FIGURE 13.12. Unique mutations in a nonrecombining DNA sequence can be used to reconstruct their genealogy. This example shows four sequences (nos. 2–5) sampled from a population, together with a more distantly related sequence (1) termed an **outgroup**. Each unique mutation defines a group of related sequences, or clade; for example, sequences 3, 4, and 5 all share an A→T substitution (*green*), which shows that they form a single clade, and sequences 4 and 5 share a G→C substitution (*dark blue*), which shows that they also form a clade. In this example, enough mutations have occurred that the genealogy can be reconstructed unambiguously. Mutations that occurred between the outgroup and sequences 2–5 are represented by *brown dots*. However, these are of no use in reconstructing the genealogy that relates 2–5. Only variable positions in the sequence are shown: In the full sequence, the great majority of sites would not vary. See Chapter 27 (online) for a full discussion.

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