

RESEARCH ARTICLE

Insights into *Penicillium roqueforti* Morphological and Genetic Diversity

Guillaume Gillot¹, Jean-Luc Jany¹, Monika Coton¹, Gaétan Le Floch¹, Stella Debaets¹, Jeanne Ropars^{2,3,4}, Manuela López-Villavicencio², Joëlle Dupont², Antoine Branca^{3,4}, Tatiana Giraud^{3,4}, Emmanuel Coton^{1*}

1 Université de Brest, EA 3882 Laboratoire Universitaire de Biodiversité et d'Ecologie Microbienne, ESIAB, Technopôle Brest-Iroise, Plouzané, France, **2** Origine, Structure, Evolution de la Biodiversité, UMR 7205 CNRS-MNH, Muséum National d'Histoire Naturelle, CP39, Paris Cedex 05, France, **3** Ecologie, Systématique et Evolution, Université Paris-Sud, Orsay cedex, France, **4** CNRS, Orsay cedex, France

* Current address: Canadian Institute for Advanced Research, Department of Biology, University of Ottawa, Ottawa, Ontario, Canada

* emmanuel.coton@univ-brest.fr



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Abstract

Fungi exhibit substantial morphological and genetic diversity, often associated with cryptic species differing in ecological niches. *Penicillium roqueforti* is used as a starter culture for blue-veined cheeses, being responsible for their flavor and color, but is also a common spoilage organism in various foods. Different types of blue-veined cheeses are manufactured and consumed worldwide, displaying specific organoleptic properties. These features may be due to the different manufacturing methods and/or to the specific *P. roqueforti* strains used. Substantial morphological diversity exists within *P. roqueforti* and, although not taxonomically valid, several technological names have been used for strains on different cheeses (e.g., *P. gorgonzolae*, *P. stilton*). A worldwide *P. roqueforti* collection from 120 individual blue-veined cheeses and 21 other substrates was analyzed here to determine (i) whether *P. roqueforti* is a complex of cryptic species, by applying the Genealogical Concordance Phylogenetic Species Recognition criterion (GC-PSR), (ii) whether the population structure assessed using microsatellite markers correspond to blue cheese types, and (iii) whether the genetic clusters display different morphologies. GC-PSR multi-locus sequence analyses showed no evidence of cryptic species. The population structure analysis using microsatellites revealed the existence of highly differentiated populations, corresponding to blue cheese types and with contrasted morphologies. This suggests that the population structure has been shaped by different cheese-making processes or that different populations were recruited for different cheese types. Cheese-making fungi thus constitute good models for studying fungal diversification under recent selection.

Introduction

Fungi display huge diversity with a widely accepted estimation of 1.62 M species [1]. However, as recognized by Hawksworth himself, this number is underestimated [2], mainly due to the