Genetic Architecture Promotes the Evolution and Maintenance of Cooperation

Antoine Frénoy, François Taddei, Dusan Misevic

HAL Id: inserm-02140178

https://www.hal.inserm.fr/inserm-02140178

Submitted on 27 May 2019

Genetic Architecture Promotes the Evolution and Maintenance of Cooperation

Antoine Frénoy*, François Taddei, Dusan Misevic

INSERM U1001, Université Paris Descartes, Sorbonne Paris Cité, Faculté de Médecine Paris Descartes, Paris, France

Abstract

When cooperation has a direct cost and an indirect benefit, a selfish behavior is more likely to be selected for than an altruistic one. Kin and group selection do provide evolutionary explanations for the stability of cooperation in nature, but we still lack the full understanding of the genomic mechanisms that can prevent cheater invasion. In our study we used Aevol, an agent-based, *in silico* genomic platform to evolve populations of digital organisms that compete, reproduce, and cooperate by secreting a public good for tens of thousands of generations. We found that cooperating individuals may share a phenotype, defined as the amount of public good produced, but have very different abilities to resist cheater invasion. To understand the underlying genetic differences between cooperator types, we performed bio-inspired genomics analyses of our digital organisms by recording and comparing the locations of metabolic and secretion genes, as well as the relevant promoters and terminators. Association between metabolic and secretion genes (promoter sharing, overlap via frame shift or sense-antisense encoding) was characteristic for populations with robust cooperation and was more likely to evolve when secretion was costly. In mutational analysis experiments, we demonstrated the potential evolutionary consequences of the genetic association by performing a large number of mutations and measuring their phenotypic and fitness effects. The non-cooperating mutants arising from the individuals with genetic association were more likely to have metabolic deleterious mutations that eventually lead to selection eliminating such mutants from the population due to the accompanying fitness decrease. Effectively, cooperation evolved to be protected and robust to mutations through entangled genetic architecture. Our results confirm the importance of second-order selection on evolutionary outcomes, uncover an important genetic mechanism for the evolution and maintenance of cooperation, and suggest promising methods for preventing gene loss in synthetically engineered organisms.

Introduction

The evolution of cooperation in microbial populations is a fascinating, rich and controversial evolutionary problem [1–6]. The theoretical understanding of cooperation has been gradually advancing for decades, and recently those insights have also been applied to practical, medical problems, such as the treatment of infections triggered by cooperating, pathogenic bacteria [7,8]. Most evolutionary explanations of cooperation rely on kin selection and group selection theories and are constantly being improved and refined by a host of mathematical tools [9,10]. Among them, the game theory and meta-population models have proved to be especially useful in the analysis of long term versus short term, as well as the individual versus population benefit of cooperation [11–14]. However, those methods tell us practically nothing about the evolutionary pressure on the structure of genomes that encode the cooperative traits. They typically do not distinguish between genotypes and phenotypes and consider only a finite set of possible behaviors (often only two: cooperate or not) with a constant extrinsic probability of switching between them. Although some recent papers do go further than evolving classical binary behavior by considering more complex stochastic strategies that take into account past interactions [15], they also remain "one

locus = one parameter" models, unable to consider genetic architecture of cooperation genes. Several experimental studies have shown the need to go beyond these limitations to understand cooperation in microbial systems. Specifically, Foster *et al.* demonstrated that the pleiotropic effect of a *Dictyostelium discoideum* gene involved in a cooperative behavior (differentiation into prestalk cells) causes the mutations inducing cheating behavior to be associated with a direct fitness cost to the individual [16]. Similarly, cheating mutations induce a cost in *Pseudomonas aeruginosa* because of co-regulation of public and "private" goods via the same quorum-sensing mechanism [17].

We postulate that genomic architecture of metabolic and secretion genes – achieved by sense-antisense coding or frameshifts – can provide a mechanism for the evolution and maintenance of cooperation that is similar but more basic than ones relying on genetic pleiotropy or co-regulation. Here we investigate how two specific types of genomic architecture of cooperation genes may affect the evolutionary fate of cooperation itself. The first type relies on the concept of operons, already well described and investigated in the context of co-regulation or co-transfer of genes in the same operon [18,19]. We specifically consider metabolic and secretion genes that have the same promoter and terminator sequence, thus sharing an operon. The second architecture type is

PubMed
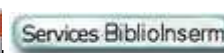
Genetic architecture promotes the evolution and maintenance of cooperation.

Frénoy A[1], Taddei F, Misevic D.

⊖ **Author information**

1 **INSERM** U1001, Université Paris Descartes, Sorbonne Paris Cité, Faculté de Médecine Paris Descartes, Paris, France.

Abstract

When cooperation has a direct cost and an indirect benefit, a selfish behavior is more likely to be selected for than an altruistic one. Kin and group selection do provide evolutionary explanations for the stability of cooperation in nature, but we still lack the full understanding of the genomic mechanisms that can prevent cheater invasion. In our study we used Aevol, an agent-based, in silico genomic platform to evolve populations of digital organisms that compete, reproduce, and cooperate by secreting a public good for tens of thousands of generations. We found that cooperating individuals may share a phenotype, defined as the amount of public good produced, but have very different abilities to resist cheater invasion. To understand the underlying genetic differences between cooperator types, we performed bio-inspired genomics analyses of our digital organisms by recording and comparing the locations of metabolic and secretion genes, as well as the relevant promoters and terminators. Association between metabolic and secretion genes (promoter sharing, overlap via frame shift or sense-antisense encoding) was characteristic for populations with robust cooperation and was more likely to evolve when secretion was costly. In mutational analysis experiments, we demonstrated the potential evolutionary consequences of the genetic association by performing a large number of mutations and measuring their phenotypic and fitness effects. The non-cooperating mutants arising from the individuals with genetic association were more likely to have metabolic deleterious mutations that eventually lead to selection eliminating such mutants from the population due to the accompanying fitness decrease. Effectively, cooperation evolved to be protected and robust to mutations through entangled genetic architecture. Our results confirm the importance of second-order selection on evolutionary outcomes, uncover an important genetic mechanism for the evolution and maintenance of cooperation, and suggest promising methods for preventing gene loss in synthetically engineered organisms.