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Research Information Resources Unit
24 February 2022

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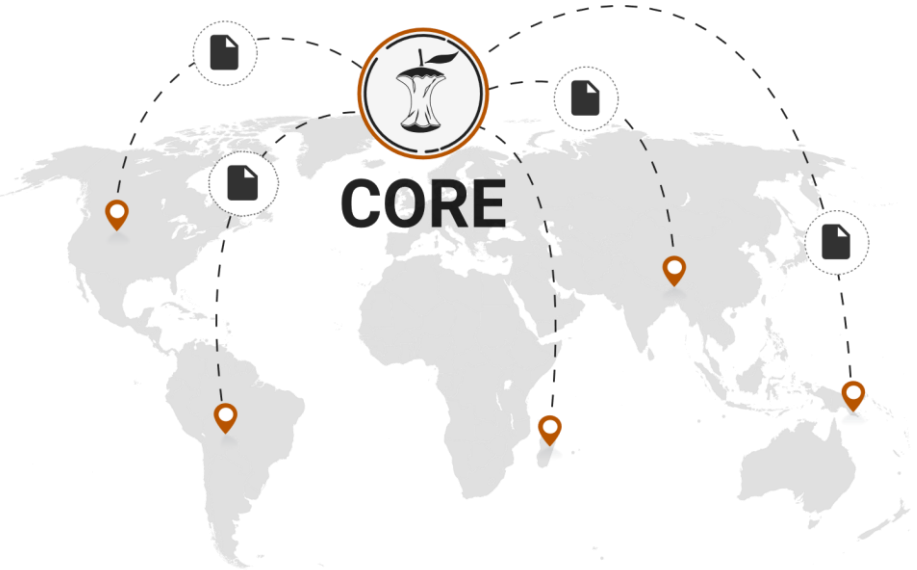

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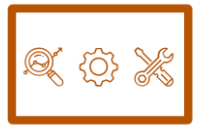

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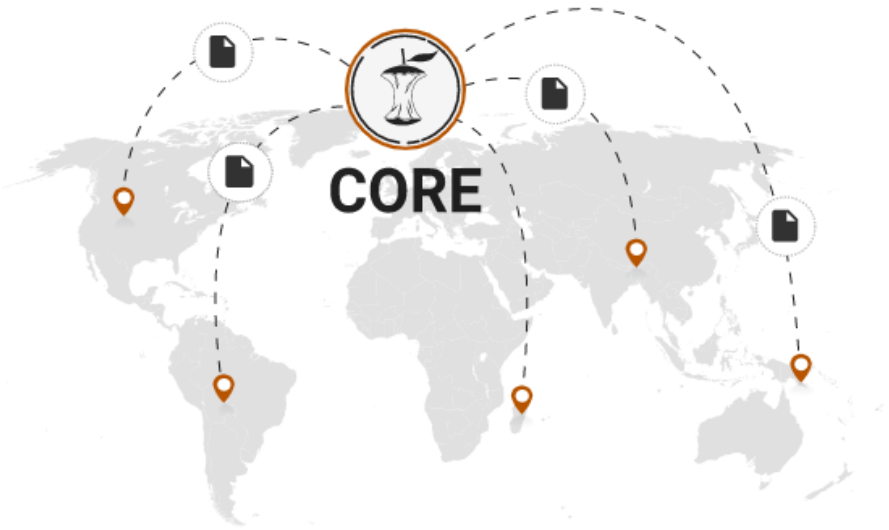

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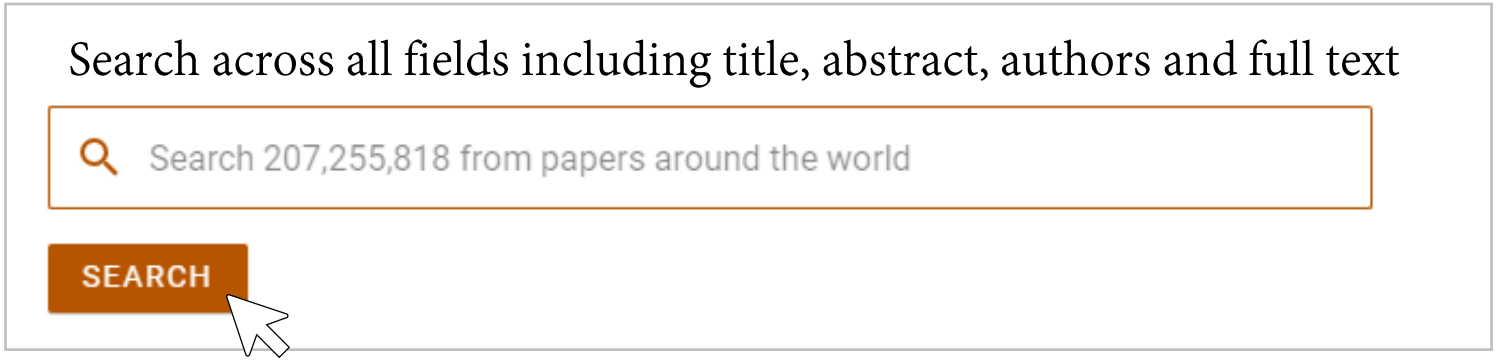

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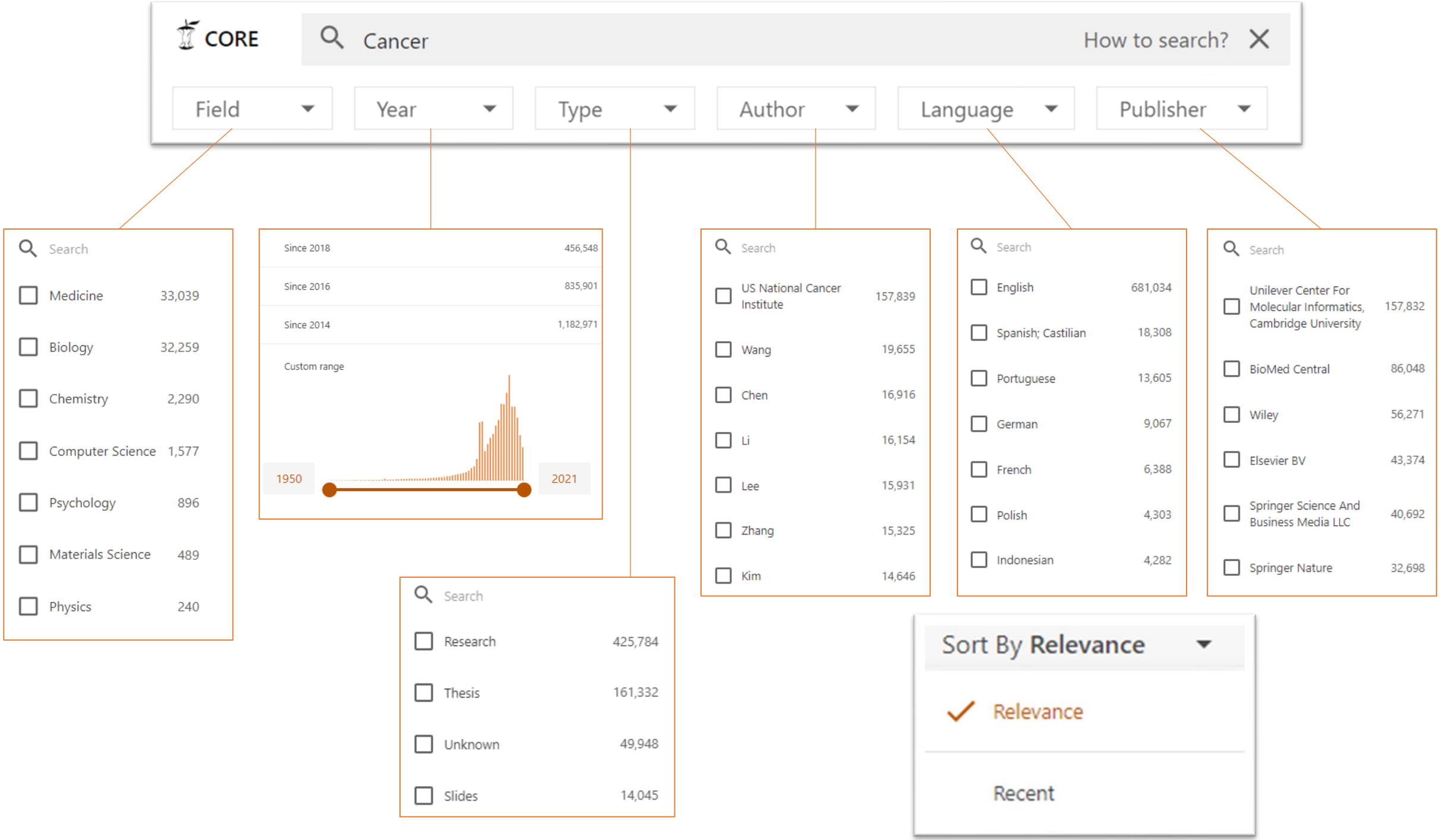
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Genetic structure in populations of Euterpe precatoria Mart. in the Brazilian Amazon.

S. L. F. RAMOS, G. DEQUIGIOVANNI, +9 MORE , • 1 January 2021 • 'Frontiers Media SA'

Abstract

Euterpe precatoria is a palm tree belonging to the Arecaceae family, occurring inWestern and Central Brazilian Amazonia. Its fruit, which is very appreciated in the Amazon region, produces pulp that is consumed in fresh form. Its production is carried out almost exclusively by extractive farmers. In order to establish adequate strategies to sustain this genetic resource, we need knowledge about the diversity and genetic structure in natural populations. This study aimed to evaluate the influence of geographic distance on genetic structure in the main extractive populations of E. precatoria in the Brazilian Amazon. Leaves from 377 plants were collected in 19 populations located in 16 municipalities in the State of Amazonas and three in the State of Rondônia. Twelve microsatellite loci were used to genotype the plants. The diversity and genetic structure among populations were estimated. The average number of alleles per locus was 5.97. The observed heterozygosity means (HO) were higher than expected (HE) at the population level (HO = 0.72, HE = 0.66) and fixation index (f = -0.100) was negative. The FST value (0.1820) and the AMOVA results (8 = 0.1796) showed population structure. The populations were clustered into three groups (K = 3) in the Bayesian analysis. The Discriminant Analysis of Principal Components (DAPC) confirmed eight clusters, with the populations close to those identified by the Bayesian analysis. The geographic differentiation was confirmed by the groupings obtained in the Structure analysis and the DACP function. Information related to phenotypic, genetic and environmental characterization of populations is important to guide conservation and management strategies and the formulation of public species management policies in Amazonia.bitstream/item/220109/1/Ananda-fevo-08-603448.pd

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Genetic Structure in Populations of *Euterpe precatoria* Mart. in the Brazilian Amazon

Santiago Linorio Ferreyra Ramos[1], Gabriel Dequigiovanni[2], Maria Teresa Gomes Lopes[3], Ananda Virginia de Aguiar[4], Ricardo Lopes[5], Elizabeth Ann Veasey[6], Jeferson Luis Vasconcelos de Macêdo[5], Alessandro Alves-Pereira[7], Therezinha de Jesus Pinto Fraxe[1], Marcos Silveira Wrege[4] and José Nivaldo Garcia[8]*

[1] Universidade Federal do Amazonas, Manaus, Brazil, [2] Centro Universitário UNIVEL, Avenida Tito Muffato, Cascavel, Brazil, [3] Faculdade de Ciências Agrícolas, Universidade Federal do Amazonas, Manaus, Brazil, [4] Embrapa Florestas, Colombo, Brazil, [5] Embrapa Amazônia Ocidental, Manaus, Brazil, [6] Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, Brazil, [7] Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas (UNICAMP), Campinas, Brazil, [8] Escola Superior de Agricultura Luiz de Queiroz/Universidade de São Paulo (ESALQ/USP), Departamento de Ciências Florestais, Piracicaba, Brazil

Euterpe precatoria is a palm tree belonging to the Arecaceae family, occurring in Western and Central Brazilian Amazonia. Its fruit, which is very appreciated in the Amazon region, produces pulp that is consumed in fresh form. Its production is carried out almost exclusively by extractive farmers. In order to establish adequate strategies to sustain this genetic resource, we need knowledge about the diversity and genetic structure in natural populations. This study aimed to evaluate the influence of geographic distance on genetic structure in the main extractive populations of *E. precatoria* in the Brazilian Amazon. Leaves from 377 plants were collected in 19 populations located in 16 municipalities in the State of Amazonas and three in the State of Rondônia. Twelve microsatellite loci were used to genotype the plants. The diversity and genetic structure among populations were estimated. The average number of alleles per locus was 5.97. The observed heterozygosity means (H_O) were higher than expected (H_E) at the population level (H_O = 0.72, H_E = 0.66) and fixation index (f = -0.100) was negative. The F_{ST} value (0.1820) and the AMOVA results (Φ = 0.1796) showed population structure.

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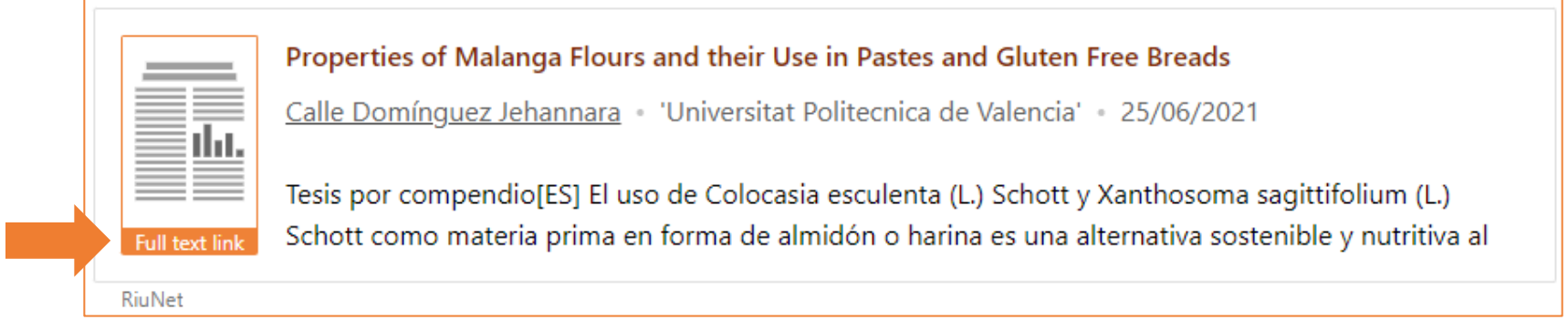

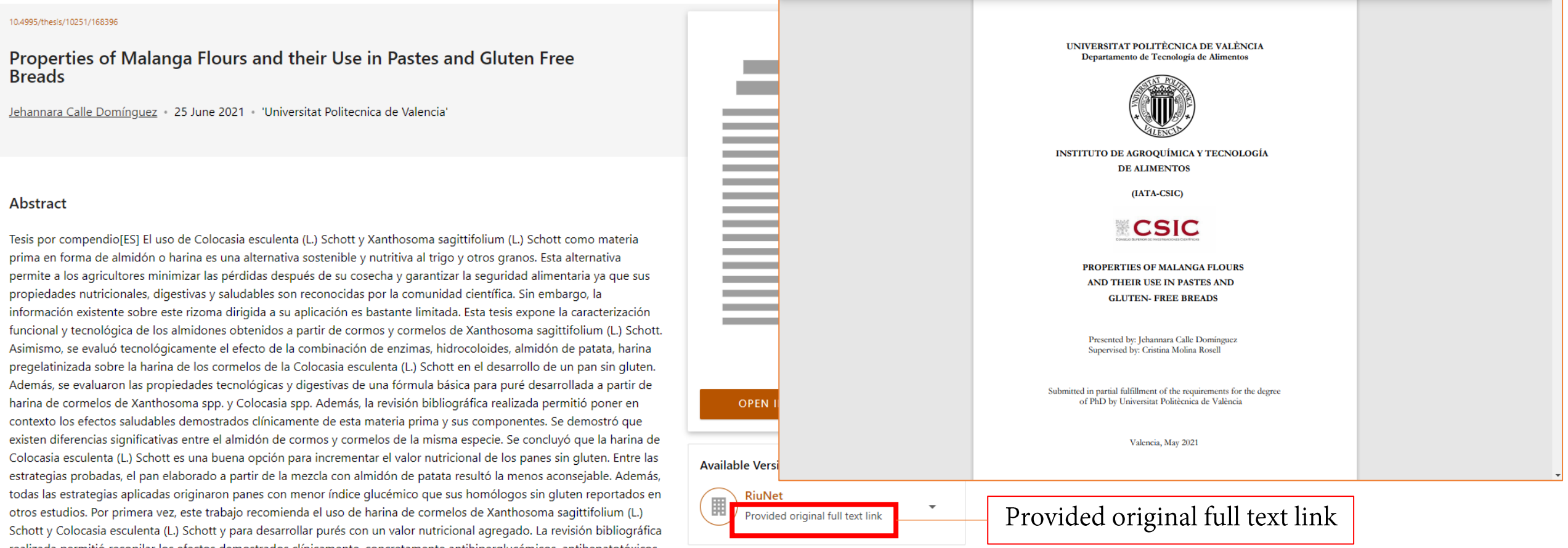

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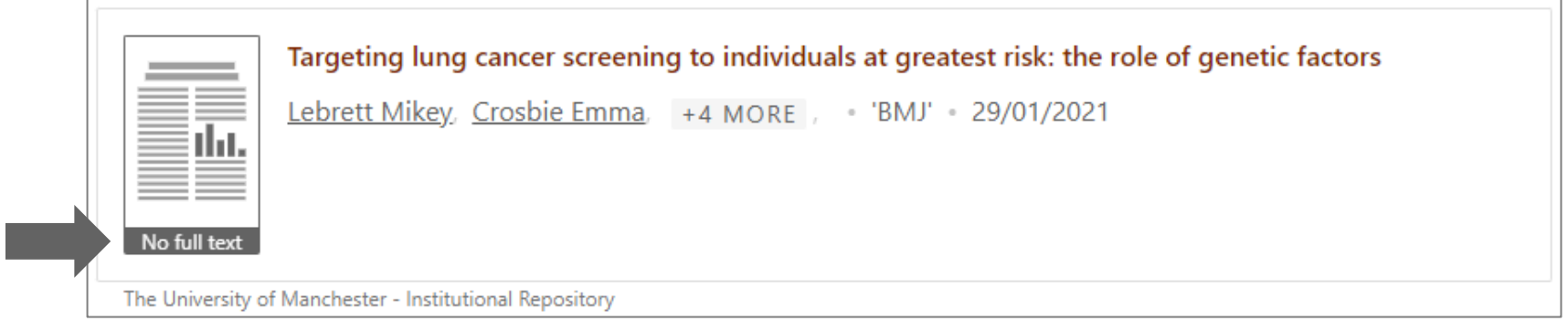

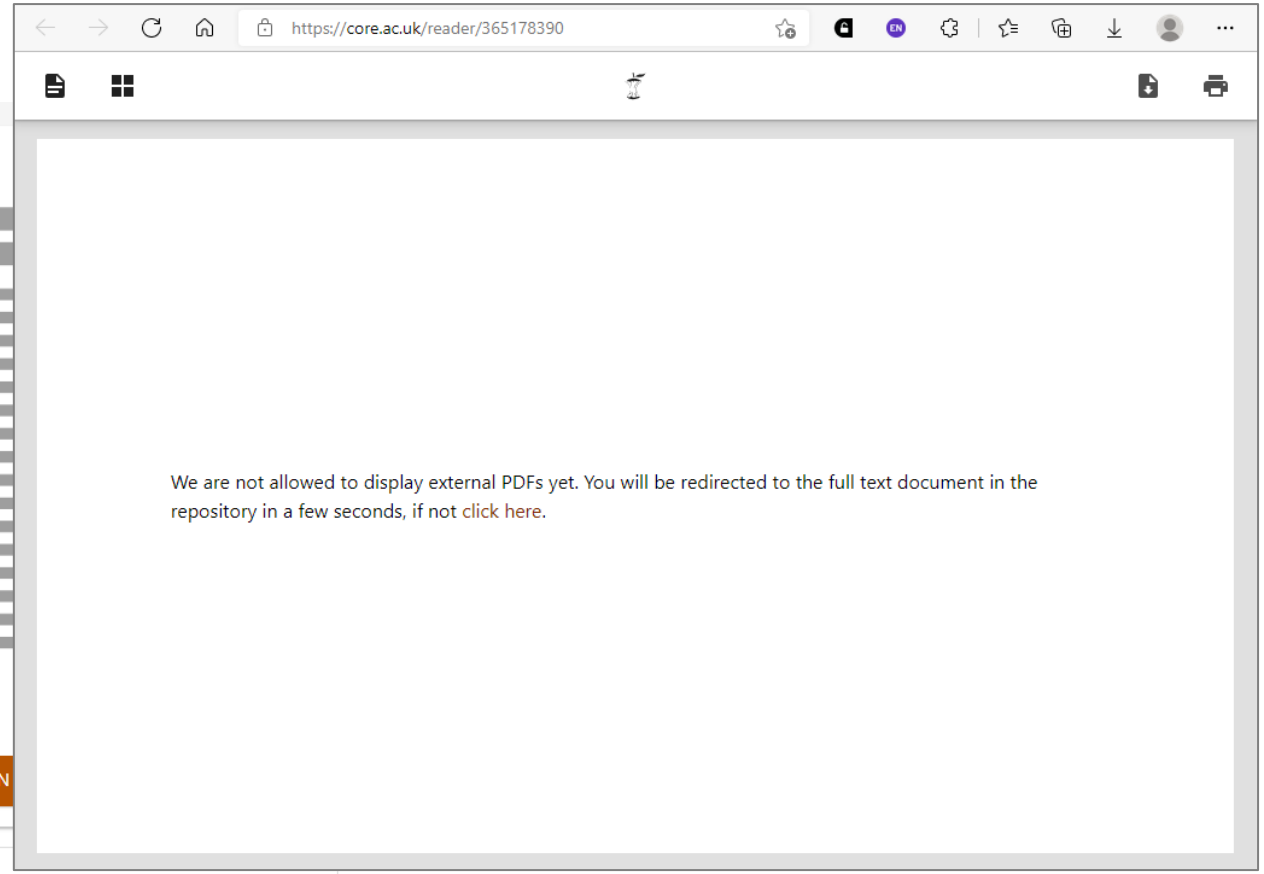

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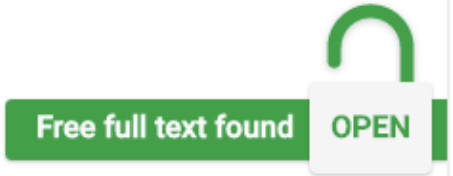

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Arie Altman

In Vitro Cellular & Developmental Biology - Plant **55**, 590–594 (2019) | Cite this article

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Abstract

The evolutionary route from plant tissue culture (IAPTC) to plant biotechnology (IAPB). Plant biotechnology is an evolutionary scientific process, formulated and maintained by our accumulated cultural-societal knowledge and the invention of new technologies (Altman and Mesoudi submitted). It emerged thousands of years ago when wheat, rice, chickpeas, potatoes, and coffee (and other plants) were first domesticated; when grains were fermented by yeasts to produce bread; and when grape juice, barley, and tubers fermentation resulted in wine, alcohol, and beer. The modern era of plant biotechnology started in the beginning of the twentieth century and is associated with the ability to grow plant cells and tissues *in vitro*, to regenerate and clone new plants and, later, to modify their genetic characteristics by molecular breeding, including molecular marker-assisted selection (MAS), genetic

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Nuclear spin-wave quantum register for a solid-state qubit

Andrei Ruskuc, Chun-Ju Wu, Jake Rochman, Joonhee Choi ✉ & Andrei Faraon ✉

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Abstract

Solid-state nuclear spins surrounding individual, optically addressable qubits[1,2] are a crucial resource for quantum networks[3,4,5,6], computation[7,8,9,10,11] and simulation[12]. Although hosts with sparse nuclear spin baths are typically chosen to mitigate qubit decoherence[13], developing coherent quantum systems in nuclear-spin-rich hosts enables exploration of a much broader range of materials for quantum information applications. The collective modes of these dense nuclear spin ensembles provide a natural basis for quantum storage[14]; however, using them as a resource for single-spin qubits has thus far remained elusive. Here,

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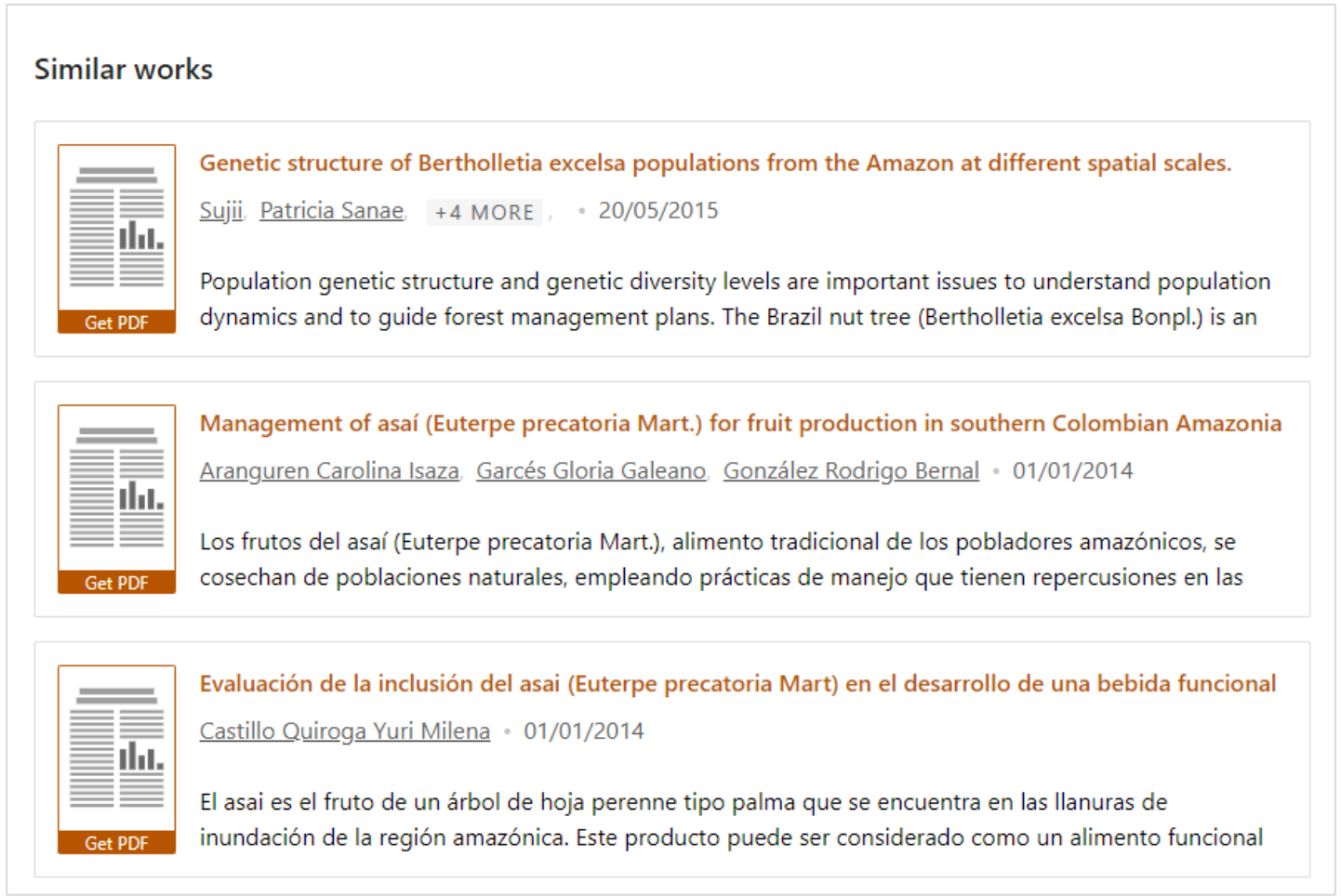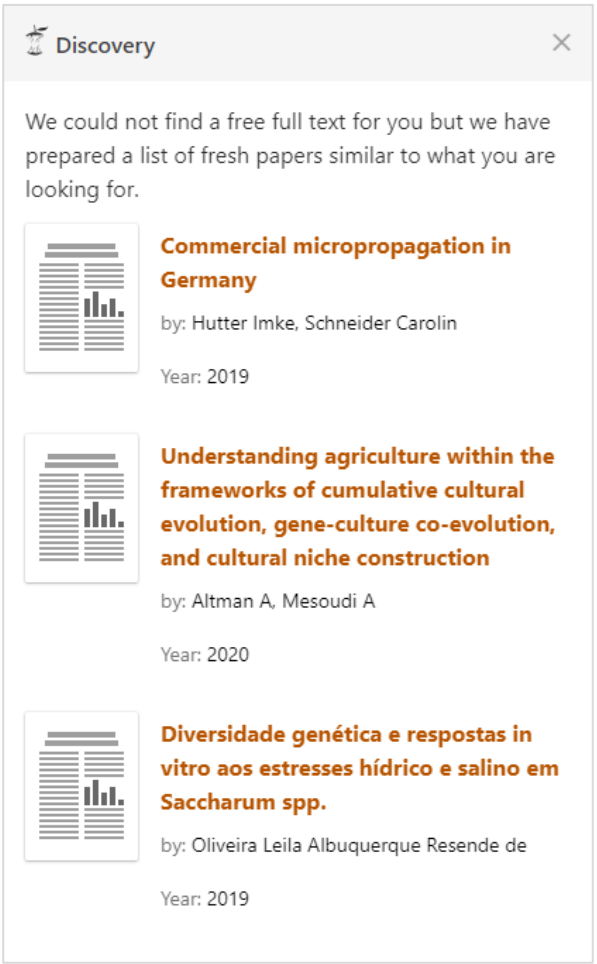
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