



Figure 8.1. Locations of the 110 leaf litter collection sites. Grid lines are shown for every 20° of latitude (between 60°N and 60°S) and for every 20° of longitude.

continued until no further distinctions could be made. All point-mounted specimens were retained as vouchers. I drew upon my experience as an ant taxonomist to make judgments about the kinds of morphological discontinuities that would indicate the presence of two biological species. The morphospecies so designated can be thought of as working hypotheses about species identities, which can be independently assessed in the future by examination of the voucher specimens. Specific names were assigned where feasible (i.e., for taxonomically well-understood genera), but in many instances it was necessary to develop a system of code names for the species in a given geographical area (e.g., *Pheidole* BOL-32 for one of about 40 *Pheidole* species from eastern Bolivia). Such code numbers have local applicability only, and the task of reconciling the specific identities of code-named taxa from different geographic regions has not yet been completed.

Indeed, although sorting species from samples taken within the same geographical area is challenging and time consuming, such difficul-

ties pale in comparison to those that attend any attempt to resolve species identities over large geographical scales. As a result, this study is primarily about patterns of alpha diversity (i.e., geographical variation in *within-site* species richness) and about regional variation in faunal composition at higher taxonomic levels (genera, subfamilies). Large-scale measurements of species beta diversity (species turnover) remain constrained by insufficient taxonomic knowledge.

All the results reported here are based on workers only, although the presence of other castes was noted. For each sample the number of individual workers of each morphospecies was recorded. Variables of interest for each sample include the total number of workers and the numbers of species, genera, and subfamilies represented. Among the independent variables recorded for each sample were biogeographic region, habitat, latitude, longitude, and altitude (see Table 8.1). Latitude was converted to absolute decimal latitude for all statistical analyses.