

Abstract

Penicillium expansum, *P. digitatum*, and *P. italicum* acidify the ambient environments of apple and citrus fruit during decay development. They use two mechanisms for this: the production of organic acids, mainly citric and gluconic, and NH_4^+ utilization associated with H^+ efflux. Exposure of *P. expansum* and *P. digitatum* hyphae to pH 5.0 increased their citric acid production, compared with the production of organic acids at acidic ambient pH. In decayed fruit, both pathogens produced significant amounts of citric and gluconic acids in the decayed tissue and reduced the host pH by 0.5 to 1.0 units. Ammonium depletion from the growth medium or from the fruit tissue was directly related to ambient pH reduction. Analysis of transcripts encoding the endopolygalacturonase gene, *pepg1*, from *P. expansum* accumulated under acidic culture conditions from pH 3.5 to 5.0, suggesting that the acidification process is a pathogenicity enhancing factor of *Penicillium* spp. This hypothesis was supported by the finding that cultivars with lower pH and citric acid treatments to reduce tissue pH increased *P. expansum* development, presumably by increasing local pH. However, organic acid treatment could not enhance decay development in naturally acidic apples. Conversely, local alkalization with NaHCO_3 reduced decay development. The present results further suggest that ambient pH is a regulatory cue for processes linked to pathogenicity of postharvest pathogens, and that specific genes are expressed as a result of the modified host pH created by the pathogens.