



## Inter-basin dispersal through irrigation canals explains low genetic structure in *Diplomystes* cf. *chilensis*, an endangered freshwater catfish from Central Chile



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### ABSTRACT

Biotic homogenization in freshwater ecosystems is a growing concern among conservation biologists. Recent phylogeographic data has shown low genetic structure between some basins from Central Chile, suggesting that either current dispersal through irrigation canals or incomplete lineage sorting due to recent divergence might explain the observed patterns. However, these hypotheses remain untested despite their potential implications for freshwater biodiversity and conservation. We used a statistical, model-based framework (approximate Bayesian computation) to investigate the relative support for each of these hypotheses in the freshwater catfish *Diplomystes* cf. *camposensis*, an endangered species from Central Chile. Our results show strong support for the model involving current migration between basins, and rejected the model of recent divergence without migration. These results strongly suggest that irrigation canals are facilitating the dispersal between basins, posing a serious threat to biodiversity in Central Chile, an area considered a biodiversity hotspot. Finally, these results highlight the utility of model-based approaches for determining demographic processes with potential conservation implications, even with the lack of extensive molecular data.

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### Introduction

Biotic homogenization is a serious threat to the integrity of endemic species and genetic pools that can result in the loss of continental, regional, and local biodiversity (Olden et al., 2004). Human constructions such as the Suez Canal and the opening of the St. Lawrence Seaway are striking examples of human activities that have facilitated the movement of hundreds of estuarine and freshwater species (Galil, 2000; Ricciardi and MacIsaac, 2000), although better known examples are provided by the introduction of invasive species at a continental or worldwide scale (Olden, 2006). These events have shown varied negative effects on the diversity of the regions impacted, including reduction of  $\beta$ -diversity, species extinctions, and genetic homogenization (Olden et al., 2004).

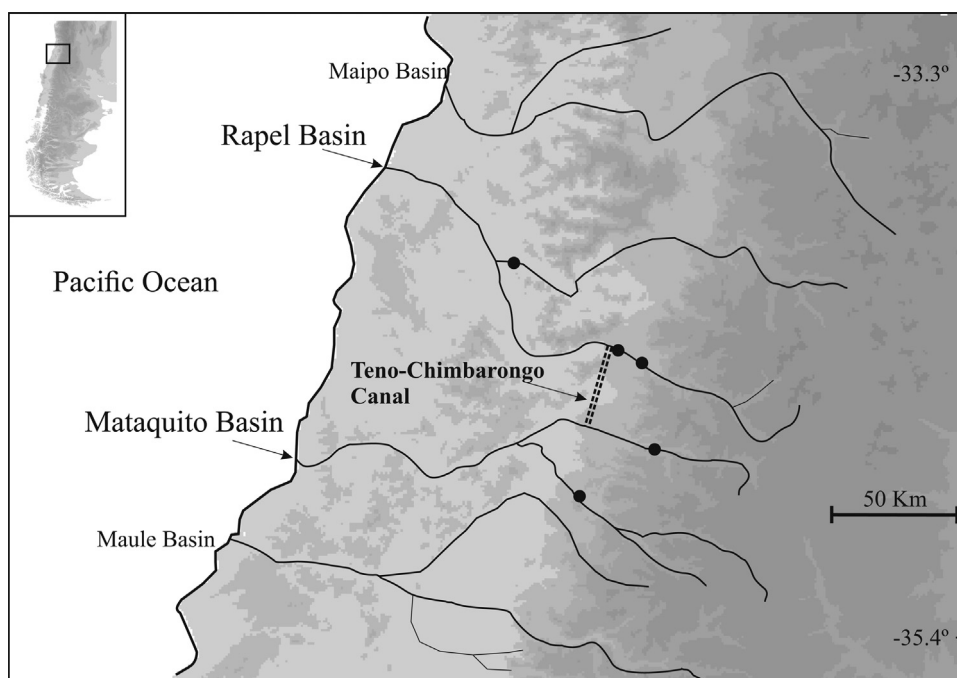
At a smaller scale, a less studied human activity that has the potential to reduce diversity in freshwater environments is the artificial connection of historically isolated river drainages. A

few cases of drainage interconnections facilitating inter-basin fish dispersal have been reported in the literature. For instance, the Snowy and Murray Rivers in Australia were artificially connected as the result of a major hydroelectric project during the early 20th century, facilitating the migration of the fish species *Galaxias brevipinnis*, an aggressive migratory species, into the Murray basin where the species was previously unrecorded (Waters et al., 2002). Similarly in New Zealand, Esa et al. (2000) reported that the connection of Otago's two major river systems, the Taieri and the Clutha, by tunnels from mining activities resulted in the introgressive hybridization of two previously allopatric galaxiid species. Although just a few studies have reported freshwater fish migration between different river basins through human mediated connections, they highlight the need for documenting these phenomena and studying its consequences for regional and local biodiversity.

The area of Central Chile concentrates the highest human population density of the country, as well as a strong agricultural activity due to optimal climatic conditions (Fuentes and Hajek, 1979). The area is drained by small and parallel river basins that originate in the Andes and discharge into the Pacific Ocean, after running just a few hundreds of kilometers. Due to the constant demand for water from

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**Fig. 1.** Study area in Central Chile showing river basins and a representation of the Teno–Chimbarongo canal. Black dots are localities from where *Diplomystes cf. chilensis* were sampled (for more details about sampling see Muñoz-Ramírez et al. 2014).

increasing agricultural activity, a number of projects have altered the natural hydrological landscape of this area by expanding the irrigation network. Some of these alterations have resulted in the current connection of previously isolated drainages, such as the Teno–Chimbarongo Canal in Central Chile that links the Rapel and Mataquito basins, and the Zañartu Canal connecting the Itata and Biobío basins. Despite the potential threat to the biodiversity of the region, there is a complete lack of studies addressing this issue, and no reports of inter-basin dispersal through these canals have been reported up to date. However, there is some evidence suggesting that dispersal through these uncovered, stream-like canals might be possible. Along with the documented presence of fish in some of these canals, which may be using them as an extension of their natural habitats (Habit and Parra, 2001; Habit, 1994), a recent phylogeographic study on a catfish genus has found low genetic structure and shared haplotypes between these basins (Muñoz-Ramírez et al., 2014). This study, which analyzed patterns of genetic variation from sequences of mitochondrial DNA, showed that even though a high amount of genetic diversity was partitioned across river basins with unique lineages in most drainages across the distribution of this group (Muñoz-Ramírez et al., 2014), some basins in Central Chile exhibited low inter-basin genetic structure, particularly between the Rapel and Mataquito basins (Fig. 1).

Two hypotheses were suggested in Muñoz-Ramírez et al. (2014) to explain the lack of genetic structure in these basins. One points out that current migrations between these basins might be occurring through irrigation canals (e.g. the Teno–Chimbarongo Canal, Fig. 1), reducing genetic structure by genetic homogenization. The second suggested that the lack of genetic differentiation could be explained by incomplete lineage sorting resulting from a relatively recent divergence following the last Pleistocene glaciation. Opportunities for headwater rearrangements and river captures might have occurred when glaciers melted approximately 10,000 years ago (Ruzzante et al., 2006).

The consequences of potential connections between historically isolated basins might bring unforeseen impacts to the diversity of this region, which is considered an important hotspot of biodiversity (Myers et al., 2000). Thus, it is urgent to know whether these

basins are exchanging fauna. However, testing these hypotheses with molecular data requires the use of methods that rigorously assess the relative support of these alternative scenarios and not simply rely on ad hoc explanations of the molecular patterns (Knowles, 2003). Current model-based approaches have proven to be powerful tools to test alternative demographic models, allowing the assessment of competing historical scenarios and the estimation of important demographic parameters (Bertorelle et al., 2010; Csilléry et al., 2010; Fagundes et al., 2007). In this study, we use a model-based simulation approach (approximate Bayesian computation) that allows the probabilistic comparison of alternative demographic models and the simultaneous estimation of demographic parameters to test whether current dispersal through irrigation canals or incomplete lineage sorting resulting from recent divergence better explain the observed genetic patterns in an endangered catfish, *Diplomystes cf. chilensis*.

## Material and methods

### Study system

Central Chile is considered a hotspot of biodiversity (Myers et al., 2000). This area is also one of the most threatened in Chile as it concentrates high levels of urbanization, forestry, and agriculture (Aronson et al., 1998; Azócar et al., 2007). One of the rarest, but also interesting group of fish inhabiting these rivers are the diplomystids, a group of endangered catfish recognized as one of the earliest branching lineages in the diverse order Siluriformes (Arratia, 1987; Sullivan et al., 2006). Diplomystids species are rare, have low fecundity (Vila et al., 1996), and exhibit generally low genetic diversity compared with other co-distributed fish species (Muñoz-Ramírez et al., 2014; Victoriano et al., 2012). All Chilean species are considered Endangered (CONAMA 2008). Their geographic distribution has decreased in recent times as they have gone extinct from two basins in the north part of their distribution (Aconcagua and Maipo basins; Muñoz-Ramírez et al., 2010), presumably as a consequence of habitat deterioration and the introduction of exotic species (Arratia, 1987). In this regard, irrigation canals may pose

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