Acinetobacter spp. Among the most complex of pathogens (a “sordid past”), Acinetobacter spp. are highly diverse, oxidase- (+) and (-), Gram-negative coccobacilli. Resistance and virulence are being linked; systems biology approach may reveal a tight association. Many genes involved in resistance may have dual roles? (OMVs, ß-Lactamase different than others; OMP A, LpxC). Acinetobacter baumannii is undoubtedly one of the most successful pathogens responsible for hospital-acquired nosocomial infections in the modern healthcare system. Due to the prevalence of infections and outbreaks caused by multi-drug resistant A. baumannii, few antibiotics are effective for treating infections caused by this pathogen. To overcome this problem, knowledge of the pathogenesis and antibiotic resistance mechanisms of A. baumannii is important. In this review, we summarize current studies on the virulence factors that contribute to A. baumannii pathogenesis, including porins, caps An increase in prevalence of multidrug-resistant Acinetobacter spp. in hospitalized animals was observed at the Justus-Liebig-University (Germany). Genotypic analysis of 56 isolates during 2000–2008 showed 3 clusters that corresponded to European clones I–III. Results indicate spread of genotypically related strains within and among veterinary clinics in Germany. Within the genus Acinetobacter, A. baumannii is clinically the most relevant species, frequently involved in hospital outbreaks and affecting critically ill humans (1,2). The strains involved are usually multidrug resistant, which limits therapeutic options (3). Many outbreaks in Europe and beyond have been associated with the European clones I–III (4–6).