vaccines

MDPI

Review

Novel Candidates for Vaccine Development Against *Mycoplasma Capricolum* Subspecies *Capripneumoniae* (Mccp)—Current Knowledge and Future Prospects

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Abstract: Exploration of novel candidates for vaccine development against *Mycoplasma capricolum* subspecies *capripneumoniae* (Mccp), the causative agent of contagious caprine pleuropneumonia (CCPP), has recently gained immense importance due to both the increased number of outbreaks and the alarming risk of transboundary spread of disease. Treatment by antibiotics as the only therapeutic strategy is not a viable option due to pathogen persistence, economic issues, and concerns of antibiotic resistance. Therefore, prophylactics or vaccines are becoming important under the current scenario. For quite some time inactivated, killed, or attenuated vaccines proved to be beneficial and provided good immunity up to a year. However, their adverse effects and requirement for larger doses led to the need for production of large quantities of Mccp. This is challenging because the required culture medium is costly and *Mycoplasma* growth is fastidious and slow. Furthermore, quality control is always an issue with such vaccines. Currently, novel candidate antigens including capsular polysaccharides (CPS), proteins, enzymes, and genes are being evaluated for potential use as vaccines. These have shown potential immunogenicity with promising results in eliciting protective immune responses. Being easy to produce, specific, effective and free from side effects, these novel vaccine candidates can revolutionize vaccination against CCPP. Use of novel proteomic approaches, including sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), two-dimensional gel electrophoresis, immunoblotting, matrix-assisted laser desorption/ionization-time-of-flight (MALDI-TOF) mass spectrometry, tandem mass spectroscopy, fast protein liquid chromatography (FPLC), bioinformatics, computerized simulation and genomic approaches, including multilocus sequence analysis, next-generation sequencing, basic local alignment search tool (BLAST), gene expression, and recombinant expression, will further enable recognition of ideal antigenic proteins and virulence genes with vaccination potential.