Explosive Speciation

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We present a theory of speciation induced by extinction. The rate of speciation should be different in different areas. There are a lot of species which resemble with each other ("genetic closeness"). It is thought that the speciation rate of these species has been very quick. Very recently, there has been a growing interest in the process of sympatric speciation. Theories heretofore have explained the process that a single species divides into two species, but they never account for the quick speciation rate. In the present work, we present a theory of explosive speciation.
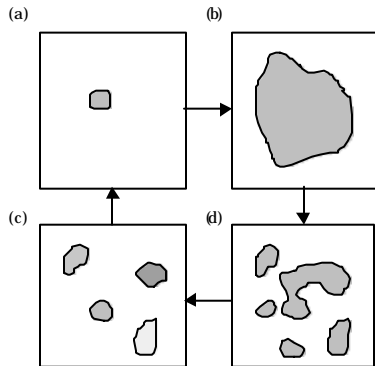

FIG. 1 Speciation process

In our model, speciation is caused by large environmental changes. When an environmental condition for a target species becomes rich, the species may have a large population size and many races (morphotypes or demes) [Fig. 1. (a) (b)]. However, if the condition becomes suddenly worse, a large contagious population may be segmented into smaller groups [(b) (c)], and many races will go extinct. In this case, both allopatric and sympatric speciation frequently occur (explosive speciation) [(c) (d)].

Consider a target species which has N races ($3 \leq N$). A couple of individuals may reproduce their offspring, even though they belong to different races. However, this does not always hold between some pair of races: when a pair of races are reproductively isolated, they cannot give birth to offspring. The reproductive isolation is mainly caused by two mechanisms. The first cause is a geographical hindrance (spatial isolation). The second cause is the sympatric hindrance.
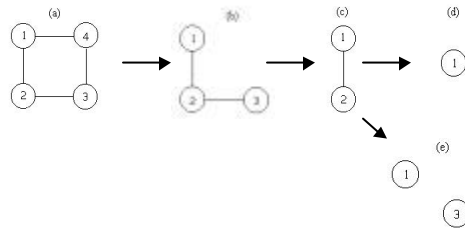

FIG. 2 Schematic illustration of polygon model for N=4.

Several models, such as polygon and star models, are possible to take into account the reproductive isolation in readiness. In this report, we mainly describe the result of polygon model. We locate N races on the vertices of polygon in order as illustrated in Fig. 2 (a). Each side (line) of polygon denotes that both ends of races of the line can reproduce their offspring. Since all races on a polygon are connected by lines, they belong to the same species. The speciation process is schematically displayed in Fig. 2.

Extinction process is performed in two different methods: individual-based model (IBM), and random extinction model (REM). Both models explains the quick speciation rate of species which have genetic closeness.
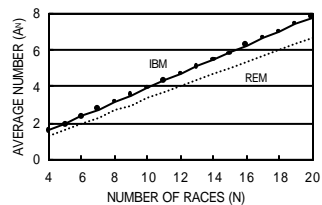

FIG. 3 The average number A_N of speciation is plotted against the initial number N of races.