Use of DNA-fingerprints for timber tracking

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1. Introduction

2. Projects and results

• Controlling the country of origin for mahogany (*Swietenia macrophylla*)

• DNA-Barcoding to distinguish tree species in the family meliaceae

• Timber tracking of Sapelli (*Entandrophragma cylindricum*) and Iroko (*Milicia excelsa*) on the level of a forest concession in Cameroon
1. Introduction - question

Need for control on different scales:

A) Logging of protected species (CITES) => control of species identity

B) Logging in countries with ban of exports or limitations in timber export volume => large scale control of geographic origin (countries)

C) Logging in protected areas or outside of certified forests => small scale control of geographic origin (landscape, forest concessions)
Requirements for control of timber origin:

Control of traits that cannot be manipulated

Method also applicable for processed timber

Spatial resolution of the control high enough

Rapid control

Low costs
1. Introduction - methods

Spatial pattern is the basis for any control!
1. Introduction - methods

Genetic fingerprinting

A microsatellite consists of a specific sequence of DNA bases or nucleotides which contains mono, di, tri, or tetra tandem repeats.
1. Introduction - methods

Causes for spatial genetic pattern of tree populations

Extinction and recolonisation
(glacial periods, natural desasters)

Spatial limited pollen and
seed dispersal

Genetic selection along gradients

Artificial regeneration from
different seed sources

The Amazon during the last glacial period
1. Introduction - methods

Spatial genetic pattern at chloroplast gene marker of the tropical tree species *Vouacapoua america* in French Guiana

1. Introduction - methods

General approach

1. Sampling of individuals in the declared location of origin and in other alternative places => good sampling design

2. Sampling of the traded wood => good sampling design

3. Genotyping (nSSRs, SNPs, Sequence Variation) => best gene markers

4. Statistical analysis => most reliable method
1. Introduction - methods

Population 1
- Allel 1: 70%
- Allel 2: 20%
- Allel 3: 10%

Population 2
- Allel 1: 70%
- Allel 2: 20%
- Allel 3: 10%

Prob = 0.04

Genotype of a wood sample

Prob = 0.28
2. Projects and results - Mahogany

Partners
Bernd Degen, vTI, Germany (co-ordination)
Stephen Cavers, CEH, UK
Carlos Navarro, CATIE, Costa Rica
Sheila Ward, University Puerto Rico, USA
Alexandre Sebbenn, Sao Paulo Forest Institute, Brazil
Maristerra Lemmes, Inpa Manaus, Brazil
Rogerio Gribel, Botanical Garden Rio de Janeiro, Brazil

Budget
vTI
EU-INCO
CNPq (Brazil)
2. Projects and results - Mahogany

**Sampling**

33 populations with 24-400 individuals
2038 trees sampled

**Genetic variation**

7 nuclear microsatellites
More than 200 alleles identified
In each population between 44 – 106 alleles
2. Projects and results - Mahogany

Genetic differentiation

Correlation between spatial and genetic distances

Strong genetic differences among populations \( (\text{delta} = 0.53; \, F_{ST} = 0.20; \, F_{ST, \text{Hedrick}} = 0.66) \)
2. Projects and results - Mahogany

Practical test with 20 mahogany wood samples of the timber trader Nagel + 11 wood samples sent by Alexandre Sebbenn

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Genotypes of the 20 wood samples from the company Theodor Nagel
# 2. Projects and results - Mahogany

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<th>Name</th>
<th>Group</th>
<th>Assigned to Pop</th>
<th>Score</th>
<th>Probability of exclusion</th>
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### List of Reference Populations ###

1. BO_m_Bolpebra / N = 92
2. BO_m_Jorge_Cruz / N = 103
3. BO_m_La_Conta / N = 59
4. BO_m_San_Borja / N = 65
5. BO_m_Sapecho / N = 52
6. BO_m_Yotau / N = 51
7. CR_N_La_Cruz / N = 50
8. CO_m_Los_Chiles / N = 51
9. CR_N_Focusol / N = 49
10. CO_H_Sardalino / N = 52
11. BO_m_La_Conta_1 / N = 80
12. BO_m_La_Conta_2 / N = 66
13. CR_h_Guanacaste / N = 34
14. GU_h_Esquitia / N = 45
15. GU_m_Peten / N = 56
16. HO_m_Colon / N = 57
17. ME_m_Veracruz / N = 98
18. ME_m_Chipas / N = 52
19. ME_m_Chamece / N = 59
20. ME_m_Quintana_Roo / N = 50
21. NI_m_Central / N = 53
22. NI_m_X / N = 53
23. PA_m_Herrera / N = 26
24. PA_m_Darien / N = 37
25. BE_m_Bast_Botes / N = 42
26. BE_m_Punta_Gorda / N = 49
27. BR_m_Agua_Azul / N = 31
28. BR_m_Cach_A / N = 32
29. BR_m_Pontes_LaCerda / N = 24
30. BR_m_Chico_Hendes / N = 34
31. BR_m_Cach_E / N = 24
32. BR_m_Fimenta_Bueno / N = 24
33. BR_m_Haraioara / N = 400
2. Projects and results - Mahogany
3. Outlook

- Create a network of involved institutions, ongoing projects => go for large international projects (ITTO)
- Further development and standardisation of methods (sample strategies, DNA-extraction from wood, gene markers (SNPs), additional isotopes)
- Merging efforts for systematic sampling and inventories with genetic and isotopic fingerprints => creation of reference data
- Setup and maintenance of free accessible data banks with reference data
- Technology transfer to private sector
- Setup of co-ordination office at Bioversity International