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# Corrigendum

**Molecular marker analysis of European *Setosphaeria turcica* populations**
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Owing to an error in the production process, symbols in the text on page 613 were missing and figure 3 of the above-mentioned article was hardly readable.

The pages as they should have been printed are presented overleaf.

The publishers extend their apologies for any inconvenience to the authors and readers.

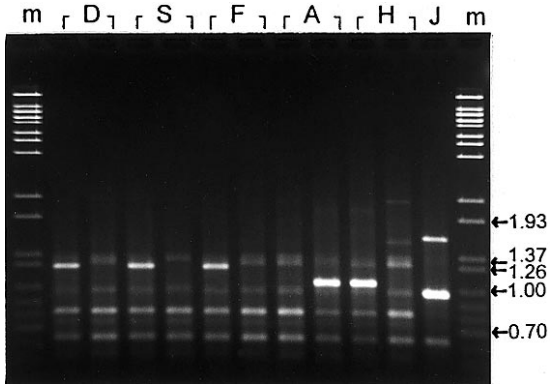


*Figure 1.* Agarose gel showing RAPD patterns generated by primer 433 with European *S. turcica* isolates. Lanes are designated m for DNA size marker, D, S, F, A, and H for two different isolates each from Germany, Switzerland, France, Austria, and Hungary, and J for an isolate from Johnson grass. Figures to the right designate DNA fragment sizes of the size marker in (kb).

ers, isolates with identical haplotypes are regarded as clonemates.

The Dice similarity coefficient (Sneath and Sokal, 1973) of two isolates x and y was calculated as $S_d = 2n_{xy} / (2n_{xy} + n_x + n_y)$, where $n_{xy}$, $n_x$ and $n_y$ are the numbers of bands possessed by both isolates, only by x, and only by y, respectively. The software NTSYS-pc (Rohlf, 1993) was used to calculate the unweighted pair-group arithmetic average (UPGMA) algorithm and to develop a dendrogram (procedures SIMQUAL, SAHN and TREE). The matrix-correspondence test (Mantel, 1967) was conducted to compare the similarity matrix with the cophenetic matrix to examine the goodness of fit of the dendrogram to the data (procedures COPH and MXCOMP). The software WINBOOT (Yap and Nelson, 1996) was used to evaluate the robustness of the groupings formed in the dendrogram by bootstrapping. From the binary data set with one isolate per haplotype, WINBOOT reconstructed the phenogram 2000 times by repeated sampling with replacement. The frequency with which a particular group was formed was considered to reflect the reliability of the group.

To investigate the question of putative clonal lineages, individual RAPD band differences between haplotypes were counted and graphically depicted for a subset of haplotypes.

An estimate of genotypic diversity was obtained with the Shannon index, corrected for different sample sizes, as $H_S = -\sum_i (g_i \ln(g_i)) / \ln N$, where $g_i$ is the frequency of the $i$th haplotype in the sample, and $N$ is the sample size. Different $H_S$-values were compared by a t-test (Poole, 1974), applying appropriate type-I errors via a sequentially rejective Bonferroni procedure (Holm, 1979).

## Results

Among the 73 isolates from maize, there were 26 different haplotypes (Figure 2). Of these, 17 haplotypes were represented by only one isolate. Eight haplotypes were detected two to ten times. The most common haplotype members, M4 (Figure 2), was represented by 22 isolates from Germany, Switzerland, and France. This is more than one third of all isolates from these three western European countries. No isolate from east of the Alps, i.e. from Austria or Hungary, was identical to haplotype M4. The dendrogram (Figure 2) shows that haplotypes of most *S. turcica* isolates from the three western countries (M1 to M12) have a higher similarity among themselves than to the Austrian and most Hungarian isolates (M15 to M22). Only four isolates (three haplotypes, M13, M14 and M20) from the three western countries were of high similarity to the eastern isolates. Just one single Swiss isolate had the same haplotype (M20) as some Austrian isolates. Two outgroups are formed by M24 to M26 (three Hungarian isolates) and M23 (a French isolate, which in 61% of all bootstrapped cases clustered together with the Hungarian outgroup haplotypes). The reliability of the dendrogram (Figure 2) is high as the cophenetic correlation is r = 0.99; it is still high (r = 0.93) when the isolates from Johnson grass were disregarded.

Genotypic diversity ($H_S$) of the whole sample of isolates from maize, regarded as one population, is 0.60, with no significant difference between the eastern (Austria + Hungary: $H_S$ = 0.70) and the western (Germany + Switzerland + France: $H_S$ = 0.51) subpopulations.

The subclustered haplotypes of western European isolates, M1 to M12, were plotted as a minimum spanning tree with single RAPD band differences between the isolates of a branch (Figure 3). Haplotype M4, the one with the most clonemates, assumes a central position. Haplotypes M1 to M9 differ from each other by as many RAPD bands as there are connecting lines between them. Haplotypes M10 to M12 differ from each other by one or two RAPD bands only, but their distance to the cluster around haplotype M4 is inconsistent: Both M10 and M12 differ by 7 bands from both M1 and M6. Further smaller subgroups with dif-

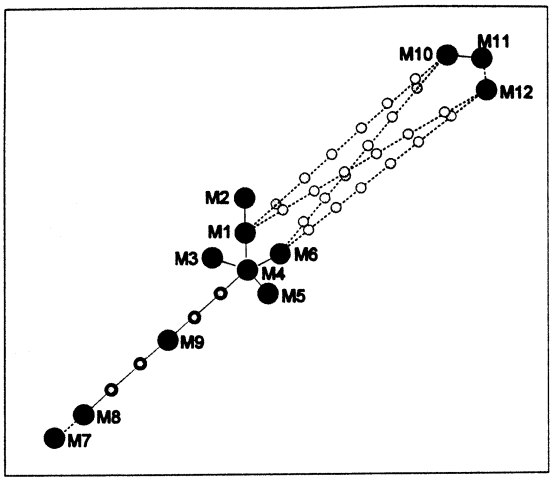


*Figure 3.* A derivative of a minimum spanning tree with haplotypes of European *S. turcica* isolates. The distance between two adjacent circles corresponds to a single RAPD band difference. Each large circle represents a haplotype found in western Europe (M1 to M12, Figure 2), while the small circles stand for hypothetical haplotypes, which were not detected. The broken lines connecting the small light circles mark possible shortest links between detected haplotypes: Haplotypes M2 and M10, M2 and M12, M6 and M10, and M6 and M12, respectively, all differ in 7 RAPD bands.

ferences in one or two bands between haplotypes and with identical mating type were found (not shown but analogous to Figure 3: M17 - M18; M21 - M20 - M22; and M24 - M25). However, none of them could be linked to other haplotypes or smaller subgroups without forming complicated loops, or without ambiguities. For example, haplotype M16 differs in two bands (and in mating type) from M14 and three other bands from M17, but M14 and M17 differ in three bands, not five.

Both mating types were found among the European *S. turcica* isolates. Isolates with identical haplotype always had the same mating type. The frequencies of MAT1 and MAT2 differed between the three western and the two eastern countries (Table 2). Most isolates from Germany, Switzerland, and France were MAT2. Only the isolates from a single field in Emmendingen (D-M7), two isolates from the experimental station Eckartsweier, and two isolates from Switzerland were MAT1. In contrast, all 12 isolates from Austria, clonemates of four different haplotypes, were MAT1. The Hungarian isolates with highest similarity to the Austrian isolates, haplotypes M16, M18, and M19 had MAT1 as well. Only the three Hungarian outgroup isolates were MAT2. No association between mating type and any RAPD marker was observed.

*Table 2.* Occurrence of mating types of *S. turcica* in the three western (Germany, Switzerland, France) and the two eastern (Austria, Hungary) European countries

| Origin of isolates | Haplotypes with MAT1 | MAT2 |
|---|---|---|
| Germany, Switzerland, France | M7, M10, M11, M20 | M1, M2, M3, M4, M5, M6, M8, M12, M13, M14, M23 |
| *Sum West*: | 4 | 10 |
| Austria, Hungary | M15, M16, M18, M19, M20, M21, M22 | M24, M25, M26 |
| *Sum East*: | 7 | 3 |

The *Setosphaeria turcica* isolates sampled from Johnson grass in a maize field in Southern Switzerland (Table 1) possessed very different RAPD banding patterns compared to all isolates from maize (Figures 1, 2). One third of all polymorphic bands distinguished between these two groups. All seven isolates from Johnson grass had the same haplotype, designated J1 (Figure 2).

## Discussion

Among the isolates from maize, there is a differentiation between the isolates from the eastern (A, H) and western (D, S, F) European countries, as characterized by similarities in marker haplotype and mating type (Figure 2). However, the differentiation was not complete, since some western isolates were most similar to eastern isolates. One Swiss isolate even shared its haplotype (M20) with Austrian isolates. Three Hungarian isolates, regarded as outgroup haplotypes according to their RAPD profiles, had MAT2 which prevailed in the western samples (Figure 2). Moreover, genotypic diversity was not significantly different between the eastern and western samples. Isolation by distance (Wright, 1942) was presumed as an important mechanism forming divergent subpopulations of *S. turcica* on different continents as well as in different regions in Kenya (Borchardt et al., 1998a, 1998b). There is an even larger geographic distance between the French and the Swiss (650 km) or German (690 km) locations than between the Austrian and the Swiss (520 km) or German (550 km) locations. Therefore we conclude that the Alps in their east-to-west extension