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# Genetic diversity of wild forage plants (genus *Urochloa*) in the West African Sahel

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## Abstract
Wild forage plants play an important role as a major natural resource basis for the local population in the Sahel region. This potential is increasingly endangered by desertification processes. The investigation of genetic diversity of wild plants is a growing research field, which has also stimulated discussion on the access to genetic resources.

Our aim was to investigate genetic diversity of the target species (e.g. the important wild Sahelian forage grasses of the genus *Urochloa*, also known as *Brachiaria*) in order to evaluate possible differences in spatial and temporal distribution. The results obtained using molecular markers clearly demonstrate a habitat-related pattern (ecotypes) of the more drought resistant (Sahelian) species *U. orthostachys* and *U. nidulans*. A discrimination in the genetic pattern according to the position of test sites for the Sahelo-Sudanian species *U. xantholeuca* could be found for test sites far apart (>300 km). In addition to the spatial pattern, the more drought resistant Sahelian species show first indications of temporal variations. According to these results, genetic diversity for the forage plants investigated is dependant on different habitats, so that a strategy of protected areas can not meet the requirements of an *in situ* conservation strategy. Transnational resource management strategies should be considered in order to maintain genetic diversity and ensure survival of the people in the area.

**Keywords:** West African Sahel, Genetic diversity, Molecular ecology, *Urochloa*, RAPD-PCR

## Introduction:

The international project presented here was conducted jointly by the Berlin Botanic Garden and Botanical Museum, the International Plant Genetic Resources Institute (IPGRI) and the Institute of Biometrics and Population Genetics, University Giessen, in cooperation with the Institute of Geoscience/Geoinformatics, Free University Berlin and the International Crop Research Institute for the Semi-Arid Tropics in Niamey/Niger between 1993 and 1997 in Niger, Mali and Burkina Faso (Kusserow 1997). The funds came from the German Ministry for Economic Cooperation (BMZ). The chief aim of the study was to explore genetic diversity of wild forage plants: Do individuals of a given species show different genetic patterns in different habitats ? And could we recognise a temporal differentiation (i.e. genetic pattern differences in samples from successive years)?

The West African Sahel is one of the most endangered ecosystems of the world. The complex process of desertification reduces biodiversity and therefore also genetic diversity. We call this process of reduction and loss of genetic diversity "genetic erosion". Not much is known

of the genetic potential of Sahelian plants, so we have little idea about what we stand to lose. One major basis of the food security in this region is livestock. An understanding of the genetic potential of wild forages is essential in order to maintain biodiversity and develop strategies for *in situ* conservation in order to ensure the survival of the people in their region. This has a significant political aspect, because reducing future migration to the South is highly important in order to reduce conflicts caused by environmental refugees. These conflicts have already reached a critical level in some northern areas of Ivory Coast, Benin, and Ghana.

The Sahelian region lies between the Sahara in the North and the semi-humid Sudanian zone to the South, between the 100 mm isohyet to the North and the 600 mm to the South. Our research region lies mainly in the southern part (South Sahelian zone) between the Canal du Sahel in Mali and the former Lake Chad in Niger. The area extends approximately 2000 km in an east-west direction, and makes up around a third of the entire Sahel.

## Material and methods

Five of the Sahelian region's most important forage plants (three grasses and two legumes) were selected for the study (Kusserow et al., 1997). Most results were obtained for one annual grass, *Urochloa xantholeuca* (better known in the agricultural sector as *Brachiaria xantholeuca*). In total, 44 test sites were laid out within an extension of 2000 km (in the states Mali, Burkina Faso and Niger). Fifteen of these were sampled repeatedly over two to three years.

The test sites were selected according to climatic and edaphic parameters. They can be classified in four different units: One unit comprises all areas on lateritic plateaux; The second and largest unit comprises sandy sites along roads; In the third unit, sites were on fallow land; The fourth unit consists of protected areas, such as the farming area of ICRISAT or the fenced sites Toukounous and Ibecetene. The latter are government managed. One criterion for the temporal study was the re-identification of test areas. Sites were selected which would be easy to find again, for example with the help of signposts, milestones, GPS and repeated visits. Test areas ranged from 1-5 m in width and 5-25 m in length. Where possible, ten individuals were collected per target species. If they grew in sufficient numbers, plants were collected by picking one, taking two steps, picking another to the right, taking two steps again and picking the next to the left, etc. For the molecular studies, leaf material was collected and stored in plastic tubes with silica gel for gentle drying.

Molecular genetic methods, specifically randomly amplified polymorphic DNA, (RAPD) were used to determine the genetic variability of the species under study (Koehler et al., 1998, Pons et al., 1998, Snowdon & Langsdorf 1998, Williams et al., 1990). In total 309 individuals from 24 test sites were investigated. From originally 100 tested primers, 10 were selected for the study, and 250 RAPD markers, approximately 25 markers could be identified per primer.

## Results

The annual *U. xantholeuca* has not been studied before with regard to its temporal and spatial genetic diversity. One of the researchers had smuggled *U. ramosa* among the collected material to test the molecular method, which was able to discriminate the samples according to their species level. The first and surprising result was that not all the samples we had collected were in fact *U. xantholeuca.* We learned that instead of two different species, five had been actually collected. With the help of the Prof. Scholz, from the Botanical Museum, it

was possible to label the five species (*U. xantholeuca , U. ramosa, U. lata, U. orthostachys* and *U. nidulans*). *U. nidulans* is a new combination (Kusserow et al., 1999).

For *U. xantholeuca*, 188 individuals collected from 14 test sites over three years were tested. The diagram presents a very heterogeneous pattern with many subclusters. A discrimination analysis shows the separation of the test sites (Fig. 1). The test site "Sevare" in Mali is discriminated first, which is interesting because this site lies far away (approx. 800 km west of most of the other sites which lie in Niger), followed by the sites Ouahigouya in Burkina and Maradi, Diffa and Takieta in Niger. The so-called H-cluster could not be very well discriminated, the distances between sites are 2 to 50 km (except H11 and H 13). The distances between Maradi and the H-cluster is approximately 650 km. Our first question: "Is it possible to see genetic diversity according to different habitats ?" can now be answered positively. In answer to the second question: "Is there a year to year variability in the genetic pattern ?" we can respond: "Yes, but it depends on the site and is not so clear as it is for *U. nidulans*".

Figure 1. Discriminant analysis of 14 test sites from *U. xantholeuca*

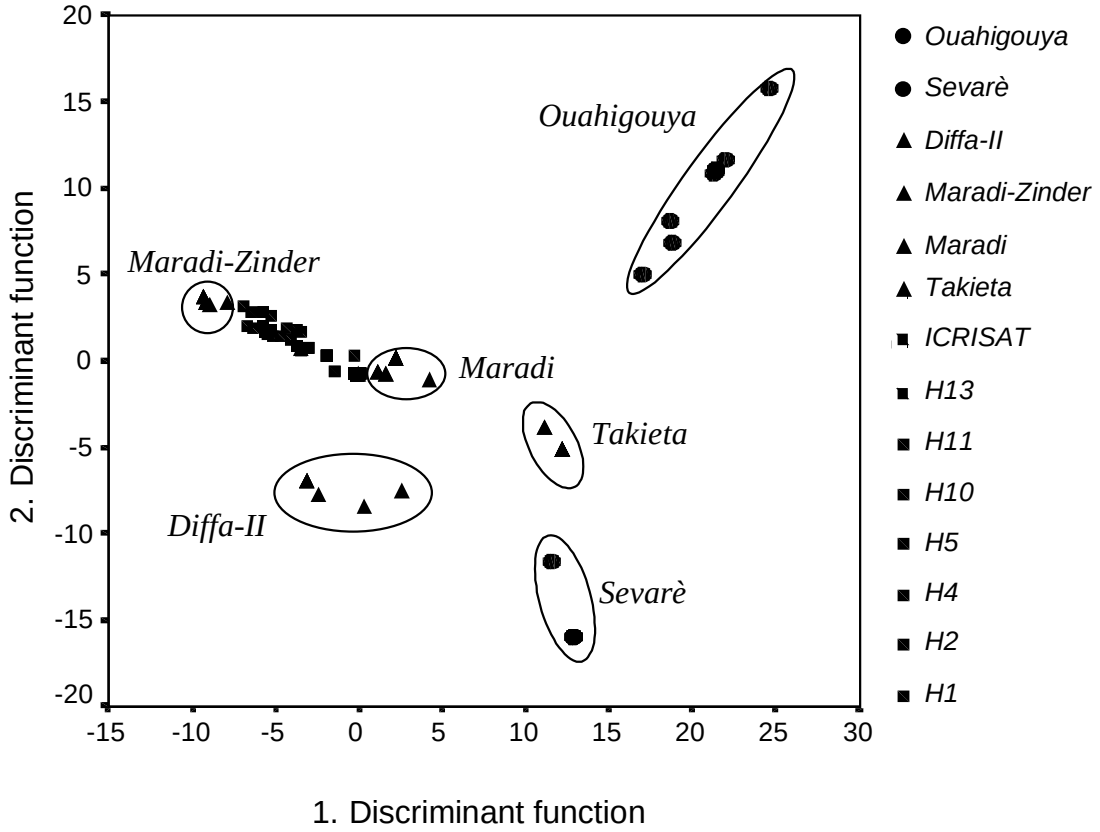
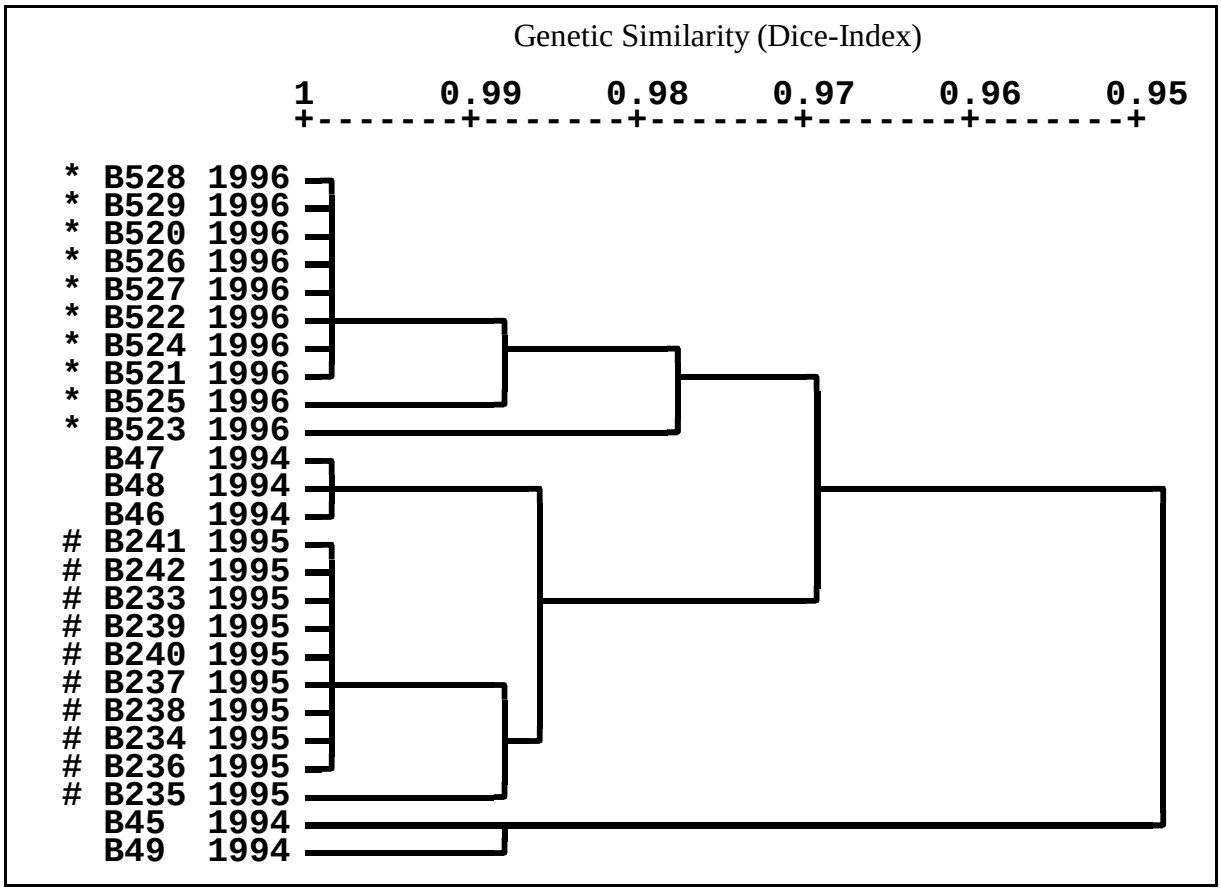



Fig. 2 demonstrates an example of temporal changes between sampling years. The site H 10, is located near Tahoua, 500 km east of the capital Niamey. The samples in 1995 and 1996 were clustered, but the individuals from 1994 do not build up a cluster. Variance analysis shows that 73% of the total variability is given by genetic differences between the collecting years and 27% is related to the genetic variability at the individual level.

Figure 2. UPGMA dendrogram of test site *H10*. 25 Individuals collected in 1994-1996 were analysed. # = Collection 1995; * = Collection 1996




Another example is given by the more drought resistant species *U. nidulans*. The distribution area lies in the more arid region of the northern Sahel and the rocky sites (e.g. Air mountains) in the Sahara. Fig. 3 shows the diagram with 81 individuals from 8 test sites and two years (1995 and 1996). All sites lie in the Sahelian part of Niger (200-400 mm). Two main points should be noted here: there is a very good spatial discrimination (sites are separated), and discrimination in time (there are different genetic patterns according to sampling year). The principal component analysis (Fig. 4) demonstrates this clear separation of test sites and same sites (Zinder I and Toukounous) from different years (Langsdorf 1999).

Figure 3. UPGMA-Dendrogramm of *U. nidulans* from 81 individuals from 8 test sites

Genetic similarity (Dice-Index)

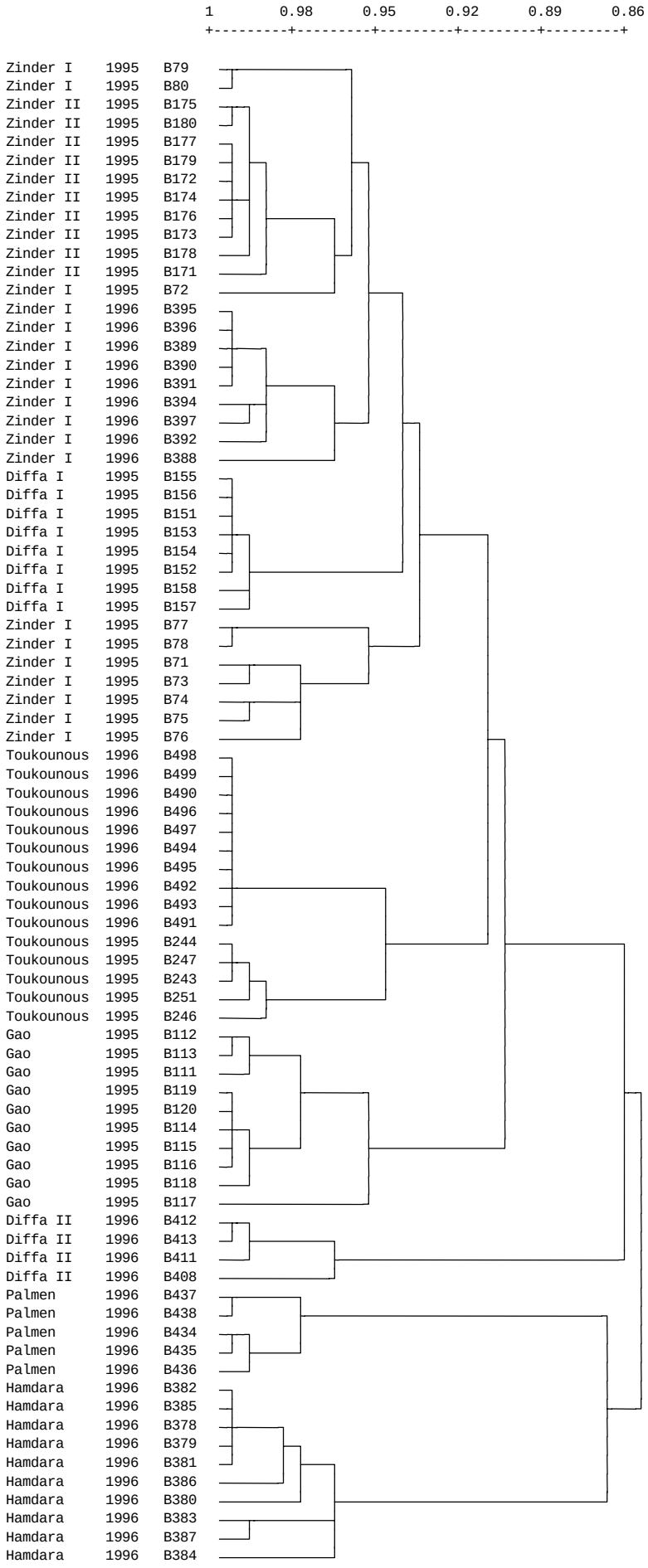
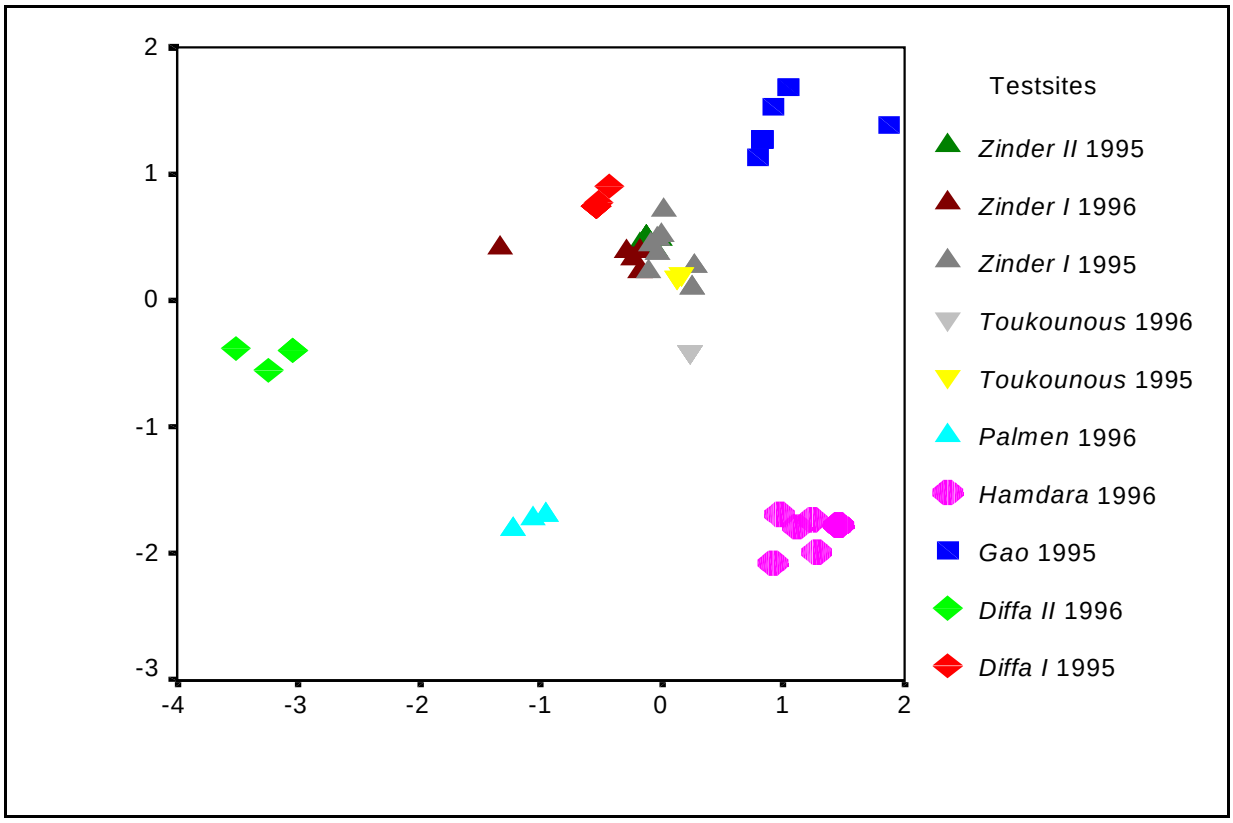

1 0.98 0.95 0.92 0.89 0.86
Zinder I 1995 B79
Zinder I 1995 B80
Zinder II 1995 B175
Zinder II 1995 B180
Zinder II 1995 B177
Zinder II 1995 B179
Zinder II 1995 B172
Zinder II 1995 B174
Zinder II 1995 B176
Zinder II 1995 B173
Zinder II 1995 B178
Zinder II 1995 B171
Zinder I 1995 B72
Zinder I 1996 B395
Zinder I 1996 B396
Zinder I 1996 B389
Zinder I 1996 B390
Zinder I 1996 B391
Zinder I 1996 B394
Zinder I 1996 B397
Zinder I 1996 B392
Zinder I 1996 B388
Diffa I 1995 B155
Diffa I 1995 B156
Diffa I 1995 B151
Diffa I 1995 B153
Diffa I 1995 B154
Diffa I 1995 B152
Diffa I 1995 B158
Diffa I 1995 B157
Zinder I 1995 B77
Zinder I 1995 B78
Zinder I 1995 B71
Zinder I 1995 B73
Zinder I 1995 B74
Zinder I 1995 B75
Zinder I 1995 B76
Toukounous 1996 B498
Toukounous 1996 B499
Toukounous 1996 B490
Toukounous 1996 B496
Toukounous 1996 B497
Toukounous 1996 B494
Toukounous 1996 B495
Toukounous 1996 B492
Toukounous 1996 B493
Toukounous 1996 B491
Toukounous 1995 B244
Toukounous 1995 B247
Toukounous 1995 B243
Toukounous 1995 B251
Toukounous 1995 B246
Gao 1995 B112
Gao 1995 B113
Gao 1995 B111
Gao 1995 B119
Gao 1995 B120
Gao 1995 B114
Gao 1995 B115
Gao 1995 B116
Gao 1995 B118
Gao 1995 B117
Diffa II 1996 B412
Diffa II 1996 B413
Diffa II 1996 B411
Diffa II 1996 B408
Palmen 1996 B437
Palmen 1996 B438
Palmen 1996 B434
Palmen 1996 B435
Palmen 1996 B436
Hamdara 1996 B382
Hamdara 1996 B385
Hamdara 1996 B378
Hamdara 1996 B379
Hamdara 1996 B381
Hamdara 1996 B386
Hamdara 1996 B380
Hamdara 1996 B383
Hamdara 1996 B387
Hamdara 1996 B384

Figure 4. Principal coordinate analysis of 81 individuals of *U. nidulans*




## Discussion

There are clear indicators for different genetic pattern according to habitats for the *Urochloa* species tested. For the widespread *U. xantholeuca*, (also found in more humid regions like Togo etc.) ecotypes like Sevaré, Ouahigouya etc. can be clearly separated. It seems that if the distance between two sites is less than 50 km the collected individuals show no different genetic pattern. For the more drought resistant *U. nidulans* the occurrence of ecotypes seems to be typical, indicating that the establishment of the plants in a more arid environment leads to a clearly different genetic pattern.

There are also indicators for a different pattern according to different collecting dates. We call this phenomenon "temporal genotypes". We can only suggest a reason for these results. There might be influences by precipitation rates, and the dormancy of the seeds as another important factor; furthermore, different parts of the seed bank in the soil may germinate in relation to different rainfalls. The more drought resistant *U. nidulans* also shows in temporal studies a very clear separation between sampling years, and even between different collecting dates within one year.

How do these results fit into an *in situ* conservation strategy ?
The most important point is the evidence that genetic diversity for the species tested depends on a variety of habitats, so that a strategy of only protected areas can not meet the requirements of an *in situ* conservation strategy. Therefore there is no alternative to transnational resource management strategies in order to maintain genetic diversity and ensure survival of the people in the area.

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