

Discussion

Although a full analysis of the evolutionary implications of our findings will appear elsewhere, we offer here a preliminary historical interpretation of the reconstructed phylogeny of sister genera *Rhinoseius* and *Tropicoseius* (Fig. 39). Table 5 summarizes, by mite species, the biological origin of all specimens studied for this monograph, plus the origin of all other specimens for which the biological source has been reported by other workers. Two preliminary comments are needed to set the stage for this discussion. First, recall that neither host information nor biogeographical information was included among the characters used to reconstruct the mite phylogeny. Second, in this discussion, we consistently refer to *Rhinoseius* in Baker & Yunker's original sense, as indicated in the cladogram (Fig. 39) and in the systematic sections of this monograph.

The most striking and immediate inference that arises from a comparison of the cladogram (Fig. 39) with the data of Table 5 is that mites of this lineage are quite conservative with regard to host plant affiliation, at least at the level of host plant genera and families. A summary of the host affiliation data of Table 5 is mapped on the cladogram in Fig. 40.

Consider, first, the genus *Rhinoseius*. With the single exception of *R. tiptoni*, every species in the genus *Rhinoseius* for which host plant records exist has been collected from plants of the family Ericaceae. In contrast, none of the species of the genus *Tropicoseius* is known from ericads, except for a single specimen of *T. steini* n. sp. collected from *Ceratostema peruvianum*. Within *Rhinoseius*, species of the *richardsoni* group are known almost exclusively from ericads, whereas several members of the sister group *rafinskii* are somewhat less restricted, with some species found also in Gesneriaceae