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Genetic variability of the Coconut Lethal Decline phytoplasma in Tanzania

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In Tanzania, the Lethal Decline (LDT), lethal yellowing-type disease, is the most destructive disease of the coconut palm. It is due to one phytoplasma (Mpunani *et al.*, Plant Pathol., 48, 109-114. 1999) belonging to the 16S-IV group. Although the disease spreads the full coastal belt of Tanzania, its incidence varies between the north where it is low and the south of the country where the incidence is very high.

To evaluate the LDT phytoplasma diversity, the 16S rRNA gene and the 16S-23S rRNA spacer region have been amplified using the P1/P7 primer pair (Smart *et al.*, Appl. Environ. Microbiol., 62, 2988-2993. 1996), and the PCR product sequenced for 15 samples of diseased coconut palms collected in the different coastal region of Tanzania.

Comparison of the sequences revealed 5 different genotypes named TZ-I to TZ-V and distributed from the north up to the south of the country. The genotype TZ-I and TZ-II are observed in the north of Tanzania only, whereas the genotype TZ-III and TZ-IV are present in the central regions and the genotype TZ-V in the south exclusively.

The distribution of the different genotypes could explain the differences in the incidence of the disease, and could be associated with the history of the coconut introduction in Tanzania also.