

DNA- Based Authentication of Alternative Plant Fibres in Textiles

Sofia Pereira de Sousa ^a, Marta W. Vasconcelos ^a, Marta Nunes da Silva ^a

mansilva@ucp.pt; s-spsousa@ucp.pt

^a Universidade Católica Portuguesa, CBQF – Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Rua Diogo Botelho 1327, 4169-005 Porto, Portugal



Introduction

Alternative plant fibres such as *Cannabis sativa* L. (**hemp**), *Ananas comosus* (**PALF**), and *Musa textilis* (**abaca**) are being increasingly recognised for their lower environmental impact compared to traditional fibres like *Gossypium hirsutum* (**cotton**) and *Linum usitatissimum* (**flax**). These fibres are **renewable**, **biodegradable**, and require **fewer resources**, making them promising solutions for **eco-friendly textiles**. However, ensuring accurate labelling and traceability remains a challenge. This study explores a **DNA-based approach** for identifying and distinguishing these fibres, supporting transparency, consumer trust, and sustainable practices across the textile value chain.



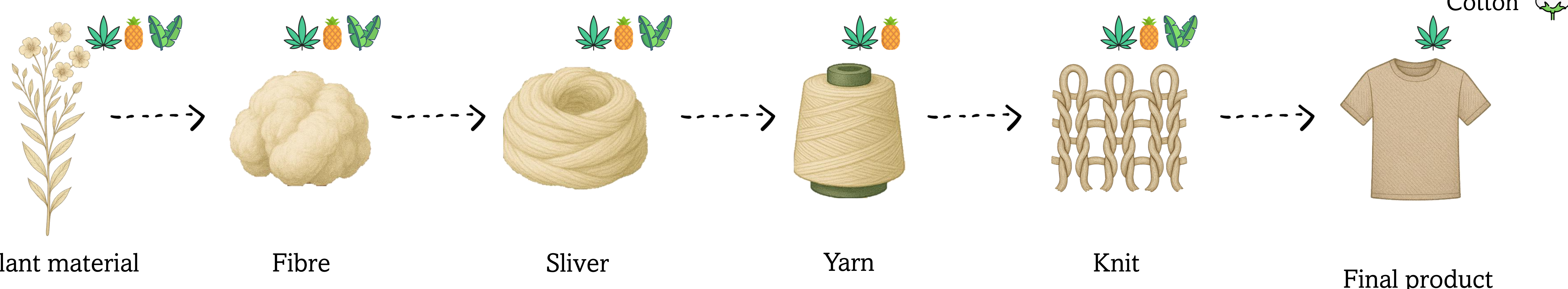
Objectives

Develop a **DNA-based tool** capable of identifying and differentiating **emerging fibres** - hemp, banana, and pineapple - in the textile industry.
To test the method's applicability in **processed** and **chemically treated textiles**.



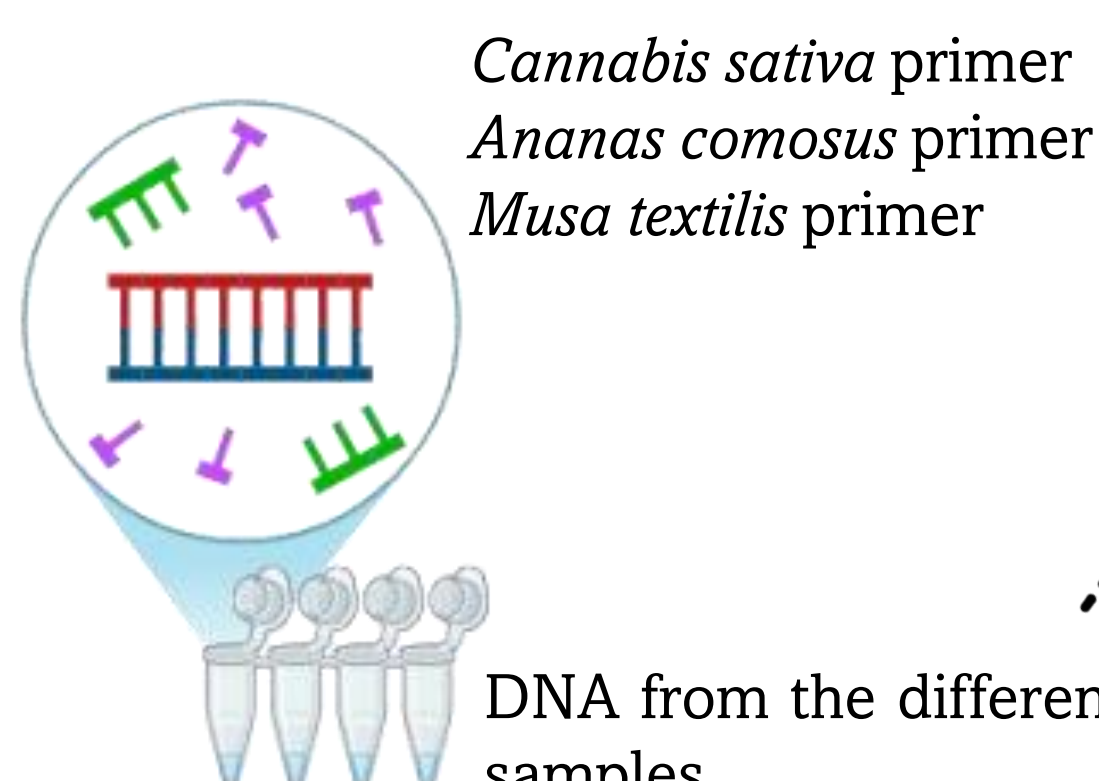
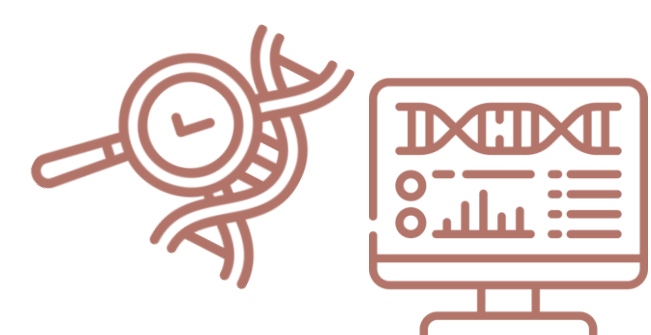
Methods

1. DNA Extraction of different samples



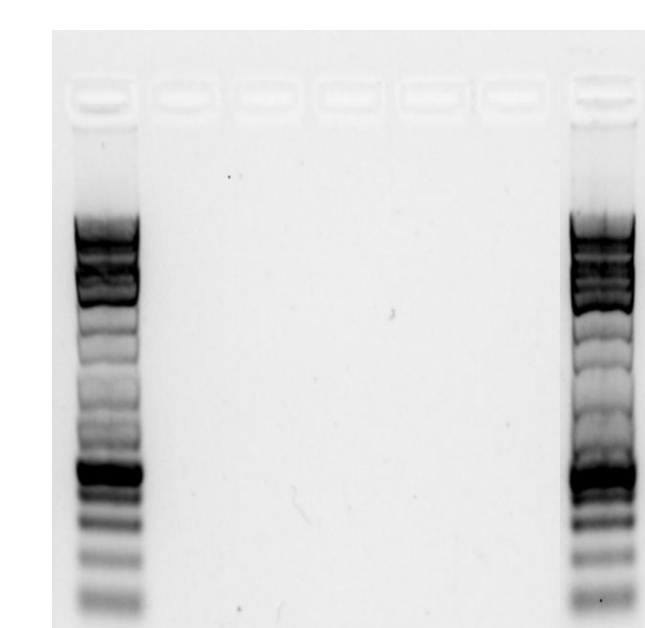
2. Design of Specific Primers for *Cannabis sativa* L., *Ananas comosus* L., *Musa textilis*

Genes of interesting: *matK* and *rbcL*

























3. PCR Amplification

Electrophoresis



Results and Discussion

Table 1. Summary of PCR amplification results using species-specific primers for hemp () PALF () abaca () cotton () and flax () across different textile processing stages. Samples include fibres, slivers, yarns (cotton blends), knitted fabrics (dyed cotton blends), and a final product (hemp-cotton blend T-shirt). Amplification outcomes indicate primer specificity and DNA detectability throughout the textile production chain. A check mark (✓) indicates successful amplification, while a cross (✗) represents no amplification.

Type of sample	Species	Treatment	Cotton mix	<i>Cannabis sativa</i> primer	<i>Ananas comosus</i> primer	<i>Musa textilis</i> primer
Plant		-	-	✓	✗	✗
		-	-	✗	✓	✗
		-	-	✗	✗	✓
		-	-	✗	✗	✗
Fibre		-	-	✓	✗	✗
		-	-	✗	✓	✗
		-	-	✗	✗	✓
Sliver		-	-	✓	✗	✗
		-	-	✗	✓	✗
		-	-	✗	✗	✓
Yarn		-	Yes	✓	✗	✗
		-	Yes	✗	✓	✗
		-	-	✗	✗	✓
Knit		Dyed	Yes	✓	✗	✗
		Dyed	Yes	✗	✗	✗
		Dyed	Yes	✗	✗	✗
Final Product		-	Yes	✗	✗	✗

Primer Performance

- Species-specific amplification achieved in plant-derived DNA;
- Flax and cotton controls showed no amplification, demonstrating high primer specificity.

Fibre and Intermediate Products

- Amplification successful in fibres;
- Sliver samples showed consistent, species-specific results;
- Yarn blends with cotton still allowed detection of target DNA.

Processing Effects

- In dyed knit samples, amplification occurred only in the hemp-cotton blend, suggesting partial DNA preservation post-treatment;
- No amplification in final product, likely due to DNA degradation caused by industrial treatments (e.g. dyeing, finishing).



Conclusion and Future Work

- The **developed primers** demonstrated **high species specificity** with no cross-reactivity;
- DNA-based** identification was **successful in early and intermediate textile stages**, even in cotton blends;
- Detection failed** in the **final product**, likely due to DNA degradation from industrial processing;
- Future work** will focus on applying **more sensitive techniques** to enable traceability in finished.

Acknowledgements

The authors acknowledge the project be@t – Textile Bioeconomy (TC-C12-i01, Sustainable Bioeconomy No. 02/C12-i01.01/2022), Next Generation EU (2021 – 2026), and by the FCT (Portugal) through PhD scholarship 2023.05224.BDANA, through 2023.06124.CEECIND, and the project UIDB/50016/2.