

UNIVERSIDADE DE SÃO PAULO  
FACULDADE DE FILOSOFIA, CIÊNCIAS E LETRAS DE RIBEIRÃO PRETO  
PROGRAMA DE PÓS-GRADUAÇÃO EM BIOLOGIA COMPARADA

Padrões e processos da diversidade genética em caranguejos (Decapoda, Brachyura): abordagem integrada com atributos biológicos, ecológicos e demográficos.  
Patterns and processes of the genetic diversity in crabs (Decapoda, Brachyura): integrative approach with biological, ecological, and demographic traits.

Pedro Augusto da Silva Peres

Tese apresentada à Faculdade de Filosofia, Ciências e Letras de Ribeirão Preto da Universidade de São Paulo, como parte das exigências para obtenção do título de Doutor em Ciências, obtido no Programa de Pós-Graduação em Biologia Comparada

Ribeirão Preto - SP

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Orientador: Prof. Dr. Fernando Luis Medina Mantelatto

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## RESUMO

Padrões e processos relacionados a diversidade genética (DG) ainda são cercados de questões ecológicas e evolutivas não resolvidas. Entre elas está a que se refere aos fatores que regulam a variação da DG dentro e entre as diferentes espécies. Tal tema ainda carece de maior quantidade de dados empíricos, principalmente em relação ao megadiverso ambiente marinho. Nesta tese, utilizamos espécies de caranguejos (*Eubrachyura*) como modelos para avaliar como atributos biológicos, ecológicos e demográficos podem estar relacionadas à DG. Esta tese é composta por quatro capítulos (um artigo publicado e três em preparação) que visam responder diferentes questões sobre o tema. No capítulo 1, testamos a hipótese de que características biológicas podem ser mais relevantes que o potencial de dispersão de organismos para explicar padrões de distribuição da DG comparando duas espécies de caranguejos filogeneticamente próximas (*Callinectes ornatus* e *C. danae*). Como resultado, mostramos que a tolerância a salinidade pode estar relacionada à estrutura genética, padrões filogeográficos e história demográfica de ambas as espécies. A partir de perguntas levantadas com os resultados anteriores, no capítulo 2 investigamos os efeitos da foz do Amazonas-Orinoco (barreira fisiológica) sobre *C. ornatus*, utilizando dados obtidos a partir de sequenciamento de nova geração (ddRAD-seq) combinados com mtDNA. Como resultados, mostramos um cenário de especiação com fluxo gênico em que grupos separados pela foz estão bastante diferenciados, mas ainda com fluxo gênico existente entre eles. No capítulo 3, investigamos os padrões espaciais da DG utilizando dados de mtDNA de 14 espécies de caranguejos ao longo de toda sua distribuição no Atlântico Ocidental e testamos a hipótese de gradiente latitudinal da DG. Encontramos que a diversidade genética interespecífica é maior em baixas latitudes, mas que os padrões intraespecíficos variam de acordo com a espécie. Por fim, no capítulo 4, investigamos a relação entre características biológicas e

demográficas (8 atributos) com a DG. Utilizamos todos os dados de mtDNA disponíveis para Eubrachyura em bancos de dados públicos junto com dados gerados durante este projeto (150 espécies), e realizamos busca padronizada das características biológicas. De maneira geral, encontramos que o tamanho populacional efetivo é o fator que mais explica a variação da DG em caranguejos, mas alguns outros atributos parecem ter importância. Portanto, temos a convicção de que esta tese abre novos horizontes a partir de propostas inéditas e relevantes sobre padrões e processos da DG utilizando caranguejos como modelo, mas também podem se estender a outros táxons, especialmente marinhos.

**PALAVRAS-CHAVE:** Brachyura; Dispersão; Filogeografia; Genética de populações; Latitude; mtDNA; ddRAD-seq.

## ABSTRACT

The patterns and processes of the genetic diversity (GD) are still surrounded by unresolved questions in the fields of ecology and evolution. One of the questions is what drives GD at the intra- and interspecific level. This topic needs further empirical data, especially regarding the megadiverse marine environment. In this dissertation, we used crabs (Eubrachyura) as models to test how biological, ecological, and demographic traits are associated to GD. This dissertation is composed of four chapters (one published paper, and three papers in preparation) that asked different questions within this framework. In chapter 1, we compared two phylogenetically close species (*Callinectes ornatus* and *C. danae*) to test the hypothesis that biological traits are more important than the dispersal potential explaining GD spatial patterns. We show that salinity tolerance can explain genetic structure, phylogeographic patterns, and the demographic history of both species. Considering the questions that remained unanswered, in chapter 2 we investigated the effects of the Amazon-Orinoco plume (physiological barrier) on *C. ornatus* employing a next-generation sequencing approach (ddRAD-seq) alongside with mtDNA. We show a speciation with gene flow scenario in that groups separated by the plume are differentiated, but we still find gene flow between them. In chapter 3, we investigated the GD spatial patterns using mtDNA of 14 crabs from the Western Atlantic and tested the latitudinal gradient hypothesis. Our results show that interspecific GD is higher at lower latitudes, but intraspecific patterns vary across species. Finally, in chapter 4, we investigated the association among biological and demographic traits (8 variables) with GD. We analyzed the most comprehensive dataset to date of Eubrachyura mtDNA available in public databases and generated during this dissertation (150 species) and did standardized searches in the literature looking for the biological traits. Overall, our results show that the historical effective population size is the primary factor determining crabs GD variation, but other

traits might also contribute to this variation. Therefore, we are sure this dissertation opens new venues by providing novel approaches on GD patterns and processes using crabs as models, but our results might also be extended to other taxa, especially marine ones.

KEY WORDS: Brachyura; ddRAD-seq; Dispersion; Latitude; mtDNA; Phylogeography; Population genetics.

## GENERAL CONCLUSIONS

The chapters we have presented here had the goal of furthering the understanding on the patterns and processes of GD using crabs as model organisms. We begin (chapter 1) showing that an ecological trait (salinity tolerance) can be a best predictor of the species phylogeographic pattern than dispersal potential. We provide empirical evidence that co-distributed and closely related species can show contrasting GD spatial patterns based on a trait-based hypothesis elaborated *a priori*. However, when a species is tolerant to variation in abiotic conditions and it is not affected by biotic interactions, long pelagic dispersion can indeed guarantee the gene flow throughout the distributional range. We believe the assumption of PLD and lack of genetic structure should be considered as a null hypothesis and trait-based hypothesis could help us on a better understanding of the drivers of intraspecific GD spatial distribution. We further explored *C. ornatus* intraspecific diversification (chapter 2) by expanding our previous dataset and also employing a NGS approach (ddRAD-seq). Overall, mtDNA and ddRAD-seq show the same patterns but the latter gives us a better resolution. We propose an incipient scenario process driven by disruptive selection coupled with a permeable barrier (the Amazon-Orinoco plume), differences in effective population size, and oceanographic currents acting together in this complex scenario. Therefore, we show a possible consequence of the plume over the diversification of species distributed along the western Atlantic by investigating *C. ornatus*. We transitioned to a different question and explored GD spatial patterns (chapter 3) exploring the effects of latitude (LGDG), species range (CMH), a combination of both (CMH-LGDG), or species dispersal potential (MH). Investigating 14 species distributed along the western Atlantic, we show that there is an interspecific LGDG pattern (higher GD at lower latitudes) that is not explained by the evolutionary speed hypothesis (ESH). Alternatively, intraspecific GD spatial

patterns varied across species and other hypotheses were evoked to explain our results. Finally, we addressed the question on the drivers of GD across crab species (chapter 4) by testing the effects of fecundity, body size, propagule size, number of larval stages, larval development time, historical effective population size, maximum longevity, and habitat. We compiled COI data for 150 species and confirm the primary influence of historical  $N_e$ , although we show other traits having minor influence. Our results add taxon-based data to a growing body of literature exploring the determinants of GD across species and confirm and refute some previous trends. Additionally, showing the association between  $N_e$  and GD in crabs, we provide a baseline for future comparisons in conservation assessments.

In many ways, this dissertation only begins to hint at the mechanisms influencing GD in crabs. We provide novel results and interpretations for current questions in the ecology and evolutionary biology fields focusing on a group frequently overlooked. Although we answered some of our questions, many others arise from here. Future studies could look at similar patterns in other marine species (Chapter 1); be benefited by sampling in hybrid zones, exploring transcriptomes from the two divergent lineages, and performing controlled mating and salinity tolerance experiments (Chapter 2); exploring co-distributed species from other regions, including depth and longitude in the analysis, so as including other types of molecular markers (Chapter 3); performing phylogenetic comparative methods, increasing species sampling, employing different markers, investigating trends in phylogenetically fine-scale (Chapter 4). In conclusion, we gained great insight and substantially increased our knowledge of the GD patterns and processes operating in crabs and provided results that can be expanded to other taxa.

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