



FIGURE 27.10. Parsimony analysis. Two possible trees relating the sequences from Fig. 27.9 are compared. (*Left column*) Possible tree #1; (*right column*) possible tree #2. (*A,B*) Two possible trees. (*C,D*) Character states from alignment column #1 are overlaid onto the trees. (*E,F*) Possible ancestral character state reconstructions are shown for each tree. Character states are indicated on the tree for ancestral nodes. State changes are indicated by arrows. For tree #1, one reconstruction (*Ea*) requires only one character state change, whereas the other (*Eb*) requires two. Thus for this tree we would infer that only one character state change is required to fit the data in alignment column 1 to the tree. For tree #2, one reconstruction requires two state changes (*Fa*), whereas the other requires three (*Fb*). Thus for this tree we would infer that two character state changes are required to fit the data in alignment column 1 to the tree. Since tree #1 only requires a single state change, this tree would be favored as more parsimonious over tree #2.