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How the Chicxulub Asteroid Impact Triggered Transposable-Element Bursts and Fungus-Farming Agriculture Across 15,000 Ant Species

Formicidae Phylogenomics * Chicxulub K-Pg Extinction * Transposable Elements (TEs)

Today, more than 15,000 described species of ants (family Formicidae) inhabit nearly every terrestrial ecosystem on Earth, collectively accounting for an estimated 20 quadrillion individuals and roughly 12 megatons of dry carbon biomass -- exceeding the combined biomass of all wild birds and mammals. Yet for the first 35 million years after eusocial ants diverged from solitary vespoid wasp ancestors in the Early Cretaceous (~100-120 million years ago), early stem-group ants such as the “hell ants” (Haidomyrmecinae) remained ecologically minor ground and canopy predators representing less than 1% of Cretaceous insect fossils. Two converging genomic studies -- a comparative assembly of 163 ant genomes led by Dr. Lukas Schrader at the University of M nster and the Global Ant Genomics Alliance (GAGA) in Science Advances , alongside a 751-taxon phylogenomic reconstruction of ant-fungus coevolution led by Dr. Ted Schultz at the Smithsonian National Museum of Natural History in Science -- show that the 66-million-year-old Chicxulub asteroid impact transformed both the internal chromosome architecture and the external trophic ecology of crown-group ants.

1. The K-Pg Extinction Bottleneck and Stress-Induced Transposable Element Bursts

To trace why specific ant lineages diversified into thousands of species while sister clades remained species-poor relicts, Schrader and colleagues sequenced and annotated 163 ant genomes spanning 12 of the 16 extant subfamilies across 100 million years of evolutionary history. Rather than accumulating mutations at a uniform clock-like pace, the ancestors of the four hyper-diverse crown subfamilies -- Myrmicinae (~7,100 species), Formicinae (~3,200 species), Dolichoderinae (~850 species), and Dorylinae (~750 species) -- experienced synchronized, independent bursts of transposable element (TE) proliferation clustered within a narrow temporal window between 66 and 60 million years ago , immediately following the Cretaceous-Paleogene (K-Pg) boundary.

In eukaryotic genomes, transposable elements -- including Class I long terminal repeat (LTR) retrotransposons, non-LTR LINEs, and Class II DNA transposons (such as Mariner/Tc1 and hAT superfamilies) -- are normally silenced in the germline by PIWI-interacting RNAs (piRNAs) and DNA/ histone methylation. However, severe abiotic and nutritional stress during the post-Chicxulub impact winter and subsequent Paleocene greenhouse warming transiently compromised epigenetic transposon silencing. Across the 163 analyzed assemblies, total TE genomic content varies from 11.4% to 54.8% of total assembly length (mean genome size ~210-550 Mb), and lineage-specific net diversification rates correlate strongly with the magnitude of

K-Pg boundary TE amplification bursts.

| Ant Subfamily / Clade | | Extant Species Diversity | | Mean Genome Size & TE Fraction | | Primary K-Pg Evolutionary Innovation (~66-55 Ma) | | Chemosensory & Trophic Regime |

| Myrmicinae (including tribe Attini) | | ~7,100 species (47% of all ants) | | 295-480 Mb * 28%-52% TEs | | K-Pg Class I/II TE burst + origin of obligate fungus farming (~66 Ma) | | 350-520 Odorant Receptors (ORs); granivory, omnivory & leucocoprineaceous fungiculture |

| Formicinae (e.g., Camponotus , Formica) | | ~3,200 species | | 240-390 Mb * 24%-44% TEs | | Post-K-Pg TE expansion + Blochmannia nutritional endosymbiosis | | 320-460 ORs; angiosperm extrafloral nectar & hemipteran honeydew tending |

| Dolichoderinae (e.g., Linepithema , Azteca) | | ~850 species | | 215-310 Mb * 19%-36% TEs | | TE-mediated tandem expansion of trail pheromone & terpenoid defense clusters | | 340-490 ORs; high-density supercolonial foraging & arboreal canopy dominance |

| Dorylinae (Army & Driver Ants) | | ~750 species | | 230-340 Mb * 22%-38% TEs | | 9-exon OR subfamily tandem duplication via unequal crossover at TE flanks | | 380-560 ORs; blind nomadic group-raiding & cuticular hydrocarbon recognition |

| Basal “Poneroid” & Relict Clades (e.g., Leptanillinae , Martialis) | | 1-80 species per clade | | 185-260 Mb * 11%-18% TEs | | Low post-K-Pg TE turnover; conserved ancestral synteny | | 140-230 ORs; specialized subterranean arthropod predation |

2. Bipartite “Two-Speed” Chromosomes and Odorant Receptor Amplification

A critical mechanistic insight from the 163-genome comparative dataset is why massive TE insertions did not drive early Paleocene ant populations to extinction through deleterious coding frameshifts. Ant chromosomes evolved a pronounced bipartite (“two-speed”) structural compartmentalization :

* Syntenic TE-Poor Core Islands: Essential housekeeping, developmental, and caste-differentiation genes (such as insulin/TOR and juvenile hormone signaling pathways) reside within tightly conserved, high-recombination syntenic blocks where purifying selection rapidly purges TE insertions.

* Dynamic TE-Rich Adaptive Compartments: Fast-evolving environmental-sensing, detoxification (cytochrome P450s), and exocrine gland biosynthesis loci cluster inside peripheral, TE-dense chromosomal islands. Within these compartments, homologous recombination between flanking interspersed repeats repeatedly generated segmental duplications, exon shuffling, and regulatory rewiring.

Most notably, TE-rich islands directly surround tandem arrays of odorant receptor (OR) genes -- particularly the ant-expanded 9-exon OR clade responsible for detecting long-chain cuticular hydrocarbons (CHCs). While solitary hymenopterans and fruit flies (Drosophila melanogaster) possess only ~60-150 OR genes, crown-group ants harbor 350 to over 550 functional OR loci . Transposon-driven tandem duplication of these chemosensory arrays enabled ancestral Paleocene ants to evolve

high-precision nestmate recognition, caste-specific queen pheromones, and multi-component chemical recruitment trails needed to coordinate colonies of tens of thousands to millions of workers.

3. The Chicxulub Impact Winter and the Birth of Ant Fungus Farming

While transposable elements rewired the ant genome from within, the ecological aftermath of the Chicxulub bolide impact reshaped ant foraging strategies from without. By sequencing 2,524 ultraconserved element (UCE) nuclear loci across 475 fungal species and 276 fungus-farming ant species (subfamily Myrmicinae , tribe Attini), Schultz and colleagues calibrated an independent time-scaled co-phylogeny of both partners. Their molecular clock analyses converge on a single synchronous origin of ant agriculture at 66.0 million years ago (95% highest posterior density: 60-72 Ma) .

When the 10-kilometer Chicxulub impactor struck the Yucat n carbonate platform, ejecta plumes, sulfate aerosols, and global wildfire soot reduced surface solar irradiance by more than 80% for months to years. As terrestrial photosynthesis collapsed and non-avian dinosaurs, pterosaurs, and roughly 50%-75% of regional plant species perished, the biosphere experienced an unprecedented global detritus pulse . Saprotrophic basidiomycete fungi -- capable of degrading lignocellulose in dead wood and leaf litter without sunlight -- proliferated globally across the K-Pg boundary (“fungal spike”).

Ancestral Neotropical attine ants, faced with the collapse of live plant and insect prey webs, transitioned from opportunistic mycophagy to actively provisioning, sheltering, and vertically transmitting basidiomycete mycelia (family Agaricaceae , tribe Leucocoprineae). This mutualism subsequently underwent a second major transition ~27 million years ago during Oligocene global cooling and South American dry-biome expansion, when one fungal lineage -- Leucoagaricus gongylophorus -- became completely isolated from free-living wild populations and evolved specialized nutrient-swollen hyphal tips called gongylidia , giving rise to the obligate “higher agriculture” practiced by modern Atta and Acromyrmex leaf-cutter ants.

4. Ecological Synthesis: From Cretaceous Minorities to Cenozoic Ecosystem Engineers

Together, the 163-genome transposable-element atlas and the 751-taxon attine-fungal UCE phylogeny resolve a long-standing macroevolutionary puzzle: why ants originated alongside mid-Cretaceous angiosperms (~100-110 Ma) yet waited 40 million years before achieving numerical and ecological dominance in the Eocene. The Chicxulub catastrophe acted as a dual evolutionary catalyst -- simultaneously clearing archaic Cretaceous competitors, triggering stress-activated transposon bursts that expanded ant chemosensory and social communication toolkits, and forging agricultural symbioses that turned post-extinction decay into a permanent trophic foundation.

References & Primary Sources

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