

## Acknowledgments Preface

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The primary motivating force for preparing this book was the dramatic change in our understanding of angiosperm phylogeny during the past 10 years. Many long-standing views of deep-level relationships were altered suddenly and substantively as a direct result of molecular analyses. Many of the major angiosperm clades do not correspond to the classes, subclasses, and orders of modern classifications. For example, monocots (class Liliopsida) were derived from within a basal grade of families traditionally considered to be dicots (class Magnoliopsida). Hence, the long recognized monocot–dicot split does not accurately reflect phylogenetic relationships revealed by analyses of DNA sequence data. Furthermore, long-recognized subclasses of both monocots and “dicots” required revision or abandonment. Although significant differences exist among modern classifications at the ordinal level, clades identified by molecular analyses often fail to match the orders of any recent classifications. The circumscriptions of many families have also required modification for the same reasons.

As a result of the major modification in our understanding of angiosperm relationships, the usefulness of the classifications of Cronquist (1981) and Takhtajan (1997) has therefore declined, although these references are still widely consulted and are still a rich source of information. The Angiosperm Phylogeny Group’s (APG 1998; APG II 2003) reclassification of angiosperms, based on recent inferences of phylogeny, offers an alternative to the classification systems of previous decades. We follow the APG classification in this book. In addition, a wealth of recent data, coupled with our current understanding of phylogenetic relationships, permits reevaluation of many evolutionary hypotheses posed by Cronquist (1981, 1988), Takhtajan (1997), and Stebbins (1974).

Our major goals in this book are threefold. First, we provide a comprehensive summary of current concepts of angiosperm phylogeny. We then illustrate the profound effect that this phylogenetic framework has on interpretations of character evolution. It has not been possible to summarize all aspects of angiosperm evolution, of course, so we selected examples involving a diverse array of characters, including chromosomes, chemistry, and a sample of morphological features, especially floral and fruit characters. The coverage provided is meant to illustrate several

themes. For example, some chemical characters or pathways previously considered to have evolved many times have instead been demonstrated to have originated rarely in the course of angiosperm evolution. Conversely, other characters long thought to be of taxonomic utility are highly dynamic in their evolution. Finally, we point to inadequacies in current understanding of both phylogeny and morphology and to the need for additional study. We hope that our efforts will stimulate future research to identify morphological synapomorphies for DNA-based clades and to refine the hypotheses of angiosperm phylogeny and evolution presented here.

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