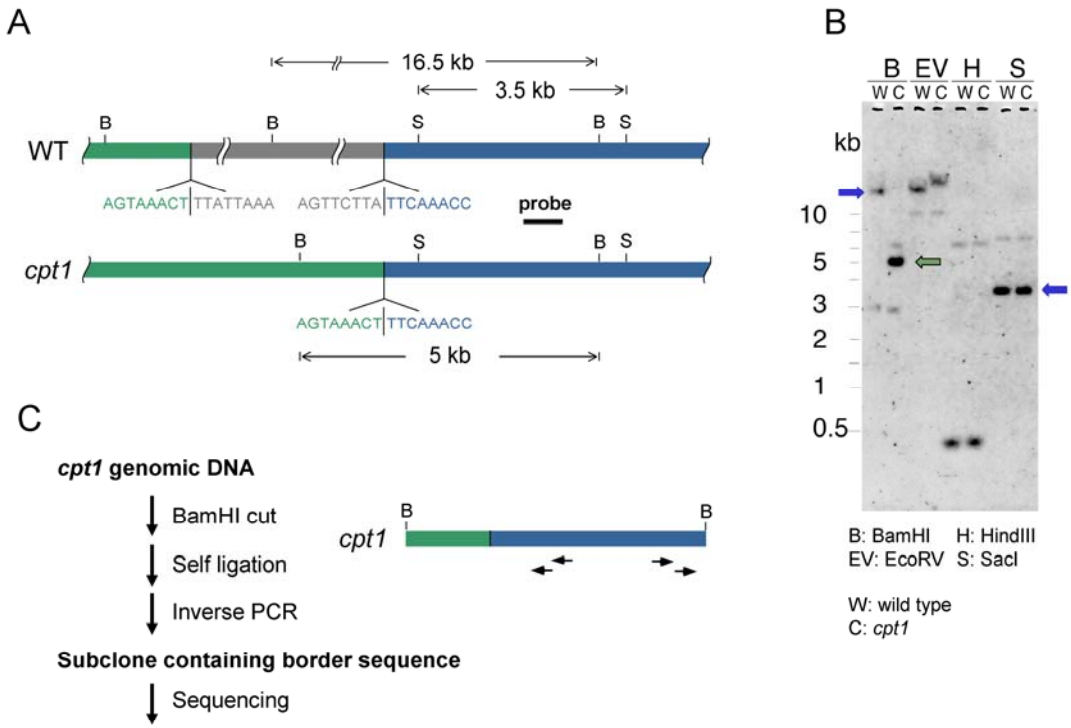

Figure 1. Identification by inverse PCR of the sequence deleted in the *cpt1* mutant. **A** Restriction map of genomic DNA encompassing the region deleted in the *cpt1* mutant (gray bar). The restriction map for the wild type (WT) is shown together with that for the *cpt1* mutant. Lengths of the restriction fragments that correspond to the hybridized bands in **B** (arrows) are indicated. B, BamHI; S, SacI. **B** Southern blot analysis with the probe indicated in **A**. Digestion with BamHI (B) gave hybridized bands of different lengths for WT (W, blue arrow) and *cpt1* (C, green arrow) while digestion with SacI gave a 3.5-kb band for both WT and *cpt1* (blue arrow). EV, EcoRV; H, HindIII. **C** Strategy for determining the border sequence. Inverse PCR was performed with nested primer sets indicated by arrows (see Methods for the primer sequences). By this analysis, the deletion indicated in **A** was determined.