Application of Fungal Communities Fingerprintings to Determine the Geographic Origin of Tropical Timbers

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Introduction

from forest to its postmarketing use, tropical timber is subjected to colonization by many fungi (endophytes, wood rotting fungi, ...). Traceability for timber production through the world is a key resource for buyers looking to secure timber of verifiable origin from certified suppliers. The objective is to use the fungal community fingerprints as microbiological marker to identify the geographical origin of wood imported from tropical countries. Many molecular tools have common approaches to understanding the genetic variation within microbial communities. Among these techniques, the CE-SSCP approach has been applied in order to profile fungal biodiversity colonizing tropical timber.

Material and methods

Table 1: Tropical species and origins of timber used in this study: Limba (*Terminalia superba*), Limbali (*Gilbertiodendron dewevrei*) and Teak (*Tectona grandis*), from six different countries.

Wood	*Geographical origin*	*Code*
Limba *Fraké*	Central African Republic	L RCA
	Benin	L Be
	Côte d'Ivoire	L Ci
	Congo	L Co
	Cameroon	L Ca
Limbali *Vaa*	Central African Republic	Li RCA (1 and 2)
	Côte d'Ivoire	Li Ci
	Cameroon	Li Ca
Teck	Polynesia	T Pol
	Côte d'Ivoire	T Ci

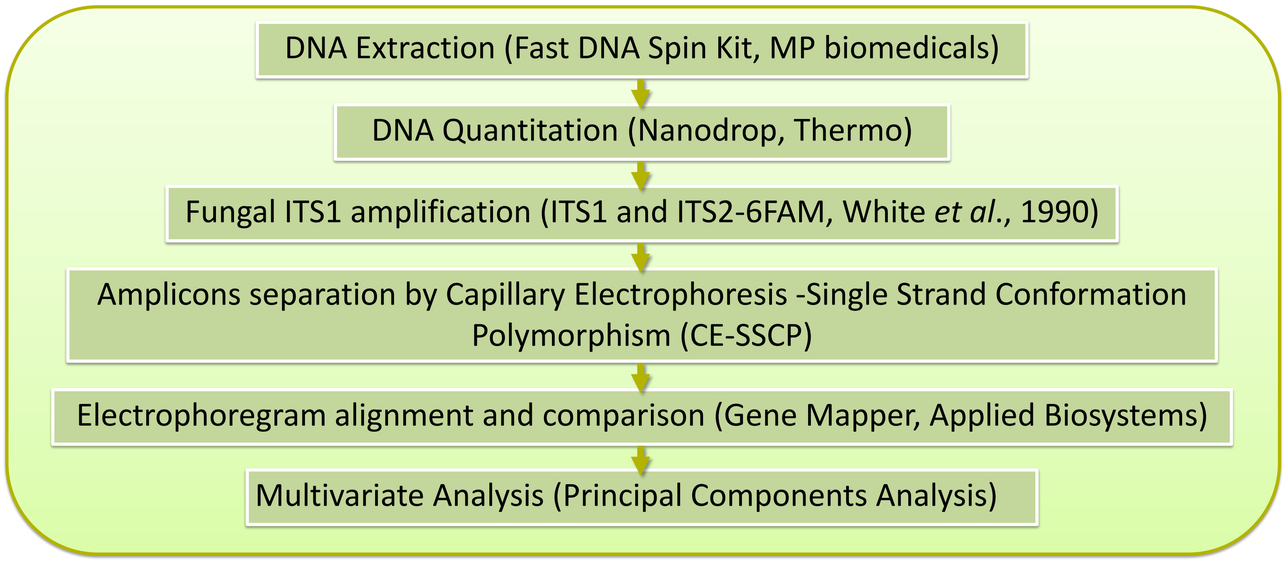

Figure 1: Technical procedure to profiling fungal biodiversity in tropical timber (adapted from Maurice *et al.*, 2010)

Results

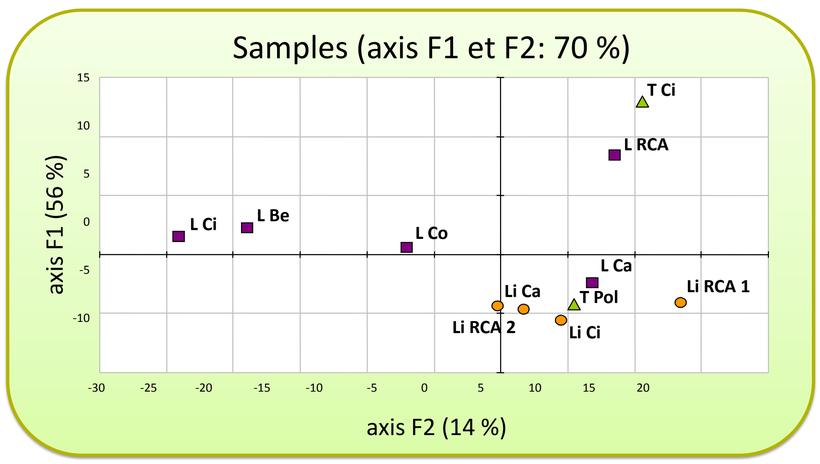

Figure 3: PCA results extracted from CE-SSCP profiles of fungal community from tropical timber. Only the first principal component was shown. The % variance explained by each component is given in parenthesis. Score plot showing the relations between samples. Communities seem to be structured according to the wood: Limba left of the F1 axis and Limbali to its right.

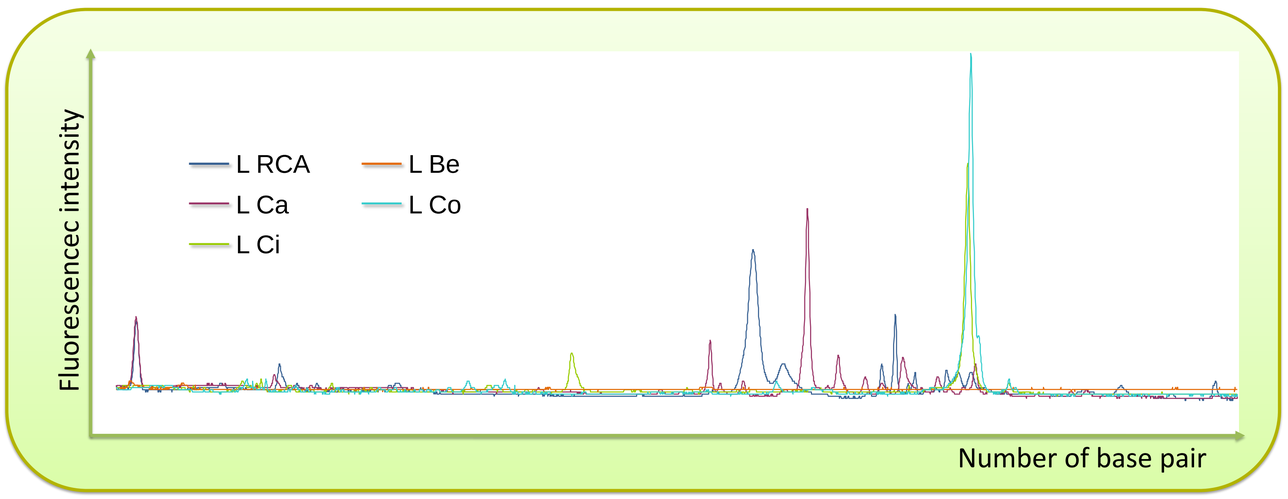

Figure 2: CE-SSCP analysis of PCR fungal amplicons (ITS1 rDNA) of Limba from distincts origins. A peak represents an Operational Taxonomic Unit (OTU). The y-axis value denotes the fluorescence intensity of each OTU which was used as quantitative data for the multivariate analysis (Principal Components Analysis).

Conclusions

Multivariate analysis seems to distinguish samples by wood type which are colonized by specific fungal communities. For origin determination using fungal communities, a focus on dominant taxa is needed. Further, it would be preferable to achieve cloning and sequencing of amplicons to determine the name of fungal taxa prior to use more accurate and informative fingerprint tool like D-HPLC (Maurice *et al.*, 2010).

References:

Maurice *et al.*, 2010 Profiling fungal community in wood decay ecosystem by Denaturing High-Performance Liquid Chromatography, 9–13 mai 2010, *41st International Research Group conference on Wood Protection*. Biarritz, France.

White *et al.*, 1990 Amplification and sequencing of fungal ribosomal RNA genes for phylogenetics. pp.315–322.: *PCR protocols: a guide to methods and applications*, Academic Press, Inc., New York, N.Y.

Conception et réalisation : Cirad, Martine Duportal, juillet 2010