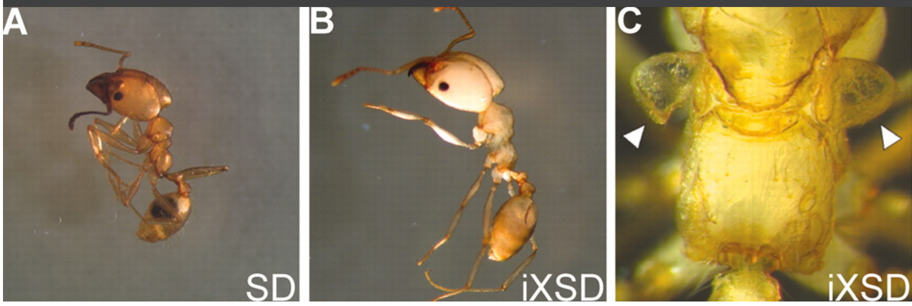
WWU MÜNSTER

1st June 2017

More than meets the eye: The role of cryptic genetic variation in the evolution of novel phenotypes



© Rajakumar et al. 2012, Science 335: 79-82: In *Pheidole* ants, the ancestral potential to form super-soldiers (B) which are significantly larger than normal soldiers (A) can be evoked by environmental cues.

Abstract:

There is a prevalence in evolutionary thought that novelty typically arises through either incremental change or the co-option of previously existing traits or genes. Oft ignored in this framework is the capacity of the environmental-developmental interaction to yield novel or re-awakened ancestral phenotypes without changes to the underlying genetic architecture of the trait. Because these phenotypes were not previously expressed (or at least not under normal conditions), the genetic underpinnings of the traits evolve through drift or indirect selection (i.e., selection on correlated traits). Environmental change and stress are, thus, mechanisms that can release new phenotypes, and these can be strikingly different in form and function from the status quo phenotype(s). The unmasking of cryptic genetic variation has the capacity to rapidly modify the phenotype space of a population, and thus the selective landscape. It is currently unclear how large a role cryptic genetic variation has had over evolutionary time, but the theoretical capacity of this process to shape major evolutionary events is now starting to be appreciated. The goal of this workshop is to consider the mechanisms of phenotypic plasticity and its regulation, how environmental change/stress act on mechanisms governing plasticity, and what the evolutionary capacity of cryptic genetic variation is in the evolutionary past, current and future.

Organizers:

- **Prof. Dr. Chris Smith**
  Department of Biology, Earlham College, Richmond
- **Prof. Dr. Jürgen Gadau**
  Institute for Evolution and Biodiversity, University of Münster

Speakers:

- **Prof. Dr. Ehab Abouheif**
  Department of Biology, McGill University, Montreal
- **Prof. Dr. Emilie C. Snell-Rood**
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For those unfamiliar with the terms phenotypic plasticity and cryptic genetic variation, consider the hypothetical example described below and the following definitions:

Phenotypic plasticity: "the ability of individual genotypes to produce different phenotypes when exposed to different environmental conditions" (Pigliucci et al. 2006, J Exp Biol 209: 2362-2367).

Cryptic genetic variation: "Cryptic genetic variation (CGV) is defined as standing genetic variation that does not contribute to the normal range of phenotypes observed in a population, but that is available to modify a phenotype that arises after environmental change or the introduction of novel alleles." (Gibson and Dworkin 2004, Nat Rev Genet 5:681-90).

Example: Once upon a time there was a hominid of size and proportions similar to present day humans, and with a size distribution similar to current day. A population of these hominids began living in a subterranean network of caves to escape increasing competition. While food was present in the caves, the nutrients in the food differed from the ancestral diet, not to mention that they lived in the absence of light. The first generation born and raised in the new environment were far smaller than their parents, well outside the range of size observed in the ancestral size distribution. Furthermore, the limb proportions were also altered, with reduced femur length relative to the rest of their body. Overall, the suite of phenotypes observed in this population were quite radically different than anything previously observed in the hominid fossil record.

Questions to consider:

- What is the difference, semantic and biological, between phenotypic plasticity and cryptic genetic variation?
- Was the cave-dwelling hominid a new species?
- Is the variation observed in the cave-dwellers a result of phenotypic plasticity?
- What environmental mechanisms may have driven the changes in phenotype?
- What developmental mechanisms may have driven the changes in phenotype?
- What genes/pathways/networks could've been responsible for these changes?

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