No Genome is an Island: Developing a 21st Century Agenda for Experimental Evolution

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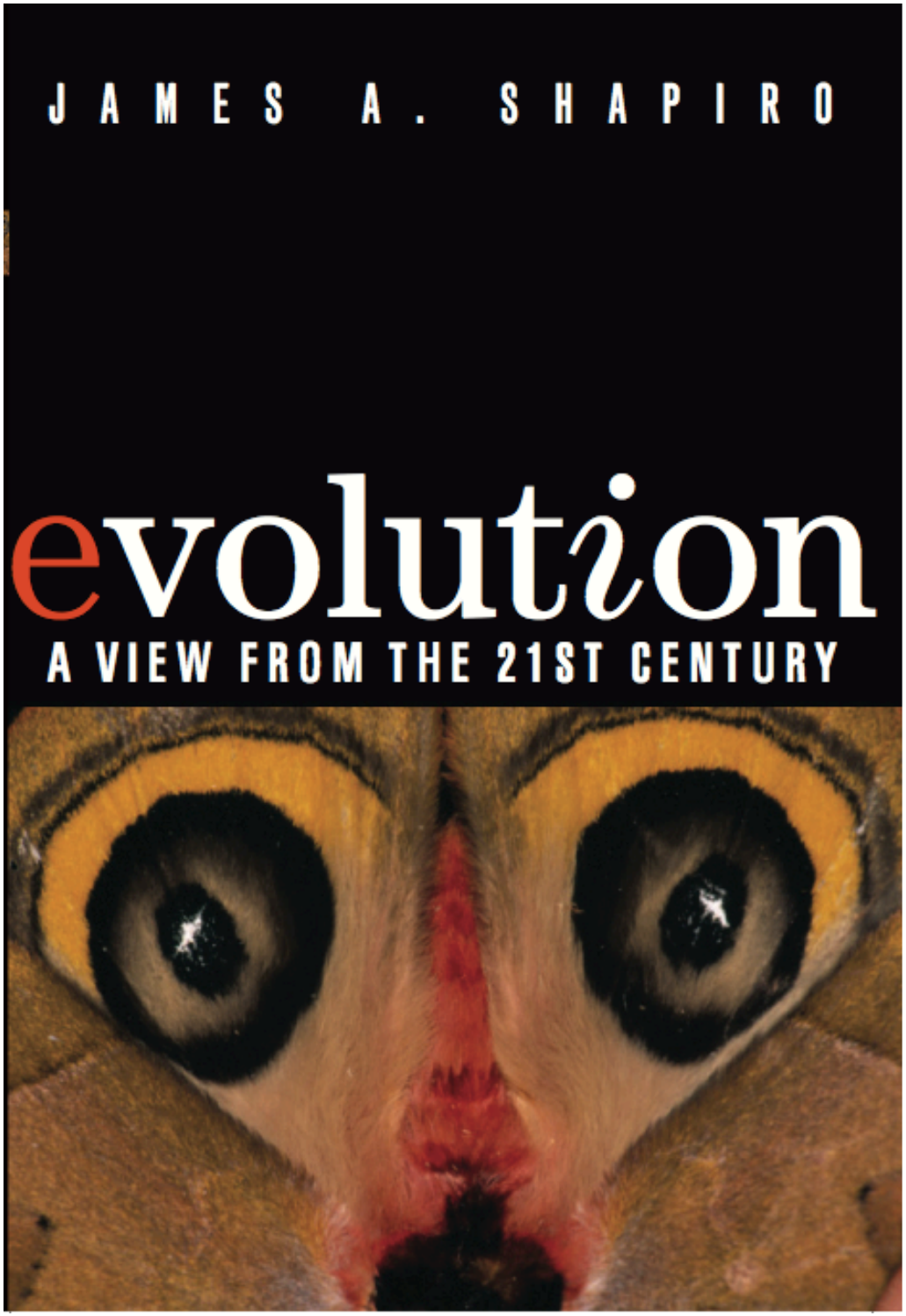
July 4, 2018



Abstract

Conventional 20th Century evolution thinking was based on the idea of isolated genomes for each species. Any possibility of life-history inputs to the germ-line was strictly excluded (Weismann's doctrine), and genome change was attributed to random copying errors. Today we know that many life-history events lead to rapid and non-random evolutionary change mediated by specific cellular functions. These include cell mergers and activation of natural genetic engineering by stress, infection and interspecific hybridization. In addition, we know of molecular mechanisms for transmitting life history information across generations through gametes. These discoveries require a new agenda for evolutionary experiments to determine the genomic impacts of abiotic stresses, biotic interactions, and sensory inputs from environmental conditions. The presentation will offer some generic recommendations for enriching evolution experiments to incorporate new knowledge and find answers to previously excluded questions.

Prevailing 20th Century Assumptions (ca. 1968)

- Reproductively isolated organismal genomes
- All hereditary change takes place within the species' genome
- No transmission of life-history information to the germline
  - Weismann doctrine
  - Central Dogma (molecular Weismannism)
- Random, accidental genome change leading to numerous small selective advantages

What's New 50 Years Later

- Cell mergers and intracellular DNA transfers producing taxonomic and adaptive divergence
  - Origin of eukaryotic cell
  - Origins of photosynthetic eukaryotes (primary, secondary, tertiary symbiogenesis)
- Microbiomes & holobionts
- Adaptive & reproductive changes through endosymbiosis & intracellular DNA transfer
- Innovative role of the virosphere
- Horizontal DNA transfers across taxa
- Cell-mediated non-random genome change ("Natural Genetic Engineering")
- Abiotic stresses triggering genome change
- Biotic interactions triggering genome change
- Real time massive genome changes in cancer
- Cross-generational transmission of life history-responsive RNA and protein molecules via gametes.

Non-Random Natural Genetic Engineering

- NGE functionalities (DNA/RNA elements, proteins and ribozymes):

  Nucleases, ligases, error-free and mutagenic DNA polymerases, reverse transcriptases, RNAseH, RdRPs, helicases, deaminases, recombinases, integrases and transposases, terminal transferases, mobile DNA elements, etc.

- Regulation of NGE activity:
  - DNA-level responses to invaders (CRISPRs, piRNA loci, adaptive immunity)
  - Stress-induced mutable and hypermutable states (≥93 proteins in *E. coli* DSB response)
  - Developmental control of DNA restructuring (phase, antigenic, and mating-type variation, ciliate macronucleus, chromatin diminution, immune system)
  - Rapid genome restructuring in cancer cells
- Targeting of NGE action:
  - DNA sequence and chromatin recognition (*e.g.,* site-specific recombinases, transposases, retrotransposons, retroviruses)
  - Protein-protein interactions (*e.g.,* yeast retrotransposons)
  - Transcription linkage (*e.g.,* kataegis, retrovirus insertion)
  - Sub-nuclear positioning (*e.g.,* translocations, chromothripsis)
  - RNA targeting (*e.g.*, DGRs, CRISPRs, ciliate macronucleus, lncRNA targeting AID)

Importance of Abiotic Factors

- Stresses inducing mutable and hypermutable states
  - UV and ionizing radiation
  - Heavy metals
  - Reactive oxygen species
  - Temperature
  - Salt and drought
  - Pesticides and other pollutants
- Abiotic triggers of specific NGE activities
  - Heat induces *Arabidopsis, Brassica* retrotransposon *ONSEN*
  - As, V, Fe induce VL30 retrotransposition in mice
  - Hg induces LINE-1 retrotransposition in human cells
  - laser irradiation stimulates *mPing* DNA transposition in rice

Importance of Biotic Interactions

- Nutritional challenges as agents of quantitative and **qualitative** mutability changes
  - Starvation-induced hypermutability in *E. coli*, *A. baumanii*
  - Starvation-induced genome restructuring in *S. cerevisiae*
  - Distinct nutritional **stress-specific mutation spectra** in *E. coli*
- Biomolecules as activators of genome variability (genotoxins, antibiotics, alcohols, pheromones/signaling molecules)
- Infectious agents as genome change vectors (viruses, etc.)
- Microbiome components facilitating stress adaptations (plants)
- **Interspecific mating**, hybrid dysgenesis as evolutionary triggers (allopolyploid hypermutability in yeast, plants and animals)
- Infection and symbiosis as evolutionary triggers
  - For host: *Wolbachia*-induced mating incompatibilities, bacterial pathogens producing genotoxins
  - For infectious agent: *P aeruginosa* hypermutability in cystic fibrosis lungs, IS elements modifying *Sinorhizobium* host-range in soybean root nodules

Some Experimental Evolution Questions

- Is most or all of eukaryotic taxonomic origination triggered by interspecific hybridization?
- How important are infectious agents in evolutionary change?
- To what extent do sensory inputs bias genome changes?

Novel Experimental Evolution Methods Based on Interactive Genome Model

- Testing role of mixed populations on efficiency of genome innovation
  - Sibling species (hybridization potential)
  - Competitors (*e.g.,* mixed microbial, plant populations)
- Testing effect of infectious agents on efficiency of genome innovation for characters unrelated to infection (e.g., photosynthesis)
  - Viruses (endogenous, external)
  - Microbial symbionts, parasites and pathogens
- Testing influence of external conditions on mutational outcomes (prior growth history, stresses and sensory inputs)

Generic Suggested Experiments To Explore the Role of Sensory Inputs on Genome Changes

1. Test starvation following growth of pure or mixed microbial populations on different substrates for alterations in the spectrum and location of genome changes (determined by WGS methods).
2. Effect of cyanophage infection on spectral shifts in photosynthesis capacity.
3. Test the effects of interspecific hybridization plus physically or visually distinct environments on the emergence of novel wing patterns in butterflies or moths.
4. Determine the synergistic effects of abiotic stresses and microbial associations on genomes of plants evolving adaptations to novel ecologies.