Origin of diversity within species

The question to whether there is a universal common ancestor is one that has queried scientists for years, and, though so far unsuccessful, the evolutionary pathways of most species can be traced back to xmya years. The taxonomic group Araneae is one of the most ancient and diverse groups of species on earth. The earliest Aranae fossil is Attercopus fimbriunguis; it dates back to the Middle Devonian period (380-374 million years ago). (Coddington, 1991) There are almost 40, 000 identified extant species, making spiders the most significant arthropod predators of the insect kingdom. (Dimitrov, 2011) There are two types of evolution that can take place within any taxonomic group: divergent evolution, where speciation occurs due to some form of isolation, and convergent evolution, where two species take different evolutionary pathways, yet end up with similar traits.

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A major contribution to within-species diversity, (and hence, in some cases, speciation) are genetic mutations. Mutations occur randomly and spontaneously during DNA replication, and can be one of three types. Substitution mutations occur when one nucleotide is substituted for another. Due to the degeneracy of the triplet code (more than one triplet codes for each amino acid; eg. Both GAA and GAG both specify for glutamic acid) substitutions only have a mutative effect if another amino acid is coded for, which does not always happen in which case this mutation is silent. If another amino acid is coded for, the mutation is ‘ mis-sense’ and may affect the tertiary structure and functionality of the protein. If a ‘ nonsense’ mutation occurs, this refers to the substitution being in the stop codon at the end of the sequence, and may result in the transcription of the polypeptide chain to be stopped prematurely, or too late, again causing the protein to be unable to carry out its function. In deletion and addition mutations, an extra nucleotide is added into or taken away from the sequence of bases and may cause a ‘ frame shift’, where the rest of the amino acid chain is translated wrong in protein synthesis. The severity of the frame shift depends on how far down the DNA base sequence the mutation occurs. (Crick, 1961) The formation of a dysfunctional protein may be disadvantageous to the organism, and due to selection pressures this genetic mutation will not be passed on.

Figure 3. Map of the Hawaiian islands showing the Theridion grallator sample sites. They were collected directly from the undersides of the leaves belonging to plants such as Broussaisia arguta and Clermontia arborescens are numbered according to the volcano on which they were collected. (Croucher et al, 2012)However in the case of an advantageous mutation, for example Theridion grallator; a small spider largely found in the forests of the Hawaiian Islands: Oahu, Molokai, Maui, and Hawaii. (Croucher et al, 2012) The spiders’ genitalia in the samples from the four islands showed no obvious differences (a sign of speciation in arthropods), and along with the viability of offspring from crosses between individuals from different islands (Oxford and Gillespie 1996) suggest that these spiders belong to a single species. The spider displays striking colour-polymorphism[1]. Laboratory rearing experiments have indicated that this polymorphism is inherited in a Mendelian (dominance and independent assortment) fashion through alleles at one (possibly two-see below) genetic locus, with the phenotypes

exhibiting a dominance hierarchy that reflects the extent of expressed pigmentation (Oxford and Gillespie 1996a, b, c).

On the islands of Ohau, there more than 20 distinct colour morphs within the Theridion grallator species. The consecutive formation of the Hawaiian Islands (Clague, 1996) shows the source of Hawaiian populations of Theridion grallator is likely to be Maui; an island adjacent to Ohau, where Theridion grallator originates. The article theorises that a small number of Theridion grallator moved across from Ohau to Hawaii in order to escape competition and find a plentiful food source. The small founder population in Hawaii was subject to inescapable genetic mutations, which produced the mode of inheritance found on Hawaii today. As the initial population expanded to fill suitable habitats, the new genetic architecture underlying the color variation spread across the island. (Oxford and Gillespie, 2001) Due to the founder effect, the gene pool on the newly colonised islands was small and the species was subject to being unable to adapt. The genetic variation within the few founder individuals, and indeed within any population, is maintained somewhat by the processes of independent assortment and crossing over.

Independent assortment is the random orientation of pairs of homologous chromosomes (bivalents) at metaphase of meiosis 1. At metaphase 1, where the centrioles are at opposite poles of the cell, the homologous pairs (one maternal, one paternal chromosome) can be located at the metaphase plate[2]. Each pair may orient with either its maternal or paternal homolog closer to a given pole. Thus, there is a 50% chance that any daughter cell of meiosis 1 will get the maternal chromosome of a particular homologous pair, and 50% chance that it will be the paternal. Because each pair is positioned independently of the other pairs at metaphase 1, the first meiotic division causes each pair sorting its maternal and paternal homologs into daughter cells independently of every other pair. (Campbell biology) Bit about crossing over This ensures variation in the resulting gametes, and allows combinations of alleles to be expressed in the offspring that may not have been expressed in the parents- allowing more chances for an advantageous trait to be conceived.

Figure 1. Mygalomorph spider (left) showing downward motion of fangs. Araneomorph spider (right) in which fangs move sideways towards one another (Cloudsly, 1958)Origin of diversity between species

All spiders spin silk. Primitive spiders' main use for silk was for building retreats and cocoons for eggs, (Cloudsly, 1958) however this ability evolved into a predatory device. It has been suggested that early predation by spiders on wingless insects stimulated the evolution of insect wings (Bristowe, 1958). However when their prey took to the air, spiders evolved aerial webs. Predation by spiders has also developed in the jaw. Primitive suborders such as Mygalomorphae and Liphistiomorphae have chelicerae that strike forward and down (parallel to the body axis), whereas Araneomorph spiders have fangs that move laterally inwards, as the chelicerae pivots horizontally (right angle to the body axis). (Cloudsly, 1958) Bristowe suggested that the evolution of these fangs coincided with the evolution of winged insects; vertically moving fangs would be less effective in aerial webs and on branches of tree ferns.

The evolution of this silk, however, The two important evolutionary events in spiders – the divergence of the advanced spiders (Araneomorphae) from the primitive spiders (Mygalomorphae) and the divergence of modern orb weavers (Araneoidea) from the primitive orb weavers (Deinopoidea) coincide with the evolution of two types of silk-producing glands, the major ampullate gland (MA) and the flagelliform gland (Flag). This suggests a link between silk protein evolution and spider evolution.

Figure 2. Eriauchenius species, lateral view, legs removed, showing elongated cephalic area. (Wood, 2007)An example of the significance of between-species variation is the convergent evolution that has occurred in ‘ assasin spiders’. In the Eriauchenius gracilicollis group, elongated cephalic area has evolved more than once. The ‘ assassin spiders’ found in Madagascar are unique due to the extreme elongation of the cephalic area and chelicerae. (Wood, 2007)

Significance of diversity between species