



CICLO

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GENOMIC FOOTPRINTS OF A BIOLOGICAL INVASION: INTRODUCTION AND DISPERSAL OF THE TOPMOUTH GUDGEON IN EUROPE



MIGUEL BALTAZAR-SOARES

CONSERVATION ECOLOGY
AND ENVIRONMENTAL SCIENCES GROUP;
BOURNEMOUTH UNIVERSITY, UK

Facilitated by the intensification of global trading, the introduction and dispersal of species to areas in which they are historically non-native is nowadays common. From an evolutionary standpoint, invasions are paradoxical: not only non-native environments are likely different from those introduced individuals are adapted to, but also small founding population size should be associated with reduced adaptive potential. As these odds are overcome, successful biological invasions are considered valuable real-time evolutionary experiments. Here, we investigated the population structure and adaptive potential of the notorious top mouth gudgeon (*Pseudorasbora parva*) across Europe and Asia Minor. We RAD-sequenced 302 specimens from 16 populations and 3 distinct invasion fronts as well as 2 locations in the native range. With 13 785 single nucleotide polymorphisms, we provide conclusive evidence for a genome-wide signature of two distinct invasion fronts, via Slovakia and Turkey, each originating from a specific area in the native range. A third invasion front found in France appears to be the product of dispersal within the invasive range. Few loci showed signs of selection, the vast majority being identified in the Slovakian region. Functions linked to those loci suggested that faster early stage development, resistance to pollution and immunocompetence might have played a role in the invasion success. Overall and by showing that invasive fronts have different evolutionary histories, our study reinforces the idea that populations, instead of species, are the units to consider in invasion biology.

13 MAIO 2019
12H30 | SALA DE ATOS

HOST
**SARA
FRANCISCO**

ENTRADA LIVRE



ISPA
INSTITUTO UNIVERSITÁRIO

RUA JARDIM DO TABACO, 34
1149 - 041 LISBOA
T. 218 811 700 | F. 218 860 954
CII@ISPA.PT | WWW.ISPA.PT
f FACEBOOK/ISPA.IU