Long-distance dispersal (LDD) pathogens pose challenges not only for modeling epidemic spread but also for inferring epidemic origins. We propose a two-stage modeling pipeline in which (i) spatiotemporal models of disease spread are fitted for discrete time transitions (forward model), and (ii) parameter estimates from the forward model inform a backward model that identifies a single epidemic source of high posterior probability by placing priors on the number (4, 8, or 16) and orientation (horizontal or vertical) of candidate source groups using a mixture modeling framework. We applied this method to a field experiment of wheat inoculated with stripe rust (Puccinia striiformis) and to accompanying simulations. In the field experiment, the backward model correctly identified the true source group in 94% of replicates under a prior of four larger source groups, decreasing to 82% with 16 smaller groups. Simulation results revealed modest bias in estimating forward-model regression parameters, but predictive accuracy of the backward model remained robust, particularly in early epidemic transitions (late May–early June) before plots were saturated with disease. This pattern was most pronounced when true sources lay near the border between candidate groups. While the current implementation assumes a single epidemic source, we note that epidemic outbreaks of LDD pathogens are more often composed of multiple sources. Our findings suggest that extending this framework to multiple-source epidemics represents a natural and necessary next step.