, four classes of events are scored: matching bands, nonmatching bands in the unknown and reference electrophoregrams, and bands that differ significantly only in staining intensity. These parameters are used in an equation to quantify electrophoretic pattern homology that determines the order of cultivar ranking. A separate computer program evaluates the uniqueness of the unknown electrophoregram and identifies diverse genotypes. Plotting software that provides a graphic analysis of electrophoretic pattern composition was developed to identify and differentiate matching and nonmatching bands in compared electrophoregrams. User-established parameters include least significant difference thresholds for comparing relative mobility and band density. The user may supply pedigree information and coded wheat class, quality, or region attributes for each reference electrophoregram. These data assist in the interpretation of program output and provide a basis for differentiation of cultivars according to functional type by gliadin composition. Two versions of the cultivar-ranking formula are described, and the performance of the computerized system is illustrated for several test input electrophoregrams against a PAGE pattern data base of 122 common spring, winter, and durum wheat cultivars.

The extensive heterogeneity of gliadin electrophoretic composition can confer a high level of discrimination among wheat cultivars. This attribute, combined with the stability of the gliadin electrophoregram in response to common environmental factors (Feillet and Bourdet 1967, Lee and Ronalds 1967, Wrigley 1970), gives the electrophoresis test its utility for cultivar identification (Autran and Bourdet 1975, Bushuk and Zillman 1978, du Cros and Wrigley 1979). However, experimental variation inherent in the electrophoretic method together with the multiplicity of gliadin components make the task of visually assessing the resemblance or composition of electrophoregrams both time consuming and imprecise.

Different approaches have been proposed to evaluate wheat cultivar identity using gliadin electrophoretic data (Wrigley et al 1982a). Diagnostic keys (Autran and Bourdet 1975, Ellis and Beminster 1977) or catalogs of cultivar formulas (Dal Belin Peruffo et al 1981, Jones et al 1982, Zillman and Bushuk 1979) based on band relative mobility (Rm) and relative staining intensity (density) values can reduce the arbitrariness of the identification process. These methods have limited value in routine applications where accuracy and speed are best achieved by computerized analysis.

An automated approach to expedite wheat cultivar identification was first reported by Bushuk et al (1978), who quantified gliadin electrophoregrams by minicomputer processing of densitometric scanning profiles. Computer programs to manipulate the derived Rm and band density data encoded as "cultivar signature arrays" were outlined (Sapirstein et al 1980) for wheat cultivar identification and other comparative analyses. Wrigley (1980) used a computerized strategy to identify Australian varieties by implementing a program designed to solve problems in taxonomy. Apart from the need for a large mainframe computer to run this program, this approach depended upon an a priori classification of bands which had limited precision. Lookhart et al (1983) described a computer program for identifying wheat cultivars similar to our earlier approach based on Rm and band density features; however, only integer accuracy was used to encode band relative mobilities. A second factor limiting discrimination was use of a similarity coefficient that left out the contribution from nonmatching bands. Program evaluation was limited to a single computer plot that traced the declining distribution of data base cultivars as a function of computed similarity to the unknown.

This study considers a more rigorous methodology for computer-based wheat cultivar identification. A set of programs designed for generalized comparative analysis of two-value parameterized lists is described which, in the present application, encodes the gliadin electrophoregram.

MATERIALS AND METHODS

Wheat Cultivars

Wheat cultivars used to establish a data base of gliadin electrophoregrams are listed along with their data base identification numbers (DBIN) in Table I. Represented are 122 common spring, winter, and durum wheat cultivars licensed in Canada before 1984. The list includes cultivars of commercial and historic importance as well as those possessing regional or restricted licenses. Several U.S.-registered hard red spring (HRS) wheats (DBIN 84-92) were also included in the data base.

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[2]Department of Plant Science, University of Manitoba.

Gliadin Extraction and Electrophoresis

Gliadin extraction and polyacrylamide gel electrophoresis (PAGE) in 6% gels were performed as described by Sapirstein and Bushuk (1985a). For each cultivar listed in Table I an average of three gliadin extracts was prepared for electrophoresis. These were derived from at least one single kernel and one ground sample of grain. All replicates were run on separate gel slabs. Gaps in the sequence of DBIN (Table I) indicate that offtype electrophoregrams were obtained for the preceding cultivar sample in the list. A characterization of offtype patterns observed is reported elsewhere (Sapirstein 1984).

Determination of Gliadin Band Mobilities and Densities

Mean band Rm values from replicated gliadin electrophoregrams were determined as described by Sapirstein and Bushuk (1985a). First, band migration distances were computed from photographs of gel slabs using a digitizing tablet, and then the absolute positional data were adjusted to the Rm scale using a new three reference band standardization implemented by means of a computer program.

Subjectively determining relative band densities from photographs of electrophoregrams was found to be sufficient, in terms of precision and speed, for cultivar comparisons. Bands were assigned an integer value from 1 (very faint) to 9 (very dense), relative to the band densities in the Neepawa reference electrophoregram run as an internal standard on each gel slab. This procedure adequately minimized run-to-run variation in the absolute level of band densities which may occur from gel staining and destaining. The precision of this method was ±1 density level. However, for computerized determination of electrophoregram homologies, a band density variation of ±2 units was routinely used as the margin of experimental error. As only sound and mature kernels were used for gliadin extraction, we generally observed no significant difference in the distribution of relative band densities in electrophoregrams from single kernels, or between single kernels and ground samples of grain.

Data Base Encoding of Gliadin Electrophoregrams

To encode Rm and band density data for computer analysis, each reference PAGE pattern entry in the data base was represented by three character and six numerical records in a set structure (Fig. 1). Character records specify the cultivar name and pedigree. The numerical portion comprises a 110-element, one-dimension cultivar signature array (row vector) of integer data. The first 100 positions contain paired Rm and density values, in order of increasing mobility, for up to 50 gliadin bands per electrophoregram. The remaining 10 element positions are used to store ancillary information on the cultivar and PAGE result. Included are the total number of gliadin bands in the pattern, the number of replicates averaged in computing Rm values, the DBIN, and three index codes specifying the class of grain, functional quality, and production region. These codes are subsequently used to print an attribute summary, along with the name and pedigree for each cultivar, listed by the ranking program of the cultivar identification system (refer to following section).

TABLE I
Wheat Cultivars Analyzed by Polyacrylamide Gel Electrophoresis for Cultivar Identification Data Base

DBIN[a]	Hard Red Spring Wheats
1	Early Red Fife
3	Garnet
4	Pioneer
5	Prelude
8,9[b]	Preston
11	Red Fife
12	Ruby
14	Acadia
15	Apex
16	Canus
17	Ceres
22	Coronation II
23	Lake
24	Lee
27	Marquis
28	Redman
29	Regent
30,32	Reliance
37	Renfrew
38	Renown
39	Reward
40	Selkirk
44	Benito
45	Canthatch
46	Columbus
47	Katepwa
52	Manitou
53	Napayo
56	Neepawa
57	Park
58	Pembina
59	Saunders
61	Sinton
62	Thatcher
63	Canuck
66,69	Chester
76	Chinook
77	Cypress
78	Leader
79	Rescue
84	Alex
85	Butte

DBIN	
86	Chris
87	Coteau
88	Era
89	Len
90	Olaf
91	Polk
92	Waldron
	Utility or miscellaneous class/type wheats
95	Bishop
96	Concorde
97	Dundas
99	Glenlea
101	Huron
102	Kota
103	Laval 19
104	Milton
105	Norquay
107	Opal
108	Pitic 62
109,110	Red Bobs 222
111	Vernon
	Soft white spring wheats
112	Cascade
113	Fielder
115	Kenhi
118	Lemhi 53
122	Lemhi 62
124,127	Quality A
128	Springfield
	Hard red winter wheats
129	Kharkov 22 M.C.
130	Lennox
131	Monopol
132	Norstar
133	Ridit
134	Sundance
135	Valor
136	Vuka
137	Wasatch
138	Westmont

DBIN	
139	Winalta
141	Yogo
	Soft white winter wheats
142	Cornell 595
143	Dawbul
147	Dawson's Golden Chaff
148	Favor
149	Fredrick
150	Gaines
151	Genessee
152	Gordon
153	Houser
154,155	Jr. No. 6
156	Nugaines
157	O.A.C. 104
158	Richmond
162	Rideau
163	Talbot
164	Yorkstar
	Soft red winter wheats
165	Egyptian Amber
166	Fairfield
167	Jones Fife
170	Kent
171	Sun
172	Thorne
	Durum wheats
174	Carleton
177	Coulter
178	Goldenball
179	Hercules
180	Macoun
181	Medora
182	Mindum
183	Nugget
184	Pelissier
185	Ramsey
186	Stewart 63
187	Wakooma
189	Wascana

[a] DBIN = Data base identification number.
[b] Two DBINs indicate different electrophoregrams for cultivar samples obtained from different sources.

The standard format of a data base reference PAGE pattern entry for Neepawa is shown in Figure 1. Because the cultivar name appears without an extension, a homogeneous cultivar sample is implied. To distinguish homogeneous from heterogeneous cultivar samples, the name of a cultivar appended with the code letter "M" indicates that the electrophoregram from the ground sample was a composite pattern derived from a mixture. The additional numbers specified by the signature array (element positions 103–109) indicate that the electrophoregram encodes 37 gliadin bands with Rm values averaged using 13 replicate PAGE patterns, and that the cultivar is a HRS wheat, superior to Marquis quality, grown in western Canada, and represents entry number 056 in the data base. A listing and definition of attribute summary codes (signature array element positions 106–108) is presented in Table II.

RESULTS AND DISCUSSION

Calculation of Electrophoretic Pattern Homology

Rm and band density values for each protein band in an electrophoregram were treated as continuous variables, where Rm represented the primary feature to assess the overall similarity in protein composition for two PAGE patterns. As such, the process did not require a classification of gliadin bands into a character set structure, as this can involve some simplification and interpretation (Wrigley 1980) and is otherwise time consuming. This problem is discussed in another article (Sapirstein and Bushuk 1985b).

For each comparison of an unknown and a reference cultivar, the pair of electrophoregrams were scanned from low to high mobility to quantify the extent of pattern homology. Compared bands were scored as matching if the differences in respective Rm and density values were within prescribed threshold levels. The least significant difference in Rm was programmable in increments of 0.1 distance units and was set in accord with the uncertainty in Rm measurements; in this study it was fixed at 0.5 Rm units, which corresponds to a significant difference ($P = 0.05$, two degrees of freedom) when comparing mean relative mobilities with a standard error of ±0.08 Rm units. The precision in determining Rm for the data base was previously found to be at least equal to this level, for all band positions in the electrophoregram field (Sapirstein and Bushuk 1985a). For band densities, which were quantified on an integer scale from one to nine, a difference of three units was arbitrarily used as the threshold to reject a match for compared bands not significantly different in mobility. Thus, for bands sharing only a positional homology, this event was scored as a band difference.

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NEEPAWA[1]
THATCHER*7/FRONTANA//THATCHER*6/KENYA FARMER/3/THATCHER
*2//FRONTANA/THATCHER, CANADA[2]
 121 2 152 3 173 2 183 1 206 4 220 4 225 1 239 4 264 4 278 2
 293 2 305 5 318 5 372 5 383 5 437 3 457 7 478 8 500 9 520 6
 543 5 570 8 583 5 594 7 618 6 638 6 644 3 680 1 708 4 723 3 [3]
 736 3 750 2 789 4 805 1 812 1 821 1 836 2   0 0   0 0   0 0
   0 0   0 0   0 0   0 0   0 0   0 0   0 0   0 0   0 0   0 0
   0 0  3713   0 2   4 2  56 0
    |    | |   | |   | |  | |
    4    5 6   7 8   9 10  11 12
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[1] Cultivar name; maximum 16 characters including extension.
[2] Pedigree; 110 characters, 55/record maximum.
[3] Signature array element positions (SAEP) 1-100 comprise paired Rm and band density parameter values in odd and even array element locations respectively. Rm values are in integer data type with the decimal point implicit after the second digit.
[4] SAEP 101-102 set=0.
[5] SAEP 103 = gliadin bands encoded for electrophoregram.
[6] SAEP 104 = replicates averaged to compute mean Rm values.
[7] SAEP 105 = blank, not assigned.
[8] SAEP 106 = kernel class code.
[9] SAEP 107 = general functional quality or utility code.
[10] SAEP 108 = production region code.
[11] SAEP 109 = data base identification number.
[12] SAEP 110 = blank, not assigned.

Fig. 1. Standard data base coding format for the gliadin electrophoregram of cultivar Neepawa.

In the algorithm which analyzes the composition of two electrophoregrams (denoted below as "A" for an unknown and "B" for a reference cultivar), four classes of events were differentiated: 1) m, pairs of bands with matching relative mobility and density values; 2) j, bands present in the unknown "A" but absent from the reference "B"; 3) k, bands present in "B" but absent from "A"; 4) l, pairs of bands that share a positional homology but possess significantly different levels in density. Percent pattern homology (% PH), which determined the basis for cultivar ranking in several programs of the cultivar identification system, was expressed as the ratio

$$\frac{100 \times (\text{No. of pairs of matching bands})}{\text{No. of pairs of matching bands} + \text{No. of different bands}}.$$

This definition is similar to the simple matching coefficient described by Sneath and Sokal (1973) and is a common form used to assess the variation in seed protein banding patterns of two electrophoregrams (Ladizinsky and Hymowitz 1979). In the present application, the above ratio was specified as follows

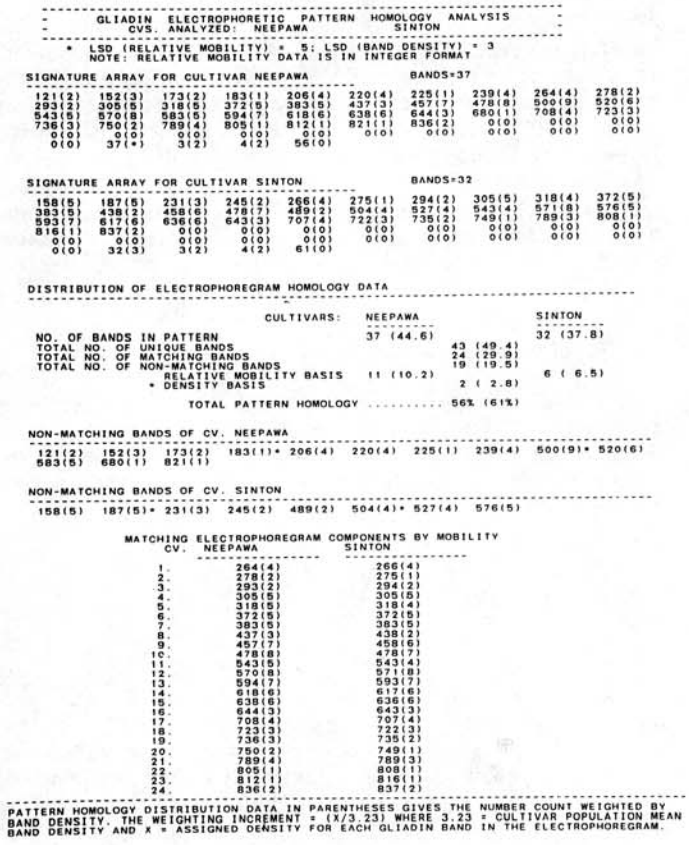
$$\%\ \text{PH} = \frac{100 \times m}{m + (j + k + l)}. \qquad (1)$$

No weights are attached to the terms in equation 1. This means, for example, that extremely faint bands (density = 1), which are commonly observed in electrophoregrams but tend to be nonreproducible as they are difficult to visualize, carry the same weight in the equation as the most intensely stained components. Because a gliadin band represents a multistate character with a relative intensity that is largely an expression of genotype, the problem can be resolved by weighting band number counts as a function of individual band densities. In this way, the protein composition of an electrophoregram can be quantified in addition to the presence or absence of bands.

TABLE II
Cultivar Signature Array Attribute[a] Summary Index Codes and Definitions

Attribute Index No.	Signature Array Element Position: 106 Class Code	Definition	107 Quality Code	108 Region Code
1	Blank		Blank	Blank
2	HRS	Hard red spring	NEMQ[b]	W.CAN
3	SHRS	Semi-hard red spring	EMQ[b]	SAWFLY
4	HWS	Hard white spring	SMQ[b]	S.ALTA
5	SHWS	Semi-hard white spring	FEED	BC
6	SWS	Soft white spring	PASTRY	ONTARIO
7	SRS	Soft red spring	BW[c]	QUEBEC
8	SHPS	Semi-hard purple spring	PASTA	ATLANTIC
9	HRW	Hard red winter	GHP[d]	ATL/BC
10	SHRW	Semi-hard red winter	nd[e]	R/W.Can[f]
11	SWW	Soft white winter	nd	USA
12	SRW	Soft red winter	nd	UTILITY
13	DURM	Durum	nd	E.CAN
14	nd		nd	E.CAN/BC

[a] Source of attribute data: Handbook of Canadian Varieties of Barley, Field Beans, Field Peas, Flax, Oats, Rye, and Spring, Durum, and Winter Wheat, prepared by Research Branch, Canadian Department of Agriculture; varietal description reports prepared by The Production and Marketing Branch, Plant Products Division, Agriculture Canada, Ottawa, Ontario.
[b] NEMQ = HRS wheat not equal to Marquis, EMQ = HRS wheat equal to Marquis, and SMQ = HRS wheat superior to Marquis in milling and baking quality.
[c] BW = non-HRS bread wheat.
[d] GHP = general household purpose.
[e] nd = not defined.
[f] R/W.CAN = restricted from West Canadian region by kernel characteristics.



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GLIADIN ELECTROPHORETIC PATTERN HOMOLOGY ANALYSIS
CVS. ANALYZED: NEEPAWA SINTON
* LSD (RELATIVE MOBILITY) = 5; LSD (BAND DENSITY) = 3
NOTE: RELATIVE MOBILITY DATA IS IN INTEGER FORMAT

SIGNATURE ARRAY FOR CULTIVAR NEEPAWA  BANDS=37
121(2) 152(3) 173(2) 183(1) 206(4) 220(4) 225(1) 239(4) 264(4) 278(2)
293(2) 305(5) 318(5) 372(5) 383(5) 437(3) 457(7) 478(8) 500(9) 520(6)
543(5) 570(8) 583(5) 594(7) 618(6) 638(6) 644(3) 680(1) 708(4) 723(3)
736(3) 750(2) 789(4) 805(1) 812(1) 821(1) 836(2) 0(0) 0(0) 0(0)
0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0)
0(0) 37(*) 3(2) 4(2) 56(0)

SIGNATURE ARRAY FOR CULTIVAR SINTON  BANDS=32
158(5) 187(5) 231(3) 245(2) 266(4) 275(1) 294(2) 305(5) 318(4) 372(5)
383(5) 438(2) 458(6) 478(7) 489(2) 504(4) 527(4) 543(4) 571(8) 576(5)
593(7) 617(6) 636(6) 643(3) 707(4) 722(3) 735(2) 749(1) 789(3) 808(1)
816(1) 837(2) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0)
0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0) 0(0)
0(0) 32(3) 3(2) 4(2) 61(0)

DISTRIBUTION OF ELECTROPHOREGRAM HOMOLOGY DATA

CULTIVARS:        NEEPAWA          SINTON
NO. OF BANDS IN PATTERN          37 (44.6)        32 (37.8)
TOTAL NO. OF UNIQUE BANDS        43 (49.4)
TOTAL NO. OF MATCHING BANDS      24 (29.9)
TOTAL NO. OF NON-MATCHING BANDS  19 (19.5)
  RELATIVE MOBILITY BASIS        11 (10.2)        6 ( 6.5)
* DENSITY BASIS                  2 ( 2.8)
TOTAL PATTERN HOMOLOGY ..... 56% (61%)

NON-MATCHING BANDS OF CV. NEEPAWA
121(2) 152(3) 173(2) 183(1)* 206(4) 220(4) 225(1) 239(4) 500(9)* 520(6)
583(5) 680(1) 821(1)

NON-MATCHING BANDS OF CV. SINTON
158(5) 187(5)* 231(3) 245(2) 489(2) 504(4)* 527(4) 576(5)

MATCHING ELECTROPHOREGRAM COMPONENTS BY MOBILITY
CV.  NEEPAWA  SINTON
1.   264(4)    266(4)
2.   278(2)    275(1)
3.   293(2)    294(2)
4.   305(5)    305(5)
5.   318(5)    318(4)
6.   372(5)    372(5)
7.   383(5)    383(5)
8.   437(3)    438(2)
9.   457(7)    458(6)
10.  478(8)    478(7)
11.  543(5)    543(4)
12.  570(8)    571(8)
13.  594(7)    593(7)
14.  618(6)    617(6)
15.  638(6)    636(6)
16.  644(3)    643(3)
17.  708(4)    707(4)
18.  723(3)    722(3)
19.  736(3)    735(2)
20.  750(2)    749(1)
21.  789(4)    789(3)
22.  805(1)    808(1)
23.  812(1)    816(1)
24.  836(2)    837(2)

PATTERN HOMOLOGY DISTRIBUTION DATA IN PARENTHESES GIVES THE NUMBER COUNT WEIGHTED BY
BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = CULTIVAR POPULATION MEAN
BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.
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Fig. 2. Pattern homology analysis printout (program HOMOLOGY2) for cultivars Neepawa and Sinton.

In the case of a single electrophoregram with an average distribution of band densities, it can be determined that

$$\Sigma_{i=1}^{n} (d)_i / \mathrm{Dav} = n, \tag{2}$$

where $(d)_i$ represents the density assignment for the ith band in the electrophoregram, and Dav is a constant equal to the average density value for all bands in the data base cultivar population. The term on the left-hand side of equation 2 gives the weighted-by-band density (WBD) score for the electrophoregram. A WBD value significantly lower or higher than the number (n) of bands in the pattern indicates that the electrophoregram contains bands with a lower or higher than average level of staining intensity or protein concentration.

In an analogous fashion, equation 1 was modified to quantify significant departures from average band density for matching and nonmatching bands in compared electrophoregrams:

$$\text{Weighted \% PH} = \frac{100 \times \Sigma_{i=1}^{m} (d\mathrm{A} + d\mathrm{B})_i / 2\mathrm{Dav}}{\Sigma_{i=1}^{m}(d\mathrm{A} + d\mathrm{B})_i / 2\mathrm{Dav} + \Sigma_{i=1}^{j}(d\mathrm{A})_i / \mathrm{Dav} + \Sigma_{i=1}^{k}(d\mathrm{B})_i / \mathrm{Dav} + \Sigma_{i=1}^{l} |(d\mathrm{A}\text{-}d\mathrm{B})|_i / \mathrm{Dav}}, \tag{3}$$

where dA and dB represent band densities for the ith band or pair of bands in cultivars "A" and "B." For cultivar identification, an algorithm implementing equation 3 was found to provide better discrimination than simple matching and nonmatching band count ratios (Sapirstein 1984).

Outline of Computer Programs

The identification system is comprised of three cultivar ranking procedures dedicated to different aspects of the comparative analysis problem. The scope of each is outlined below as follows:

1. The program designated "CVID" produces a short list ranking of data base reference cultivars in order of declining pattern

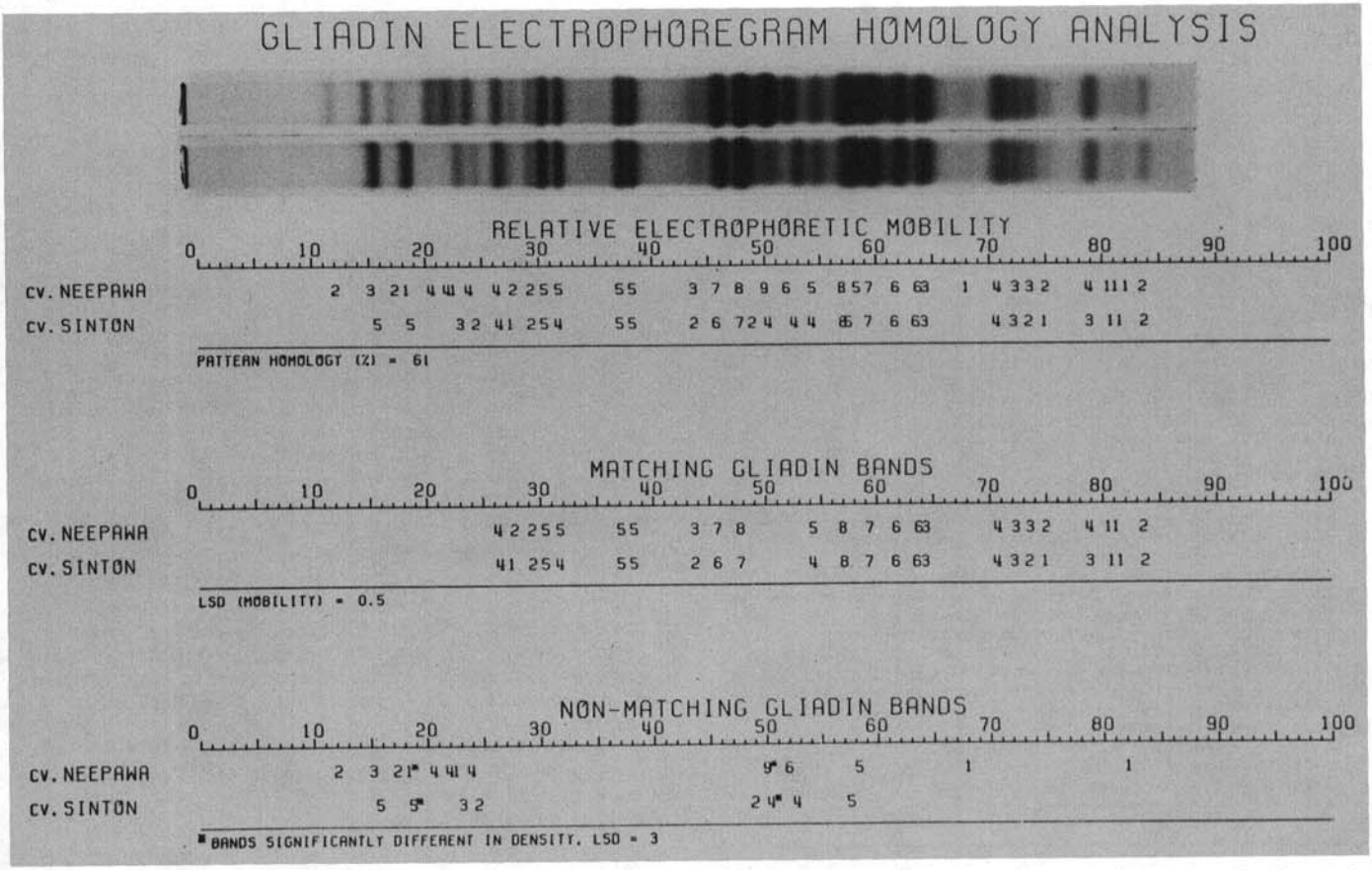

Fig. 3. Cultivar formula plots of pattern homology analysis (program HOMPLOT2) for cultivars Neepawa and Sinton, along with photographs of respective electrophoregrams.

homology with the unknown electrophoregram. A threshold value for % PH, which may be set by the user, controls entry into the list. Printed output includes the cultivar name, pedigree, class/quality attributes, and tabulation of matching and nonmatching bands for each paired comparison.

2. Programs "IDHOM" and "IDPLOT" combine to produce a graphic analysis of electrophoregram composition for cultivars specified in the list generated by program CVID. IDHOM identifies matching and nonmatching bands for each comparison of cultivar PAGE data between the unknown and data base member. The printout gives a detailed summary of results on standard forms. Program IDPLOT uses as input the data derived from the IDHOM routine to graphically visualize the composition of matching and nonmatching bands, which are isolated in separate plots for the list of ranked cultivars.
3. Program "CVMAP" computes the minimum number of bands that must be deleted from the unknown and each reference electrophoregram to yield patterns of identical composition. The printout is a frequency distribution that plots each cultivar's data base identification number and pattern homology score against the value of the independent variable, i.e., the total number of differences with the unknown electrophoregram. The result assists in evaluating the uniqueness of the unknown and identifies cultivars lying at the margins of the distribution which are of diverse genotype.

In addition to these ranking programs of the cultivar identification system, the comparative analysis could be focused on selected pairs of electrophoregrams to produce numerical data ("HOMOLOGY2") and graphic output ("HOMPLOT2") results for two cultivars of special interest. All software, with the exclusion of plotting programs IDPLOT and HOMPLOT2, was written in FORTRAN using standard data items, with the exception that character expressions were used in the source code. As such, these programs must be compiled under compilers that can translate the character data type (e.g., WATFIV, FORTRAN 77). The plotting programs IDPLOT and HOMPLOT2 were developed in FORTRAN but also incorporate several subroutines of CALCOMP basic software (California Computer Products, Anaheim, CA) to produce results on a Versatec D1200A matrix plotter or a Xerox 8700 laser printer. All programs were tested on IBM 470 and Amdahl 470/580 mainframe computers. Program implementation on a laboratory-scale mini/micro computer (256K memory) should be readily feasible, as the only major machine dependencies are in the input and output routines. Commented program source listings can be obtained from the first author on request.

Analysis of Pattern Homology for Two Cultivars

The various programs of the cultivar identification system implement a common procedure for paired comparison of electrophoregram data. The basic processing characteristics of the larger system can be well demonstrated with an analysis of two cultivars. Figures 2 and 3 show typical printout and graphic analysis results generated by HOMOLOGY2 and HOMPLOT2, respectively. In this example, electrophoregram data were analyzed for the HRS wheat cultivars Neepawa and Sinton.

An important feature of the comparative analysis printout is the comprehensive tabulation of the distribution and identity of matching and nonmatching bands in compared patterns. All pattern homology parameter values are given in their weighted and unweighted form. In the absence of computer resources for plotting data, program HOMOLOGY2 or its counterpart for cultivar identification (program IDHOM, results not shown), can be run to provide a satisfactory substitute for the graphic display described in this paper.

The measure of pattern homology between cultivars Neepawa and Sinton was determined to be 56% (unweighted), derived from

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-   WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY    -
 *  122 DATA BASE CULTIVAR PATTERNS ANALYZED
 *  DATA BASE SEARCH CUTOFF AT 55% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
 *  LSD(RELATIVE MOBILITY) = 0.5, MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3, DENSITY RANGE: 1 - 9.
 *  UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 37 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 44.6

                                                                  DISTRIBUTION OF NON-MATCHING BAND DATA
                                 GLIADIN                          ------------------------------------
                                 BANDS IN      MATCHING                  MOBILITY      DENSITY      MOBILITY
                      WEIGHTED   PATTERN       BANDS          TOTAL      BASIS-R      BASIS        BASIS-U
                      % PATTERN  ---------     ---------      ---------    ---------    ---------    ---------
     CULTIVAR         HOMOLOGY   NO.  WBD      NO.  WBD       NO.  WBD     NO.  WBD     NO.  WBD     NO.  WBD     CLASS/TYPE   REGION
     --------         --------   --  ------    --  ------     --  ------   --  ------   --  -----   --  ------   ------------ ---------
 1   NEEPAWA             100     37 (44.6)    37 (44.6)      0 ( 0.0)     0 ( 0.0)     0 (0.0)     0 ( 0.0)     HRS-SMQ      W.CAN
 2   MANITOU              98     34 (41.5)    34 (42.6)      3 ( 0.9)     0 ( 0.0)     0 (0.0)     3 ( 0.9)     HRS-SMQ      W.CAN
 3   KATEPWA              97     35 (39.0)    34 (41.2)      4 ( 1.2)     1 ( 0.3)     0 (0.0)     3 ( 0.9)     HRS-SMQ      W.CAN
 4   CANTHATCH            96     36 (39.9)    34 (39.8)      4 ( 1.9)     1 ( 0.3)     1 (0.9)     2 ( 0.6)     HRS-SMQ      W.CAN
 5   THATCHER             96     35 (42.1)    34 (42.6)      4 ( 1.5)     1 ( 0.6)     0 (0.0)     3 ( 0.9)     HRS-SMQ      W.CAN
 6   NAPAYO_M             93     40 (43.0)    35 (42.3)      7 ( 3.1)     5 ( 2.5)     0 (0.0)     2 ( 0.6)     HRS-SMQ      W.CAN
 7   CHRIS                91     38 (43.7)    34 (42.1)      7 ( 4.0)     4 ( 2.5)     0 (0.0)     3 ( 1.5)     HRS-SMQ      USA
 8   BENITO               91     36 (43.7)    34 (42.1)      5 ( 4.0)     2 ( 1.9)     0 (0.0)     3 ( 2.2)     HRS-SMQ      W.CAN
 9   CANUCK_M             82     49 (52.0)    35 (43.5)     16 ( 9.6)    14 ( 9.0)     0 (0.0)     2 ( 0.6)     HRS-EMQ      SAWFLY
10   LEADER               80     39 (43.7)    32 (37.8)     11 ( 9.6)     6 ( 5.3)     1 (0.9)     4 ( 3.4)     HRS-SMQ      SAWFLY
11   ERA                  75     39 (37.2)    30 (33.3)     13 (10.8)     6 ( 4.3)     3 (3.7)     4 ( 2.8)     HRS-NEMQ     USA
12   PARK                 63     40 (41.8)    27 (31.1)     21 (18.6)    11 ( 9.6)     2 (2.2)     8 ( 6.8)     HRS-SMQ      W.CAN
13   SAUNDERS_M           62     37 (38.7)    27 (30.8)     18 (19.2)     8 ( 8.4)     2 (2.8)     8 ( 8.0)     HRS-EMQ      W.CAN
14   SINTON               61     32 (37.8)    24 (29.9)     19 (19.5)     6 ( 6.5)     2 (2.8)     11 (10.2)    HRS-SMQ      W.CAN
15   RELIANCE_PGR_M       59     35 (42.7)    25 (30.5)     19 (21.4)     7 ( 9.3)     3 (4.0)     9 ( 8.0)     HRS-NEMQ     W.CAN
16   CHINOOK              59     37 (39.3)    26 (30.3)     21 (21.4)    10 (10.2)     1 (1.5)     10 ( 9.6)    HRS-EMQ      SAWFLY
17   COTEAU               58     32 (38.4)    22 (29.3)     23 (21.4)     8 ( 6.8)     2 (2.8)     13 (11.8)    HRS-SMQ      USA
18   SUNDANCE             56     35 (39.3)    24 (29.1)     22 (22.6)     9 (10.5)     2 (2.8)     11 ( 9.3)    HRW-BW       W.CAN
     ----------------  ------    --  ------   --  ------    --  ------   --  ------   --  -----   --  ------
          MEAN VALUE:     78     37 (41.6)    30 (36.8)     12 (10.6)     5 ( 4.9)     1 (1.4)     5 ( 4.4)

                          DATA BASE
                            INDEX
                             NO.      PEDIGREE DATA
                             ---      -------------
 1   NEEPAWA                  56      THATCHER*7/FRONTANA//THATCHER*6/KENYA FARMER/3/THATCHER*2//FRONTANA/THATCHER, CANADA
 2   MANITOU                  52      THATCHER*7/FRONTANA//CANTHATCH/3/PI 170925/6*THATCHER, CANADA
 3   KATEPWA                  47      NEEPAWA*6/RL2938/3/NEEPAWA*6//C.I.8154/2*FROCOR, CANADA(RL2938 = LEE*2/KENYA FARMER).
 4   CANTHATCH                45      THATCHER*6/KENYA FARMER, CANADA
 5   THATCHER                 62      MARQUIS/IUMILLIO/MARQUIS/KANRED, CANADA
 6   NAPAYO_M                 53      MANITOU*2/4/THATCHER*5/LEE/3/THATCHER*7/FRONTANA//THATCHER*6/KENYA FARMER, CANADA
 7   CHRIS                    86      FRONTANA/3*THATCHER/3/KENYA 58/NEWTHATCH/2*THATCHER,   USA
 8   BENITO                   44      NEEPAWA/3/RL4255*4/MANITOU/CI7090, CANADA
 9   CANUCK_M                 63      CANTHATCH/3/MIDA/CADET//RESCUE, CANADA
10   LEADER                   78      FORTUNA/CHRIS, CANADA
11   ERA                      88      II-50-10/4/PEMBINA/II-52-329/3/II-53-38/III-58-4//II-53-546, USA
12   PARK                     57      MIDA/CADET//THATCHER, CANADA
13   SAUNDERS_M               59      HOPE/REWARD//THATCHER, CANADA
14   SINTON                   61      MANITOU/3/THATCHER*6/KENYA FARMER//LEE*6/KENYA FARMER,   CANADA
15   RELIANCE_PGR_M           30      KANRED/MARQUIS, USA
16   CHINOOK                  76      THATCHER/S-615-11, CANADA
17   COTEAU                   87      ND496 S18//ND487/FLETCHER, USA (ND496=WALDRON/ND269; ND487=ND259/CONLEY//CONLEY/ND122/3/
18   SUNDANCE                134      JUSTIN/ND142) CHEYENNE/KHARKOV 22 M.C., CANADA
-----------------------------------------------------------------------------------------------------------------------------------
     WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT  WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23)
     WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.
```

Fig. 4. Cultivar identification short list ranking (program CVID) printout for hard red spring wheat Neepawa. The "Mobility Basis-R" data column scores the number of bands in ranked cultivar electrophoregrams lacking positional homology with the unknown pattern. The "Mobility Basis-U" data column scores the converse band number count for the unknown. See text for additional details.

equation 1 as follows:

$$\text{Unweighted \% PH} = \frac{24 \times 100}{24 + (11 + 6 + 2)} = 56\%.$$

The weighted % PH score (61%) is somewhat higher, owing to the higher WBD count for the 24 bands that matched.

The performance of the process is illustrated with clear detail in the computer plot of electrophoregram composition (Fig. 3), which isolated matching and nonmatching bands from the total patterns. The computed result is largely confirmed by visual inspection of the Neepawa and Sinton electrophoregrams, which lack homology in the regions of low and intermediate mobility.

Cultivar Identification System Program Output

To evaluate the performance of the identification system, representative gliadin electrophoregrams for wheats of various class types were selected as test input data to represent unknown samples, namely Neepawa (HRS bread wheat), Wascana (durum wheat), Yorkstar (soft white winter [SWW] wheat), Springfield (soft white spring [SWS] wheat), Sundance (hard red winter [HRW] bread wheat), and Opal (HRS feed wheat).

The typical complement of computer printouts and plots for a complete cultivar identification analysis is shown in Figures 4 through 6. The summary report produced by program CVID (Fig. 4) represents a short list of data base cultivars ranked in order of decreasing weighted % PH compared to the unknown

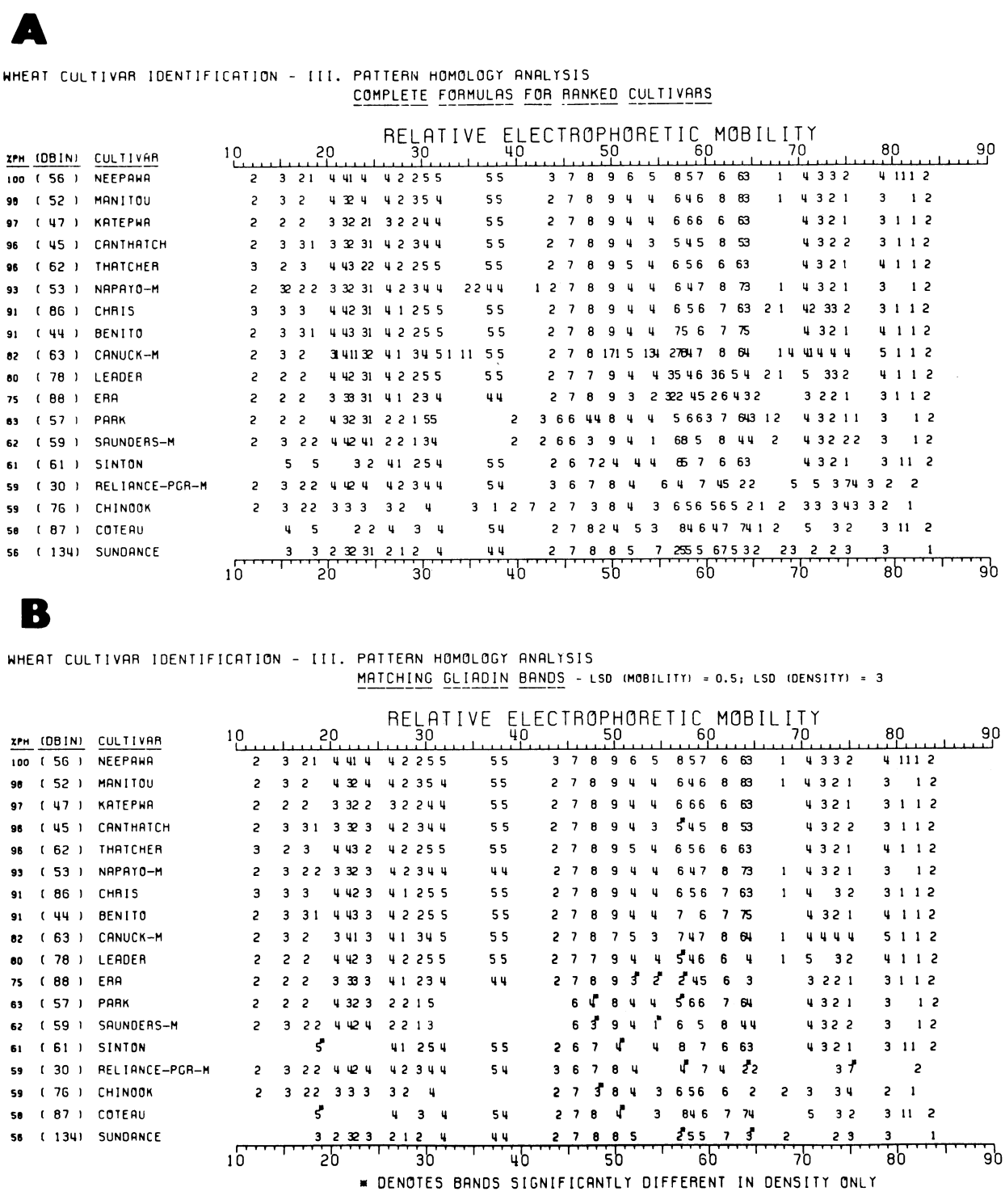
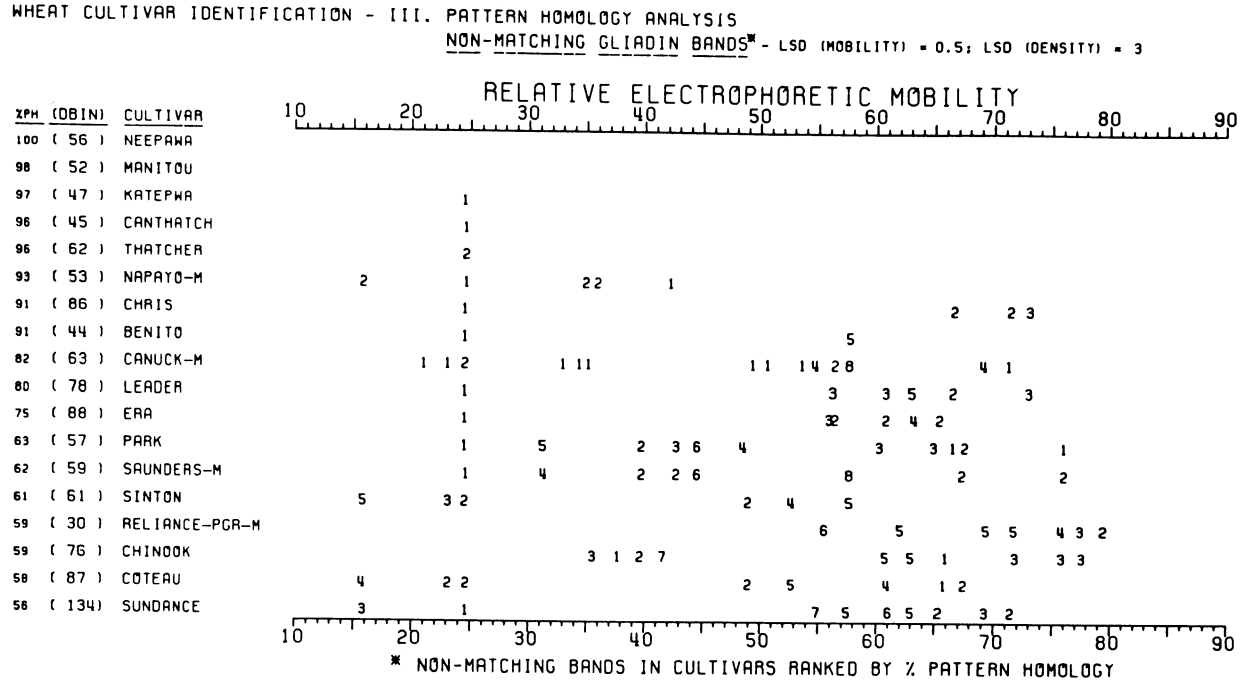


Fig. 5. Cultivar identification pattern homology analysis plots (program IDPLOT) for cultivar Neepawa.

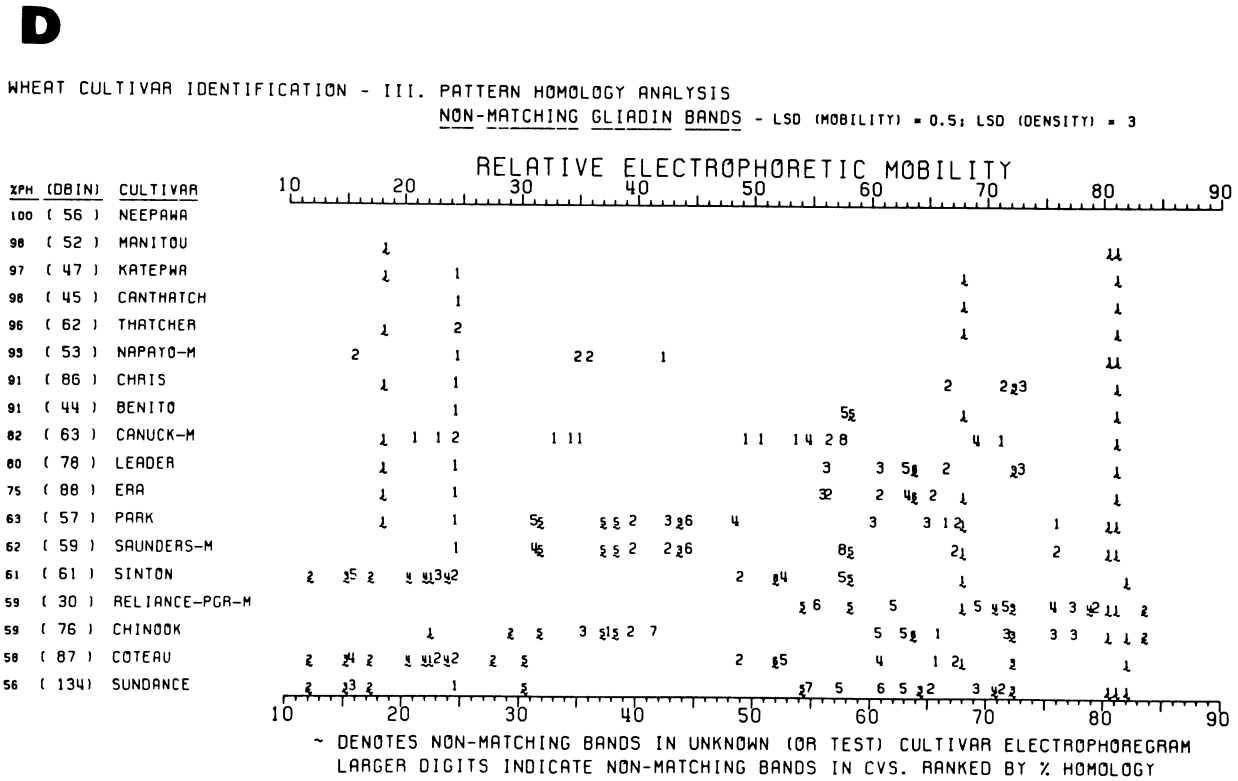
electrophoregram. At the head of the output are several lines specifying the various free parameters chosen for the program run. As indicated, 55% PH was selected as the cutoff value for cultivar entry into the short list ranking. This limit, in combination with the selected difference thresholds for gliadin band identity (i.e., 0.5 Rm units, 3 density units), generally resulted in ranking 10 to 20% of the primary population (excluding biotypes) of 122 common spring, winter, and durum wheat reference cultivars in the data base. The number of ranked cultivars varies depending on the uniqueness of the input electrophoregram. For example, the ranking by pattern homology to the Marquis electrophoregram (result not shown) lists 43 cultivars above the 55% PH threshold, evidence of the significant contribution of this historic Canadian variety to the genetic composition of other wheat cultivars in the data base.

The top-ranked cultivar in Figure 4 shows that the identification program was successful in precisely matching the input PAGE pattern for Neepawa with its data base counterpart. Successive % PH values indicate further that the Neepawa electrophoregram is very similar in composition to band patterns of a group of seven cultivars that have been isolated with very high levels of pattern homology (>90%). The influence of common genetic background has contributed largely to this result, as all eight cultivars are dominated by the cultivar Thatcher or a related genotype as the recurrent parent in respective pedigrees. Not surprisingly, these

C



D



cultivars all share common class attributes for HRS bread wheats with excellent milling and baking quality characteristics.

Apart from providing cultivar names, % PH scores, class attributes, and pedigrees, the CVID printout includes an extensive tabulation of the distribution of matching and nonmatching bands for compared electrophoregrams. The total nonmatching band data column shows that WBD scores (in parentheses) for the six cultivars ranked below Neepawa are considerably less than the paired number count. This provides evidence that cultivar discrimination was derived primarily from differences involving very faint bands.

The cultivar formula plots shown in Figure 5 were produced by program IDPLOT and provide the means to evaluate the CVID printout (Fig. 4) by visualizing the pattern homology analysis process for the entire set of ranked wheats. The detail and precision of the computerized methodology is especially well demonstrated in the plot of cultivar formulas for isolated matching bands (Fig. 5B), which clearly identifies common groups of gliadins similar in density or otherwise. The plots for nonmatching bands (Fig. 5C and D) confirm that only extremely faint bands are the basis for discrimination. Considerable uncertainty therefore exists in differentiating Neepawa from cultivars with pattern homology scores greater than 95%. Fortunately, the need to discriminate among these closely related genotypes has no present commercial relevance, as they all possess similar end-use quality characteristics.

These computer-generated plots also illustrate the potential of the method for studying genetic relationships, where large numbers of progeny are to be evaluated in terms of discrete electrophoregram similarities, differences, and recombinants compared to parental type protein patterns. In this application, the electrophoregram (or portion thereof) of a parent genotype would replace the unknown as the input pattern, and electrophoregrams for the F2 generation or other derived material would constitute the data base.

The third and final element (program CVMAP) of the cultivar identification system, illustrated in Figure 6, computes the frequency distribution of band position differences between the gliadin electrophoregram of an input cultivar and counterpart patterns in the data base. For each pair compared, the positional difference variable scores the total nonmatching band count, including bands that significantly differ by density alone. Removal of these differences will yield electrophoregrams of identical composition. The strategy implemented by program CVMAP complements results shown previously by using a different criterion for ranking. It also provides an output extended to include the entire reference population of common and durum wheats, in which each entry is explicitly identified.

A typical result is illustrated in Figure 6, which depicts the frequency distribution for weighted positional differences between the Neepawa electrophoregram and 122 reference cultivars. The difference distribution, which we termed a "cultivar distance map" (CVMAP), shows a wide gap or genotypic distance separating the cultivar Neepawa (DBIN 56) from the bulk of the data base population. Cultivars that are relatively distinct in electrophoregram

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-    WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES    -

  * INPUT TEST CULTIVAR = NEEPAWA
  * 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES
-------------------------------
      0     56(**)
      1     47(97) 52(98)
      2     45(96) 62(96)
      3     53(93)
      4     44(91) 86(91)
      5
      6
      7
      8
      9
     10     63(82) 78(80)
     11     88(75)
     12
     13
     14
     15
     16
     17
     18
     19     57(63) 59(62)
     20     61(61)
     21     30(59) 76(59) 87(58)
     22
     23    134(56)
     24     37(52)156(51)
     25     69(51)150(43)
     26     11(52)133(51)
     27     46(52) 79(44) 91(50)
     28      4(49) 40(46) 58(43) 66(45)124(52)137(51)
     29     12(46) 15(47)112(47)
     30     27(46) 95(43)110(44)
     31     97(38)101(47)141(43)158(44)
     32      8(36) 85(45)118(37)139(41)
     33     99(37)122(37)163(39)
     34      3(37) 16(41) 17(39)109(42)151(40)170(43)
     35    142(37)147(35)152(27)153(34)164(36)
     36     32(35)113(32)129(40)148(29)
     37     84(35)128(34)138(29)
     38     22(34) 28(36) 77(33) 92(33)154(35)157(28)
     39
     40    167(36)
     41      1(28)102(29)103(24)115(26)132(29)
     42      9(26) 14(34) 96(30)105(22)107(24)111(23)130(28)165(21)166(26)
     43    104(28)131(24)143(27)171(18)172(16)
     44    178(28)
     45    135(23)162(28)
     46     29(24) 38(21)108(20)136(27)180(25)186(24)
     47     89(19)
     48     90(23)
     49     24(26)127(20)149(20)155(21)184(12)
     50    179(20)187(20)
     51
     52
     53     39(18)181(19)
     54      5(19)174(20)185(19)189(21)
     55     23(11)177(12)
     56    183(15)
     57
     58    182(16)

CULTIVARS MOST SIMILAR TO CV. NEEPAWA
-------------------------------------
DIFFS.=  0 (**%PH)    DBIN -  56  CV. NEEPAWA
DIFFS.=  1 (97%PH)    DBIN -  47  CV. KATEPWA
DIFFS.=  1 (98%PH)    DBIN -  52  CV. MANITOU
DIFFS.=  2 (96%PH)    DBIN -  45  CV. CANTHATCH
DIFFS.=  2 (96%PH)    DBIN -  62  CV. THATCHER
DIFFS.=  3 (93%PH)    DBIN -  53  CV. NAPAYO_M
DIFFS.=  4 (91%PH)    DBIN -  44  CV. BENITO
DIFFS.=  4 (91%PH)    DBIN -  86  CV. CHRIS
DIFFS.= 10 (82%PH)    DBIN -  63  CV. CANUCK_M
DIFFS.= 10 (80%PH)    DBIN -  78  CV. LEADER
DIFFS.= 11 (75%PH)    DBIN -  88  CV. ERA
DIFFS.= 19 (63%PH)    DBIN -  57  CV. PARK
DIFFS.= 19 (62%PH)    DBIN -  59  CV. SAUNDERS_M

CULTIVARS MOST DIFFERENT FROM CV. NEEPAWA
-----------------------------------------
DIFFS.= 58 (16%PH)    DBIN - 182  CV. MINDUM
DIFFS.= 56 (15%PH)    DBIN - 183  CV. NUGGET
DIFFS.= 55 (11%PH)    DBIN -  23  CV. LAKE
DIFFS.= 55 (12%PH)    DBIN - 177  CV. COULTER
DIFFS.= 54 (19%PH)    DBIN -   5  CV. PRELUDE_M
DIFFS.= 54 (20%PH)    DBIN - 174  CV. CARLETON_PGR
DIFFS.= 54 (19%PH)    DBIN - 185  CV. RAMSEY
DIFFS.= 54 (21%PH)    DBIN - 189  CV. WASCANA
DIFFS.= 53 (18%PH)    DBIN -  39  CV. REWARD
DIFFS.= 53 (19%PH)    DBIN - 181  CV. MEDORA
DIFFS.= 50 (20%PH)    DBIN - 179  CV. HERCULES
DIFFS.= 50 (20%PH)    DBIN - 187  CV. WAKOOMA_M

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    WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY
    BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT
    = (X/3.23)  WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY
    FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR
    EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.
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Fig. 6. Cultivar identification distance map (program CVMAP) printout for Neepawa. Framed data in the frequency distribution corresponds to cultivars ranked in Figures 4 and 5. Data in inset represents a separate segment of program CVMAP output which identifies diverse genotypes relative to the input electrophoretic pattern. See text for details.

A

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY

* 122 DATA BASE CULTIVAR PATTERNS ANALYZED
* DATA BASE SEARCH CUTOFF AT 35% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
* LSD(RELATIVE MOBILITY) = 0.5, MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3, DENSITY RANGE: 1 - 9.
* UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 35 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 43.0

	CULTIVAR	WEIGHTED % PATTERN HOMOLOGY	GLIADIN BANDS IN PATTERN NO.	GLIADIN BANDS IN PATTERN WBD	MATCHING BANDS NO.	MATCHING BANDS WBD	DISTRIBUTION OF NON-MATCHING BAND DATA: TOTAL NO.	TOTAL WBD	MOBILITY BASIS-R NO.	MOBILITY BASIS-R WBD	DENSITY BASIS NO.	DENSITY BASIS WBD	MOBILITY BASIS-U NO.	MOBILITY BASIS-U WBD	CLASS/TYPE	REGION
1	WASCANA	100	35	(43.0)	35	(43.0)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	DURM-PASTA	W.CAN
2	STEWART 63	79	33	(36.8)	29	(35.3)	10	(9.3)	4	(4.6)	0	(0.0)	6	(4.6)	DURM-PASTA	W.CAN
3	CARLETON_PGR	77	44	(43.0)	31	(36.7)	15	(10.8)	11	(7.1)	2	(2.2)	2	(1.5)	DURM-PASTA	W.CAN
4	MACOUN	64	31	(36.2)	22	(29.9)	20	(17.0)	7	(5.3)	2	(2.8)	11	(9.0)	DURM-PASTA	W.CAN
5	NUGGET	59	44	(43.0)	26	(30.5)	24	(21.4)	15	(12.1)	3	(3.7)	6	(5.6)	DURM-PASTA	W.CAN
6	MINDUM	58	42	(44.6)	25	(30.8)	24	(22.3)	14	(12.4)	3	(3.7)	7	(6.2)	DURM-PASTA	W.CAN
7	WAKOOMA_M	49	30	(35.3)	19	(25.7)	26	(26.3)	10	(9.9)	1	(1.5)	15	(14.9)	DURM-PASTA	W.CAN
8	MEDORA	43	34	(38.7)	15	(23.5)	36	(31.0)	16	(13.3)	3	(4.0)	17	(13.6)	DURM-PASTA	W.CAN
9	HERCULES	40	37	(37.8)	16	(22.8)	39	(34.1)	20	(15.8)	1	(0.9)	18	(17.3)	DURM-PASTA	W.CAN
10	GOLDENBALL	39	26	(36.8)	15	(21.7)	28	(33.4)	8	(11.1)	3	(4.3)	17	(18.0)	DURM-PASTA	W.CAN
	MEAN VALUE:	60	35	(39.5)	23	(30.0)	22	(20.6)	10	(9.2)	1	(2.3)	9	(9.1)		

	CULTIVAR	DATA BASE INDEX NO.	PEDIGREE DATA
1	WASCANA	189	LAKOTA*2/PELISSIER, CANADA
2	STEWART 63	186	ST 464/8*STEWART, CANADA
3	CARLETON_PGR	174	VERNAL EMMER/MINDUM, USA
4	MACOUN	180	RL 3607/ DT 182, CANADA
5	NUGGET	183	MINDUM/CARLETON//HEITI/STEWART, USA
6	MINDUM	182	? FOUND IN BREAD WHEAT FIELD, USA
7	WAKOOMA_M	187	LAKOTA*2/PELISSIER, CANADA
8	MEDORA	181	WARD/MACOUN, CANADA
9	HERCULES	179	RL 3097/RL 3304//STEWART/RL 3380, CANADA
10	GOLDENBALL	178	? FROM S. AFRICA

WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.

B

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES

* INPUT TEST CULTIVAR = WASCANA
* 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES

```
 0  189(**)
 1
 2
 3
 4
 5
 6
 7
 8
 9  186(79)
10
11  174(77)
12
13
14
15
16
17  180(64)
18
19
20
21  183(59)
22  182(58)
23
24
25
26  187(49)
27
28
29
30
31  181(43)
32
33  178(39)
34  179(40)
35  184(29)
36  177(33)
37
38
39  162(32)
40  127(24)165(23)185(31)
41   95(27)111(23)171(20)
42   23(25) 58(24) 59(30) 61(26) 76(30)
43   38(26) 40(27) 99(24)107(20)131(25)
44   79(20) 84(26)103(16)141(26)
45   22(27) 32(24) 57(26)115(20)172(14)
46    9(17) 29(24) 46(29) 47(25) 89(16)118(22)129(25)134(26)147(23)154(26)
47    3(19)  5(24) 28(23) 66(20) 87(23)104(20)148(16)
48   16(24) 37(23) 92(22)102(21)105(19)124(24)135(18)153(16)167(26)
49    8(11) 14(22) 39(23) 90(18)112(21)138(17)150(12)156(21)166(16)
50   27(22) 44(24) 62(23) 91(22)101(25)113(17)122(18)128(18)142(21)143(20)163(22)
51    4(19) 12(17) 24(21) 77(20) 78(22)108( 7)137(20)149(16)155(19)157(15)164(18)
52   15(21) 45(21) 63(26) 96(17)130(14)152( 7)
53    1(14) 17(18) 53(21) 85(21) 97( 8)109(21)
54   30(22) 56(21) 69(15) 88(16)
55   11(18)110(17)133(18)151(18)
56   52(18)136(15)170(18)
57  132(12)158(16)
58
59   86(16)
60
61
62
63
64  139( 9)
```

WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.

Fig. 7. Cultivar identification ranking (**A**) and distance map (**B**) printouts for durum wheat Wascana. Framed cultivars in (**B**) correspond to cultivars ranked in (**A**).

A

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY

- 122 DATA BASE CULTIVAR PATTERNS ANALYZED
- DATA BASE SEARCH CUTOFF AT 55% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
- LSD(RELATIVE MOBILITY) = 0.5, MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3, DENSITY RANGE: 1 - 9.
- UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 37 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 33.1

	CULTIVAR	WEIGHTED % PATTERN HOMOLOGY	GLIADIN BANDS IN PATTERN NO.	GLIADIN BANDS IN PATTERN WBD	MATCHING BANDS NO.	MATCHING BANDS WBD	DISTRIBUTION OF NON-MATCHING BAND DATA: TOTAL NO.	TOTAL WBD	MOBILITY BASIS-R NO.	MOBILITY BASIS-R WBD	DENSITY BASIS NO.	DENSITY BASIS WBD	MOBILITY BASIS-U NO.	MOBILITY BASIS-U WBD	CLASS/TYPE	REGION
1	YORKSTAR	100	37	(33.1)	37	(33.1)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	SWW-PASTRY	ONTARIO
2	FAVOR	98	37	(29.7)	36	(31.1)	2	(0.6)	1	(0.3)	0	(0.0)	1	(0.3)	SWW-PASTRY	ONTARIO
3	GENESSEE	95	40	(39.9)	36	(35.6)	5	(1.9)	4	(1.5)	0	(0.0)	1	(0.3)	SWW-PASTRY	ONTARIO
4	GORDON	94	36	(24.8)	34	(28.0)	5	(1.9)	2	(0.6)	0	(0.0)	3	(1.2)	SWW-PASTRY	ONTARIO
5	TALBOT	91	40	(38.1)	36	(33.9)	5	(3.4)	4	(2.8)	0	(0.0)	1	(0.6)	SWW-PASTRY	ONTARIO
6	CORNELL 595	90	40	(37.8)	35	(33.6)	7	(3.7)	5	(2.8)	0	(0.0)	2	(0.9)	SWW-PASTRY	ONTARIO
7	DGCHAFF	87	39	(36.2)	34	(32.2)	8	(5.0)	5	(3.4)	0	(0.0)	3	(1.5)	SWW-PASTRY	ONTARIO
8	KENT	86	40	(45.2)	35	(35.4)	6	(5.6)	4	(4.0)	1	(0.9)	1	(0.6)	SRW-PASTRY	ONTARIO
9	DAWBUL_M	76	44	(37.6)	33	(29.9)	14	(9.6)	10	(6.8)	1	(1.2)	3	(1.5)	SWW-PASTRY	ONTARIO
10	JR.NO.6	75	39	(39.6)	32	(30.3)	11	(10.2)	6	(6.5)	1	(0.9)	4	(2.8)	SWW-PASTRY	ONTARIO
11	EGYPTIAN AMBER	64	39	(31.0)	28	(24.6)	19	(13.6)	10	(7.7)	1	(1.5)	8	(4.3)	SRW-PASTRY	ONTARIO
12	HOUSER	61	43	(34.7)	28	(24.8)	22	(15.8)	13	(8.4)	2	(3.4)	7	(4.0)	SWW-PASTRY	ONTARIO
13	OAC104	61	38	(34.1)	27	(25.1)	20	(15.8)	10	(7.7)	1	(1.2)	9	(6.8)	SWW-PASTRY	ONTARIO
14	THORNE_M	59	37	(24.1)	27	(19.8)	18	(13.9)	8	(5.6)	2	(1.9)	8	(6.5)	SRW-PASTRY	ONTARIO
15	FAIRFIELD	58	40	(32.8)	25	(24.0)	26	(17.3)	14	(9.9)	1	(1.9)	11	(5.6)	SRW-PASTRY	ONTARIO
16	RICHMOND_M	56	40	(41.2)	25	(25.1)	25	(19.8)	13	(9.0)	2	(3.1)	10	(7.7)	SWW-PASTRY	ONTARIO
17	FREDRICK	56	34	(36.2)	23	(23.8)	23	(18.6)	9	(8.0)	2	(3.4)	12	(7.1)	SWW-PASTRY	ONTARIO
	MEAN VALUE:	76	39	(35.1)	31	(28.8)	12	(9.2)	6	(5.0)	0	(1.1)	4	(3.1)		

	CULTIVAR	DATA BASE INDEX NO.	PEDIGREE DATA
1	YORKSTAR	164	GENESEE*5/3/YORKWIN//NORIN 10/BREVOR, USA
2	FAVOR	148	DIGA DIJON//GABO/NEW ZEALAND 496.01, CANADA
3	GENESSEE	151	YORKWIN//HONOR*2/FORWARD, USA
4	GORDON	152	CD7561(RELATED TO ETOILE DE CHOISY)/GENESSEE/2/CD7561/ KENT/3/7453-4-2-4(FREDRICK SIB)/4/2*YORKSTAR, C
5	TALBOT	163	TRUMBULL//HOPE/HUSSAR/3/DAWSON'S GOLDEN CHAFF*2/RIDIT//CORNELL 595, CANADA
6	CORNELL 595	142	HONOR/FORWARD//NURED/3/HONOR, USA
7	DGCHAFF	147	SELECTION OF CLAWSON, CANADA
8	KENT	170	CALDWELL 10/DAWSON'S GOLDEN CHAFF, CANADA
9	DAWBUL_M	143	DAWSON'S GOLDEN CHAFF/BULGARIAN, CANADA
10	JR.NO.6	154	AS GOLDCOIN, SELECTION OF REDCHAFF OR OF REDCHAFF BALD, USA
11	EGYPTIAN AMBER	165	FULTZ/LANCASTER, USA
12	HOUSER	153	BREVOR/NORIN 10//NY WHEAT RYE SEL./3/HOPE HUSSAR/YORKWIN/4/GENESSEE//CT12658/ALASKAN/3/AVON, USA
13	OAC104	157	DAWSON'S GOLDEN CHAFF/BULGARIAN, CANADA
14	THORNE_M	172	PORTAGE/FULCASTER, USA
15	FAIRFIELD	166	PURKOF/FULHIO, USA
16	RICHMOND_M	158	DAWSON'S GOLDEN CHAFF*2/RIDIT, CANADA
17	FREDRICK	149	WASHINGTON 1//GENESEE/CAPELLE, CANADA

WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.

B

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES

- INPUT TEST CULTIVAR = YORKSTAR
- 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES

```
  0   164(**)
  1   148(98)
  2   151(95)152(94)
  3   163(91)
  4   142(90)
  5   147(87)
  6   170(86)
  7
  8
  9
 10   143(76)154(75)
 11
 12
 13
 14   165(64)172(59)
 15
 16   153(61)157(61)
 17   166(58)
 18
 19   149(56)150(49)
 20   158(56)171(51)
 21    76(54) 77(53) 85(54)113(52)
 22    12(52)108(49)156(47)
 23     5(50)
 24     9(45) 27(51)103(46)115(47)138(44)
 25    15(49) 17(49) 84(48)
 26    22(47)105(41)110(48)124(47)
 27     1(43) 16(46) 32(43) 97(39)101(46)109(46)132(42)141(41)167(47)
 28    28(42) 39(43) 40(43) 79(37) 88(40) 90(42)102(40)104(43)118(42)135(40)137(43)162(43)
 29     8(36) 11(43) 14(44) 37(40) 66(40)111(40)112(42)130(41)131(37)136(43)
 30    87(37) 91(40) 92(39)134(36)
 31    38(34) 69(41) 95(37)129(40)133(38)139(37)
 32     4(38) 29(38) 61(35)127(35)128(36)
 33    23(30) 24(39) 45(35) 47(36) 57(38) 78(37) 89(34)122(36)
 34     3(36) 53(35) 62(36) 63(41) 99(33)107(32)155(35)
 35    30(31) 52(32) 56(36) 86(35) 96(36)
 36    59(32)184(24)
 37    44(31) 46(36)185(29)
 38
 39
 40   179(25)
 41    58(22)181(25)
 42
 43
 44
 45   177(15)186(19)187(18)
 46   178(16)180(17)182(19)183(19)
 47
 48   174(18)
 49
 50
 51   189(18)
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WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.

Fig. 8. Cultivar identification ranking (**A**) and distance map (**B**) printouts for soft white winter wheat Yorkstar. Framed cultivars in (**B**) correspond to cultivars ranked in (**A**).

A

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY

* 122 DATA BASE CULTIVAR PATTERNS ANALYZED
* DATA BASE SEARCH CUTOFF AT 55% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
* LSD(RELATIVE MOBILITY) = 0.5. MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3. DENSITY RANGE: 1 - 9.
* UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 35 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 39.3

	CULTIVAR	WEIGHTED % PATTERN HOMOLOGY	GLIADIN BANDS IN PATTERN NO.	GLIADIN BANDS IN PATTERN WBD	MATCHING BANDS NO.	MATCHING BANDS WBD	DISTRIBUTION OF NON-MATCHING BAND DATA: TOTAL NO.	TOTAL WBD	MOBILITY BASIS-R NO.	MOBILITY BASIS-R WBD	DENSITY BASIS NO.	DENSITY BASIS WBD	MOBILITY BASIS-U NO.	MOBILITY BASIS-U WBD	CLASS/TYPE	REGION
1	SUNDANCE	100	35	(39.3)	35	(39.3)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	HRW-BW	W.CAN
2	YOGO	67	34	(34.7)	25	(29.6)	19	(14.9)	9	(5.0)	0	(0.0)	10	(9.9)	HRW-BW	W.CAN
3	LEADER	65	39	(43.7)	26	(30.5)	19	(16.4)	10	(8.0)	3	(2.8)	6	(5.6)	HRS-SMQ	SAWFLY
4	KHARKOV 22 M.C.	65	41	(41.2)	28	(31.0)	18	(16.7)	11	(9.0)	2	(2.8)	5	(5.0)	HRW-BW	W.CAN
5	ERA	63	39	(37.2)	26	(28.2)	19	(16.4)	10	(7.1)	3	(3.7)	6	(5.6)	HRS-NEMQ	USA
6	CANUCK_M	61	49	(52.0)	28	(32.5)	26	(20.7)	19	(13.0)	2	(1.9)	5	(5.9)	HRS-EMQ	SAWFLY
7	CANTHATCH	59	36	(39.9)	25	(28.9)	20	(20.1)	10	(8.4)	1	(0.9)	9	(10.8)	HRS-SMQ	W.CAN
8	RELIANCE_PGR_M	59	35	(42.7)	24	(29.3)	20	(20.4)	9	(8.7)	2	(2.2)	9	(9.6)	HRS-NEMQ	W.CAN
9	NAPAYO_M	58	40	(43.0)	26	(28.9)	21	(21.4)	12	(9.6)	2	(2.5)	7	(9.3)	HRS-SMQ	W.CAN
10	CHRIS	57	38	(43.7)	26	(29.6)	20	(22.6)	11	(10.8)	1	(1.2)	8	(10.5)	HRS-SMQ	USA
11	BENITO	57	36	(43.7)	25	(29.6)	20	(22.6)	10	(10.2)	1	(1.5)	9	(10.8)	HRS-SMQ	W.CAN
12	RESCUE_PGR_M	57	33	(34.4)	23	(24.6)	20	(18.9)	8	(6.9)	2	(2.5)	10	(10.5)	HRS-EMQ	SAWFLY
13	THATCHER	56	35	(42.1)	24	(28.6)	21	(22.9)	10	(9.9)	1	(1.2)	10	(11.8)	HRS-SMQ	W.CAN
14	NEEPAWA	56	37	(44.6)	24	(29.1)	22	(22.6)	11	(9.3)	2	(2.8)	9	(10.5)	HRS-SMQ	W.CAN
15	NUGAINES	56	29	(32.8)	21	(24.9)	21	(19.2)	7	(5.6)	1	(0.9)	13	(12.7)	SWW-PASTRY	BC
16	KATEPWA	55	35	(39.0)	23	(26.6)	22	(22.0)	10	(8.0)	2	(2.2)	10	(11.8)	HRS-SMQ	W.CAN
17	MANITOU	55	34	(41.5)	23	(27.6)	21	(22.6)	9	(8.4)	2	(2.8)	10	(11.5)	HRS-SMQ	W.CAN
18	HOUSER	55	43	(34.7)	23	(23.7)	27	(19.2)	15	(8.7)	5	(5.6)	7	(5.0)	SWW-PASTRY	ONTARIO
	MEAN VALUE:	61	37	(40.6)	25	(29.0)	19	(18.9)	10	(8.1)	1	(2.1)	7	(8.7)		

	CULTIVAR	DATA BASE INDEX NO.	PEDIGREE DATA
1	SUNDANCE	134	CHEYENNE/KHARKOV 22 M.C., CANADA
2	YOGO	141	MINTURKI/BELOGLINA//BUFFUM, USA
3	LEADER	78	FORTUNA/CHRIS, CANADA
4	KHARKOV 22 M.C.	129	SELECTION OF KHARKOV, CANADA
5	ERA	88	II-50-10/4/PEMBINA/II-52-329/3/II-53-38/III-58-4//II-53-546, USA
6	CANUCK_M	63	CANTHATCH/3/MIDA/CADET//RESCUE, CANADA
7	CANTHATCH	45	THATCHER*6/KENYA FARMER, CANADA
8	RELIANCE_PGR_M	30	KANRED/MARQUIS, USA
9	NAPAYO_M	53	MANITOU*2/4/THATCHER*5/LEE/3/THATCHER*7/FRONTANA//THATCHER*6/KENYA FARMER, CANADA
10	CHRIS	86	FRONTANA/3*THATCHER/3/KENYA 58/NEWTHATCH/2*THATCHER, USA
11	BENITO	44	NEEPAWA/3/RL4255*4//MANITOU/CI7090, CANADA
12	RESCUE_PGR_M	79	APEX/S-615, CANADA
13	THATCHER	62	MARQUIS/IUMILLIO/MARQUIS/KANRED, CANADA
14	NEEPAWA	56	THATCHER*7/FRONTANA//THATCHER*6/KENYA FARMER/3/THATCHER*2//FRONTANA/THATCHER, CANADA
15	NUGAINES	156	SIB. OF GAINES, USA
16	KATEPWA	47	NEEPAWA*6/RL2938/3/NEEPAWA*6//C.I.8154/2*FROCOR, CANADA(RL2938 = LEE*2/KENYA FARMER).
17	MANITOU	52	THATCHER*7/FRONTANA//CANTHATCH/3/PI 170925/6*THATCHER, CANADA
18	HOUSER	153	BREVOR/NORIN 10//NY WHEAT RYE SEL./3/HOPE HUSSAR/YORKWIN/4/GENESSEE//CT12658/ALASKAN/3/AVON, USA

WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.

B

WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES

* INPUT TEST CULTIVAR = SUNDANCE
* 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES

```
      0   134(**)
      1
      2
      3
      4
      5
      6
      7
      8
      9
     10
     11
     12
     13
     14
     15   141(67)
     16    78(65) 88(63)
     17   129(65)
     18   150(54)
     19    79(57)153(55)156(56)
     20    30(59) 45(59)
     21    53(58) 63(61) 87(53) 97(52)
     22    47(55)
     23    22(53) 44(57) 52(55) 56(56) 62(56) 76(53) 86(57) 103(47)
     24    46(54) 85(61)112(52)139(50)142(50)167(54)
     25    12(50)
     26    14(49)113(45)115(41)148(40)
     27   147(44)152(35)165(40)172(35)
     28    28(45) 32(45) 37(44) 61(45) 77(43)102(46)107(43)128(42)143(41)151(43)157(40)158(46)
     29     4(47) 40(44) 90(43)111(40)136(46)
     30     1(41) 16(41) 17(43)138(36)154(44)163(41)164(36)170(45)
     31    27(43)118(40)124(45)130(42)162(42)171(34)
     32    15(42) 29(41) 69(39)
     33     3(37) 11(40) 38(35)104(37)105(35)108(34)110(39)135(36)
     34    59(36) 66(33) 95(36)131(32)133(38)
     35    57(38)122(35)166(27)
     36     8(29) 58(30) 84(32) 91(36) 92(33)101(38)
     37     9(30) 89(26)132(30)137(37)
     38
     39   127(28)184(23)
     40    99(26)178(25)187(26)
     41   186(25)
     42    24(27) 96(30)109(31)179(26)
     43   181(24)
     44   149(19)177(17)180(23)
     45    23(21)185(24)
     46    39(24)189(26)
     47     6(22)
     48   183(19)
     49   156(21)
     50   174(18)
     51   182(17)
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WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT = (X/3.23) WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.

Fig. 9. Cultivar identification ranking (**A**) and distance map (**B**) printouts for hard red winter wheat Sundance. Framed cultivars in (**B**) correspond to cultivars ranked in (**A**).

A

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-  WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY  -
 *  122 DATA BASE CULTIVAR PATTERNS ANALYZED
 *  DATA BASE SEARCH CUTOFF AT 55% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
 *  LSD(RELATIVE MOBILITY) = 0.5, MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3, DENSITY RANGE: 1 - 9.
 *  UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 42 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 35.0
```

	CULTIVAR	WEIGHTED % PATTERN HOMOLOGY	GLIADIN BANDS IN PATTERN NO.	GLIADIN BANDS IN PATTERN WBD	MATCHING BANDS NO.	MATCHING BANDS WBD	DISTRIBUTION OF NON-MATCHING BAND DATA: TOTAL NO.	TOTAL WBD	MOBILITY BASIS-R NO.	MOBILITY BASIS-R WBD	DENSITY BASIS NO.	DENSITY BASIS WBD	MOBILITY BASIS-U NO.	MOBILITY BASIS-U WBD	CLASS/TYPE	REGION
1	SPRINGFIELD	100	42	(35.0)	42	(35.0)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	SWS-PASTRY	S.ALTA
2	LEMHI 53_M	86	44	(37.2)	40	(33.4)	6	(5.3)	4	(3.4)	0	(0.0)	2	(1.9)	SWS-PASTRY	S.ALTA
3	LEMHI 62_M	78	45	(37.8)	39	(31.9)	9	(9.0)	6	(5.6)	0	(0.0)	3	(3.4)	SWS-PASTRY	S.ALTA
4	FIELDER	70	40	(34.4)	33	(28.5)	16	(12.4)	7	(5.9)	0	(0.0)	9	(6.5)	SWS-PASTRY	S.ALTA
5	LENNOX	67	41	(37.5)	32	(28.5)	18	(14.2)	8	(6.8)	1	(1.2)	9	(6.2)	HRW-FEED	ATLANTIC
6	BISHOP	65	40	(40.2)	29	(27.1)	21	(14.9)	8	(5.0)	3	(4.3)	10	(5.6)	HWS-EMQ	W.CAN
7	OPAL	64	38	(33.7)	28	(25.4)	22	(14.2)	8	(4.6)	2	(1.9)	12	(7.7)	HRS-FEED	R/ W.CAN
8	VALOR	61	37	(33.4)	28	(25.2)	21	(16.1)	7	(6.2)	2	(1.9)	12	(8.0)	SHRW-FEED	ATLANTIC
9	VERNON	60	42	(34.4)	29	(25.4)	25	(16.7)	12	(7.1)	1	(0.9)	12	(8.7)	SRS-FEED	R/ W.CAN
10	GLENLEA_M	58	40	(38.7)	27	(26.0)	26	(19.2)	11	(8.4)	2	(3.1)	13	(7.7)	SHRS-FEED	UTILITY
11	MILTON	58	39	(38.7)	27	(25.9)	26	(18.9)	11	(9.3)	1	(0.9)	14	(8.7)	HRS-FEED	R/ W.CAN
12	CASCADE	58	38	(39.6)	27	(25.2)	22	(18.6)	7	(5.9)	4	(4.6)	11	(8.0)	SHWS-GHP	E.CAN
13	GARNET	57	40	(38.1)	29	(25.7)	22	(19.2)	9	(7.1)	2	(3.4)	11	(8.7)	HRS-NEMQ	W.CAN
14	KHARKOV 22 M.C.	56	41	(41.2)	27	(25.9)	26	(20.1)	11	(7.7)	3	(4.3)	12	(8.0)	HRW-BW	W.CAN
15	RELIANCE_LTH_M	56	43	(39.3)	28	(25.9)	26	(20.1)	12	(9.9)	3	(3.7)	11	(6.5)	HRS-NEMQ	W.CAN
16	EGYPTIAN AMBER	56	39	(31.0)	26	(23.7)	29	(18.6)	13	(8.4)	0	(0.0)	16	(10.2)	SRW-PASTRY	ONTARIO
17	CHESTER_BRDR	56	42	(37.2)	30	(25.7)	23	(20.1)	11	(9.3)	1	(1.5)	11	(9.3)	HRS-SMQ	SASKFLY
18	WESTMONT	55	34	(30.0)	24	(22.8)	27	(18.3)	9	(5.6)	1	(0.9)	17	(11.8)	HRW-BW	W.CAN
	MEAN VALUE:	64	40	(36.5)	30	(27.1)	20	(15.3)	8	(6.4)	1	(1.8)	10	(7.1)		

	CULTIVAR	DATA BASE INDEX NO.	PEDIGREE DATA
1	SPRINGFIELD	128	NORIN 10/BREVOR//3*LEMHI 53/3/LEMHI 62, USA
2	LEMHI 53_M	118	CALIFORNIA 3098/5*LEMHI, USA
3	LEMHI 62_M	122	LEMHI 53*5/3/LEE*7//CHINESE/AE. UMBELLATA, USA
4	FIELDER	113	YAKTANA 54A*4//NORIN 10/BREVOR/3/2*YAQUI 50/4/NORIN 10/BREVOR//BAART/ONAS, USA
5	LENNOX	130	SELECTION, MIRONOVSKAJA, USA
6	BISHOP	95	LADOGA/GEHUN, CANADA
7	OPAL	107	TRIESDORF STAMM 21/40 X VON ROMKE ERLI; PEDIGREE INCLUDES GARNET, GERMANY
8	VALOR	135	KENT/SANGASTE (RYE), CANADA
9	VERNON	111	OPAL*4/POMPE, CANADA
10	GLENLEA_M	99	PEMBINA*2/BAGE//CB 100, CANADA
11	MILTON	104	KENTVILLE SELECTION*6/POMPE, CANADA; (KENTVILLE SELECTION = AWNED PLANT SEL. FROM OPAL).
12	CASCADE	112	QUALITY A/PACIFIC BLUE STEM//C26-59-2D/3/ONAS, CANADA
13	GARNET	3	PRESTON A/RIGA M, CANADA
14	KHARKOV 22 M.C.	129	SELECTION OF KHARKOV, CANADA
15	RELIANCE_LTH_M	32	KANRED/MARQUIS, USA
16	EGYPTIAN AMBER	165	FULTZ/LANCASTER, USA
17	CHESTER_BRDR	66	RENOWN/S-615//RESCUE/3/KENDEE/4/MIDA/CADET, CANADA
18	WESTMONT	138	RIO/REX//NEBRED, USA

```
    WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT  WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23)
    WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.
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B

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-  WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES  -
  * INPUT TEST CULTIVAR = SPRINGFIELD
  * 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES
-------------------------------
      0   128(**)
      1
      2
      3
      4
      5   118(86)
      6
      7
      8
      9   122(78)
     10
     11
     12   113(70)
     13
     14   107(64) 130(67)
     15    95(65)
     16   135(61)
     17   111(60)
     18   138(55)
     19     3(57)  58(53)  99(58) 104(58) 112(58) 131(54) 165(56)
     20    32(66)  66(56)  97(52) 118(52) 129(56) 172(49)
     21
     22     8(50) 105(50) 149(52)
     23    46(54)  77(49) 133(52) 152(44) 153(50) 162(51) 166(50)
     24    12(51)  17(51)  88(47) 110(52)
     25     4(49)  30(49)  69(50)  90(48) 103(46) 108(46) 141(43) 157(46) 171(44)
     26    11(49)  22(46)  37(45)  89(43) 132(43) 136(43) 148(42)
     27     1(44)  23(42)  24(49)  28(44)  29(45)  76(45)  91(43) 163(45) 167(49)
     28    40(44)  79(36)  92(45)  96(46) 127(41) 134(42) 137(44) 151(45)
     29    38(38)  39(43) 109(45) 139(39)
     30    16(42)  59(38)  78(42) 101(42) 102(40) 143(39) 147(39) 184(33)
     31     5(39)  84(42) 158(39)
     32    14(41)  45(35)  57(39)  62(39)  85(39) 150(29) 154(39) 164(36)
     33    15(40)  27(39)  47(34)  61(34)  86(38) 124(39)
     34     9(31)  44(36)  63(38)  87(32) 142(36)
     35    52(32) 156(28) 170(38)
     36    53(32)
     37    56(34) 155(31)
     38
     39
     40   187(23)
     41   179(26)
     42   180(23)
     43   177(17)
     44   178(15) 185(24)
     45   174(23)
     46   181(22)
     47
     48   186(18)
     49   183(19)
     50   182(18) 189(18)

    WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY
    BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT
    = (X/3.23)  WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY
    FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR
    EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.
```

Fig. 10. Cultivar identification ranking (**A**) and distance map (**B**) printouts for soft white spring wheat Springfield. Framed cultivars in (**B**) correspond to cultivars ranked in (**A**).

A

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-   WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - I. RANKING BY PATTERN HOMOLOGY   -
 *  122 DATA BASE CULTIVAR PATTERNS ANALYZED
 *  DATA BASE SEARCH CUTOFF AT 55% PATTERN HOMOLOGY (WEIGHTED BY BAND DENSITY).
 *  LSD(RELATIVE MOBILITY) = 0.5, MOBILITY RANGE: 10.0 - 90.0. LSD(BAND DENSITY) = 3, DENSITY RANGE: 1 - 9.
 *  UNKNOWN (OR TEST) CULTIVAR ELECTROPHOREGRAM CONTAINS 38 GLIADIN BANDS; TOTAL, WEIGHTED BY BAND DENSITY (WBD) = 33.7
```

	CULTIVAR	WEIGHTED % PATTERN HOMOLOGY	GLIADIN BANDS IN PATTERN NO.	GLIADIN BANDS IN PATTERN WBD	MATCHING BANDS NO.	MATCHING BANDS WBD	DISTRIBUTION OF NON-MATCHING BAND DATA: TOTAL NO.	TOTAL WBD	MOBILITY BASIS-R NO.	MOBILITY BASIS-R WBD	DENSITY BASIS NO.	DENSITY BASIS WBD	MOBILITY BASIS-U NO.	MOBILITY BASIS-U WBD	CLASS/TYPE	REGION
1	OPAL	100	38	(33.7)	38	(33.7)	0	(0.0)	0	(0.0)	0	(0.0)	0	(0.0)	HRS-FEED	R/ W.CAN
2	VERNON	96	42	(34.4)	38	(33.4)	4	(1.2)	4	(1.2)	0	(0.0)	0	(0.0)	SRS-FEED	R/ W.CAN
3	MILTON	95	39	(38.7)	37	(35.3)	3	(1.9)	2	(1.5)	0	(0.0)	1	(0.3)	HRS-FEED	R/ W.CAN
4	FIELDER	70	40	(34.4)	27	(28.0)	24	(12.1)	13	(6.5)	0	(0.0)	11	(5.6)	SWS-PASTRY	S.ALTA
5	VUKA	69	36	(39.0)	28	(29.7)	18	(13.3)	8	(8.4)	0	(0.0)	10	(5.0)	HRW-FEED	ATLANTIC
6	LEMHI 63_M	64	44	(37.2)	30	(27.6)	22	(15.8)	14	(10.2)	0	(0.0)	8	(5.6)	SWS-PASTRY	S.ALTA
7	KENHI	64	35	(33.1)	26	(24.9)	20	(13.9)	8	(5.0)	1	(1.2)	11	(7.7)	SWS-PASTRY	S.ALTA
8	SPRINGFIELD	64	42	(35.0)	28	(25.4)	22	(14.2)	12	(7.7)	2	(1.9)	8	(4.6)	SWS-PASTRY	S.ALTA
9	LEMHI 62_M	63	45	(37.8)	30	(27.6)	23	(16.4)	15	(10.8)	0	(0.0)	8	(5.6)	SWS-PASTRY	S.ALTA
10	LENNOX	62	41	(37.5)	28	(26.5)	21	(16.4)	11	(8.0)	2	(1.9)	8	(6.5)	HRW-FEED	ATLANTIC
11	MONOPOL	61	32	(31.9)	24	(24.9)	22	(15.8)	8	(6.2)	0	(0.0)	14	(9.6)	HRW-BW	ATLANTIC
12	SUN	61	42	(31.3)	27	(23.5)	23	(14.9)	12	(5.9)	3	(3.1)	8	(5.9)	SRW-PASTRY	BC
13	BISHOP	60	40	(40.2)	27	(24.9)	21	(16.7)	10	(7.7)	3	(3.7)	8	(5.3)	HWS-EMQ	W.CAN
14	PITIC 62	60	38	(31.6)	26	(24.1)	23	(16.4)	11	(6.8)	1	(0.9)	11	(8.7)	SRS-FEED	UTILITY
15	KHARKOV 22 M.C.	60	41	(41.2)	28	(27.6)	22	(18.6)	12	(9.3)	1	(2.2)	9	(7.1)	HRW-BW	W.CAN
16	PIONEER	58	40	(43.0)	25	(26.0)	25	(18.6)	12	(8.0)	3	(3.7)	10	(6.8)	HRS-EMQ	W.CAN
17	HOUSER	58	43	(34.7)	26	(24.0)	27	(17.3)	15	(9.0)	2	(2.8)	10	(5.6)	SWW-PASTRY	ONTARIO
18	EGYPTIAN AMBER	58	39	(31.0)	25	(23.1)	26	(16.7)	13	(8.4)	1	(0.9)	12	(7.4)	SRW-PASTRY	ONTARIO
19	SELKIRK_M	57	38	(38.1)	27	(25.7)	21	(19.2)	10	(9.3)	1	(1.9)	10	(8.0)	HRS-EMQ	W.CAN
20	DUNDAS_M	56	36	(31.0)	23	(20.7)	24	(16.4)	9	(6.2)	4	(4.6)	11	(5.6)	SRS-FEED	R/ W.CAN
21	ALEX	56	39	(40.2)	25	(25.7)	24	(20.1)	11	(10.5)	3	(2.8)	10	(6.8)	HRS-SMQ	USA
22	RUBY_M	55	43	(41.2)	27	(26.0)	26	(21.7)	15	(12.4)	1	(1.5)	10	(7.7)	HRS-EMQ	W.CAN
23	LAVAL 19	55	40	(32.8)	25	(22.3)	26	(18.3)	13	(8.7)	2	(1.9)	11	(7.7)	SHPS-FEED	E.CAN
24	VALOR	55	37	(33.4)	24	(23.5)	26	(18.9)	12	(7.4)	1	(0.9)	13	(10.5)	SHRW-FEED	ATLANTIC
25	EARLY RED FIFE	55	38	(37.8)	27	(24.6)	20	(19.8)	9	(9.3)	2	(3.1)	9	(7.4)	HRS-NEMQ	W.CAN
	MEAN VALUE:	64	39	(36.0)	27	(26.4)	20	(15.0)	10	(7.4)	1	(1.6)	8	(6.0)		

	CULTIVAR	DATA BASE INDEX NO.	PEDIGREE DATA
1	OPAL	107	TRIESDORF STAMM 21/40 X VON ROMKE ERLI; PEDIGREE INCLUDES GARNET, GERMANY
2	VERNON	111	OPAL*4/POMPE, CANADA
3	MILTON	104	KENTVILLE SELECTION*6/POMPE, CANADA; (KENTVILLE SELECTION = AWNED PLANT SEL. FROM OPAL).
4	FIELDER	113	YAKTANA 54A*4//NORIN 10/BREVOR/3/2*YAQUI 50/4/NORIN 10/BREVOR//BAART/ONAS, USA
5	VUKA	136	TOEERING 2/MERLIN//CARSTEN 8, FRG
6	LEMHI 63_M	118	CALIFORNIA 3088/5*LEMHI, USA
7	KENHI	115	KENYA 338 AC2E3/2*LEMHI, CANADA
8	SPRINGFIELD	128	NORIN 10/BREVOR//3*LEMHI 63/3/LEMHI 62, USA
9	LEMHI 62_M	122	LEMHI 63*5/3/LEE*7//CHINESE/AE. UMBELLATA, USA
10	LENNOX	130	SELECTION, MIRONOVSKAJA, USA
11	MONOPOL	131	PANTHUS/ADMIRAL, WEST GERMANY
12	SUN	171	AS SOL, SELECTION OF LOCAL VARIETY/ENGLISH STANDUP, SWEDEN
13	BISHOP	95	LADOGA/GEHUN, CANADA
14	PITIC 62	108	YAKTANA 54//NORIN 10/BREVOR 26-1C, MEXICO
15	KHARKOV 22 M.C.	129	SELECTION OF KHARKOV, CANADA
16	PIONEER	4	RIGA/PRESTON, CANADA
17	HOUSER	153	BREVOR/NORIN 10//NY WHEAT RYE SEL /3/HOPE HUSSAR/YORKWIN/4/GENESSEE//CT12658/ALASKAN/3/AVON, USA
18	EGYPTIAN AMBER	165	FULTZ/LANCASTER, USA
19	SELKIRK_M	40	MCMURACHY/EXCHANGE/3*REDMAN, CANADA
20	DUNDAS_M	97	OPAL/INIA 66, CANADA
21	ALEX	84	ND507/ND496, USA (ND507 = WALDRON/RL4205)
22	RUBY_M	12	DOWNY RIGA/RED FIFE, CANADA
23	LAVAL 19	103	F.W.606-A/OPAL//OPAL, CANADA
24	VALOR	135	KENT/SANGASTE (RYE), CANADA
25	EARLY RED FIFE	1	SELECTION OF RED FIFE, CANADA

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    WBD VALUES IN PARENTHESES GIVE THE PAIRED NUMBER COUNT WEIGHTED BY BAND DENSITY. THE WEIGHTING INCREMENT = (X/3.23)
    WHERE 3.23 = POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY FOR EACH GLIADIN BAND IN THE ELECTROPHOREGRAM.
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B

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-   WHEAT CULTIVAR IDENTIFICATION BASED ON GLIADIN ELECTROPHOREGRAMS - II. DISTRIBUTION BY DIFFERENCES   -
  * INPUT TEST CULTIVAR = OPAL
  * 122 DATA BASE CULTIVAR PATTERNS ANALYZED ; LSD(RELATIVE MOBILITY) = 0.5, LSD(BAND DENSITY) = 3.

WEIGHTED POSITIONAL DIFFERENCES
-------------------------------
      0   107(**)
      1   111(96)
      2   104(95)
      3
      4
      5
      6
      7
      8
      9
     10
     11
     12   113(70)
     13   136(69)
     14   115(64)128(64)
     15   171(61)
     16    97(56)108(60)118(64)122(63)130(62)131(61)
     17    95(60)153(58)165(58)172(62)
     18   103(55)
     19     4(58) 40(57)129(60)135(55)
     20     1(55) 84(56)
     21    66(54) 79(47)149(52)162(53)
     22    12(55) 37(53)138(48)
     23   108(47)112(52)157(49)
     24    58(45) 69(52) 96(48)167(52)
     25    17(48) 99(46)137(49)158(48)166(45)
     26     8(43) 77(44)127(43)148(40)152(37)184(38)
     27     3(44) 92(43)
     28     5(43)  9(40) 11(46) 15(46) 23(41) 27(45) 28(43) 32(42) 38(40) 89(38)110(45)124(45)134(43)
     29    24(44) 61(36) 87(38)102(40)141(40)155(41)
     30    22(41) 39(43) 46(45) 76(41) 85(41) 90(39)147(38)
     31    59(37)109(43)
     32   143(36)185(34)
     33    16(37) 29(36)142(36)154(39)163(38)
     34    14(35)132(31)133(36)151(35)156(32)164(32)
     35   150(26)
     36    57(34) 63(38)139(30)
     37    88(28)170(36)186(25)
     38    53(31) 78(30)177(23)182(26)187(24)
     39    30(27) 47(26)183(23)
     40    91(26)101(30)
     41   179(26)180(22)181(24)
     42    45(24) 56(24)174(21)178(18)
     43    62(23)189(20)
     44    52(23) 86(25)
     45
     46
     47
     48     44(19)

    WEIGHTED POSITIONAL DIFFERENCE GIVES THE TOTAL NUMBER OF BAND DIFFERENCES WEIGHTED BY DENSITY
    BETWEEN THE INPUT PATTERN AND DATA BASE CULTIVAR ELECTROPHOREGRAMS. THE WEIGHTING INCREMENT
    = (X/3.23) WHERE 3.23 = CULTIVAR POPULATION MEAN BAND DENSITY AND X = ASSIGNED DENSITY
    FOR EACH GLIADIN BAND. TABULATED DATA IS LISTED IN PAIRS, AND REPRESENTS RESPECTIVELY FOR
    EACH CULTIVAR ANALYZED, ITS DATA BASE INDEX NUMBER AND % PATTERN HOMOLOGY IN PARENTHESES.
```

Fig. 11. Cultivar identification ranking (**A**) and distance map (**B**) printouts for hard red spring wheat Opal. Framed cultivars in (**B**) correspond to cultivars ranked in (**A**).

composition because of their similarity to the Neepawa pattern are tightly clustered in the upper part of the CVMAP distribution. As expected, this group was exclusively comprised of cultivars listed in the CVID program ranking result shown in Figure 4.

A further distinction among the 10 remaining cultivars in the ranked subpopulation relates to the isolation of cultivars Canuck, Leader, and Era (DBINs 63, 78, and 88, respectively). Both Canuck and Leader are sawfly-resistant Canadian HRS bread wheats of good quality. Cultivar Era is a U.S.-registered HRS semi-dwarf wheat of poor breadmaking quality and relatively low protein content. These three cultivars of the same wheat class are logically different genotypes from those cultivars immediately above and below them in the CVMAP result and the ranked list provided in Figure 4. Their gliadin electrophoregrams reflect these differences. It is noteworthy particularly for Era, which cannot be visually differentiated by kernel characteristics from commercial HRS wheat cultivars of good breadmaking quality.

These observations indicate that the CVMAP analysis can stand alone as a satisfactory "summary" version of the cultivar identification procedure, requiring no input of pedigree, functional quality, or adaptation information to set up the data base. Clearly, however, the CVMAP program presents information complementary to the CVID short-list ranking. In this regard, a most useful feature is the identification of diverse genotypes with respect to the input cultivar. These are located at the margins of the CVMAP distribution and can be listed separately (illustrated in inset, Fig. 6) by the user. Cultivars in the lower tail of the distribution are in the main durum (DBIN >172) or common wheat cultivars with electrophoregrams differing in the extreme from that of Neepawa. For example, at the weighted positional difference level of 55, the durum wheat Coulter (DBIN 177) shares only a 12% PH with Neepawa. Lake (DBIN 23) also has a very low level of pattern homology (11%) with the Neepawa electrophoregram. Cultivar Lake, unlike Coulter, is an HRS bread wheat of good milling and baking quality. The CVMAP process can therefore be used to quickly and comprehensively identify inherent variability in large populations of material that could be exploited through plant breeding.

The CVMAP distribution also yields information on overall discriminative ability of the procedure using the present data base. For cultivars at the bottom end of the ranking list, pattern homology scores around 10–20% are common. In other words, the data base cultivar population is resolved over 80–90% of the pattern homology measurement scale, which indicates a significant advantage in cultivar discrimination compared to the 60–65% range of "relative percent similarity" obtained by Lookhart et al (1983).

Wheat Class Comparisons

In terms of class or quality type discrimination, the most striking results were obtained using a durum wheat cultivar as the test unknown. An example shown in Figure 7 was derived from a program run for the cultivar Wascana. The computer clearly identifies a durum wheat cultivar as the "unknown" (Fig. 7A) by exclusively ranking other cultivars of like class below the top-ranked Wascana. Note that the cutoff threshold for entry into the ranking list was reduced to 35% PH from the 55% level usually used for common wheats.

The CVMAP result (Fig. 7B) also shows how easily durum cultivars can be discriminated by gliadin electrophoregrams. The main body of the CVMAP distribution is comprised entirely of common wheats. With a mode value of 50 band differences for the Wascana electrophoregram, this level of discrimination between durum and common wheats is about 50% higher than that within each class alone. The distinction of durum wheats by gliadin electrophoregrams features a substantially different pattern distribution; and a general absence of bands with Rm <20 is consistent with their genetic composition, as all lack the D genome.

The identification of cultivars by class or quality characteristics was also easily determined for soft winter wheats. Electrophoregram data for Yorkstar (a SWW wheat) gave a ranking that included only soft white or red winter pastry wheats (Fig. 8A) with common adaptation. The remaining soft winter wheat cultivars in the data base that were excluded from the list were five genotypes with different attributes. The excluded set comprised cultivars Gaines, Nugaines, and Sun, which are all SWW types adapted to the Pacific Northwest; Jones Fife, an obscure soft to semi-hard white winter wheat grown to a limited extent in Alberta; and Rideau, with kernel characteristics similar to Jones Fife, possessing only fair quality for pastry flour, presumably as a result of inheriting relatively strong gluten characteristics from one of its parents, Kharkov 22 M.C., an HRW bread wheat.

Another feature of the soft winter wheat ranking (Fig. 8A) is the apparent unimportance of common pedigree in deriving the result. The cluster of seven cultivars with high pattern homology scores (>85%) and few positional differences (<7) with the Yorkstar electrophoregram (Fig. 8B) are relatively dissimilar in pedigree. In total, the ancestry of the 17 wheat cultivars in the Yorkstar ranking includes contributions from more than 36 different parents from at least five countries. This indicates that gliadin composition may be the predominant factor in clustering genotypes by functional type.

Compared to the soft winter wheats, HRW wheats were a less strongly associated cultivar class. A typical result is illustrated in Figure 9, which shows the ranking derived by the Sundance electrophoregram as the test unknown. Cultivar Sundance is an HRW wheat with good milling and baking quality. Of the 11 remaining HRW wheats in the cultivar identification data base, only cultivars Yogo and Kharkov 22 M.C. possess gliadin patterns with sufficient resemblance to be included in a list dominated by Thatcher-type HRS bread wheats. The ranking may be at least partly explained by the limited number of HRW bread quality wheats in the data base, as well as by the contribution of Kanred, an HRW wheat, in the pedigree of Thatcher. Nevertheless, when wheats of different classes comprised the list of ranked cultivars, as in this example, we routinely found that the common factor in the ranking could generally be reduced to end-use quality in terms of bread or so-called "nonbread" wheat status.

A similar trend was observed when the data base was ranked by gliadin pattern homology to an electrophoregram from either a soft (white or red) spring, or an HRS feed wheat cultivar. Results are shown in Figures 10 and 11 for the SWS cultivar Springfield and the HRS wheat Opal. Both cultivars may be characterized as relatively low-protein wheats, unsuitable for breadmaking. These quality attributes, and Opal's visual indistinguishability from top-grade HRS bread wheats, also account for its restricted license for production in eastern Canada or areas of British Columbia not designated under the Canadian Wheat Board Act.

The computer outputs for Springfield and Opal (Figs. 10 and 11) have several common features. The majority of wheats with high % PH in respective short rankings, correctly reflect the class of the input cultivar. Both lists are also comparable in the proportion of pastry and feed type cultivars which were isolated, as well as the high proportion of HRS bread wheat cultivars which were excluded. (The cultivar identification data base includes 59 HRS wheats, 41 of which are at least equal to Marquis in milling and baking quality.) The CVMAP distributions (Figs. 10B and 11B) also reveal that Neepawa (DBIN 56) and other Thatcher-related wheats, which presently dominate the grain commerce in western Canada, are the most distant common wheat cultivars in electrophoregram identity with Springfield and Opal type wheats.

These results point to substantial differences in gliadin composition between bread and nonbread wheat genotypes, notwithstanding grain class affiliation or distinguishability by kernel characteristics. In order to explain the similarity in the ranking lists for Springfield and Opal, it should be noted that both cultivars, despite having very different pedigrees, share a 64% electrophoretic pattern homology. This was sufficient to place each cultivar in the upper tail of the other's CVMAP distribution (Fig. 10B, DBIN 107; Fig. 11B, DBIN 128).

The foregoing provides firm evidence of the influence of gliadin composition in differentiating wheats of different functional type. Comparable results were routinely observed in extensive testing of programs of the cultivar identification system. As the ranking

results were generated by the computer based solely on gliadin composition, the latter must be considered an important factor relating to inherent wheat quality characteristics. Indeed, the relevance of gliadin composition to wheat quality parameters has been well documented for French (Branlard and Rousset 1980) and Australian (Wrigley et al 1981, 1982b) varieties, in studies where complete electrophoretic pattern data was submitted to the computer for analysis. It is not surprising, therefore, that ranking Canadian cultivars by gliadin electrophoregram homologies also exposes a similar underlying relationship.

The aims of the present study were not involved with investigating the association between gliadin protein composition and utilization quality. The relationship is nonetheless important to the successful long-term application of the electrophoresis test for wheat cultivar identification, as it suggests that grain with undesirable or different quality attributes can always be expected to be differentiated by PAGE from (otherwise visually identical) wheat of acceptable or contrasting quality.

General Considerations

With the exception of the short-list ranking results for Neepawa and Yorkstar (Figs. 4 and 8, respectively), no more than two cultivars (or <2% of the data base population) in a given ranking achieved pattern homology scores greater than 80% with the test electrophoregram. This level of discrimination was typical of cultivar identification program runs in general, for which the average number of isolated cultivars in both 90% (i.e., 90–100%) and 80% (80–89%) pattern homology classes was approximately one (of 121 cultivars) in each case.

While these numbers reflect the facility with which differences could be distinguished between cultivars by gliadin electrophoregrams, unequivocal differentiation was not possible in every instance, mainly when genetic relationship was very close. A list of nine cultivar groupings in the data base that were affected in this way is given in Table III. This list can be subdivided into 16 pairs of cultivars with similar gliadin PAGE patterns, a relatively insignificant total when compared with more than 7,380 possible pairs among 122 cultivar electrophoregrams in the data base that can be differentiated.

Of greater importance are values for % PH that were computed among cultivar groups in Table III. The data indicate that the comparative analysis of gliadin electrophoregrams characterized by pattern homology scores greater than about 94% must be interpreted with caution, as implied band differences may not be significant.

It should be emphasized that the reliability of results in general will depend on good precision in relative mobility determination and the establishment of a data base comprising a broad-based collection of reference electrophoregrams derived from authentic seed samples of known pedigree. Information concerning the presence of offtype patterns is also important if single kernels are used as the basis for cultivar comparisons.

TABLE III
Cultivar Groups in the Data Base for Which Discrimination by Gliadin Electrophoregrams is Uncertain

Attribute Index No.	Cultivars	Class	Computed % Pattern Homology Score
1	Apex-Marquis	Hard Red Spring	99
2	Regent-Renown		95
3	Manitou-Neepawa		98
	Canthatch-Katepwa		99
4	Milton-Opal-Vernon		>95
5	Lemhi 53-Lemhi 62	Soft White Spring	96
6	Lennox-Valor	Hard Red Winter	94
7	Yorkstar-Favor-Genessee-Gordon	Soft White Winter	>92
	Gaines-Nugaines		100
9	Mindum-Nugget	Durum	98

CONCLUSIONS

The complex heterogeneity of gliadin proteins demands the utility of a computerized strategy to evaluate the resemblance of electrophoregrams. Even on a small scale, the task of identifying matching and nonmatching bands in compared patterns is impractical by visual means alone. The elaborate system of programs described in this article has several practical and research applications, not the least of which is to quantify these types of assessments for cultivar identification. The power of these methods clearly relates to the comparative analysis of gliadin electrophoregram composition, especially where a large sample of patterns comprises the data base. The speed and detail of this process should therefore be well suited for determining genetic relationships, or to characterize the diversity or identify unique forms in a population of genotypes. Where satisfactory resolution and reproducibility of banding patterns exist, data on other protein fractions, notably sodium dodecyl sulfate PAGE patterns of high molecular weight glutenin subunits, should lend themselves well to similar analyses. The potential also exists to successfully apply the computer-based methodology for the comparative analysis of high-performance liquid chromatography separations of cereal proteins as described by Bietz et al (1984). In this rapidly developing field, cultivar identification based on chromatographic data can also be reduced to a process of comparing lists of two-value parameters (relative elution time and absorbance) that characterize the cultivar.

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