PROSPECTION OF PROTEIN CANDIDATES FOR DRUG AND VACCINE DEVELOPMENT AGAINST STREPTOCOCCUS PNEUMONIAE INFECTIONS

SPECIAL INTEREST GROUP
DRUG-DESIGN

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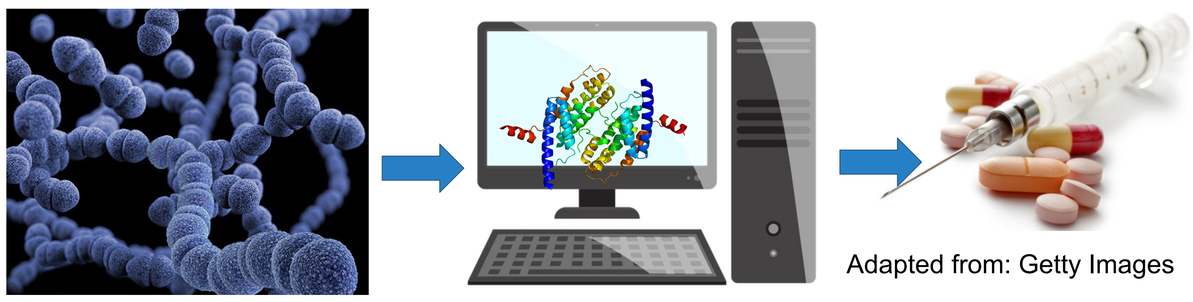
Introduction

Streptococcus pneumoniae is a Gram-positive, facultative anaerobic bacterium, and the most common cause of pneumonia, meningitis, bacteremia, and acute otitis media in humans. The World Health Organization estimates 1.6 million deaths per year due to invasive pneumococcal disease. Since 1980, isolation of strains which are resistant to several classes of antibiotics, such as beta-lactams and macrolides, has been reported.

Based on the pan-genomic analysis of *S. pneumoniae* and using bioinformatics tools, this work aims to identify proteins that could be used as targets in the development of new drugs and vaccines against this pathogen.



Adapted from: Getty Images

Results

Prediction of subunit vaccine candidates resulted in 6 highly immunogenic antigens shared by all strains analyzed. In addition, we obtained good quality three-dimensional structure models for 33 cytoplasmic proteins shared by all strains using the MHOLline workflow. Among the modeled proteins, 4 drug target candidates were found using the PBIT pipeline. The selection was made according to the involvement of protein in virulence and essentiality in bacteria, beyond the absence of homology with proteins from the human intestinal microbiota.

Acknowledgment

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Methods

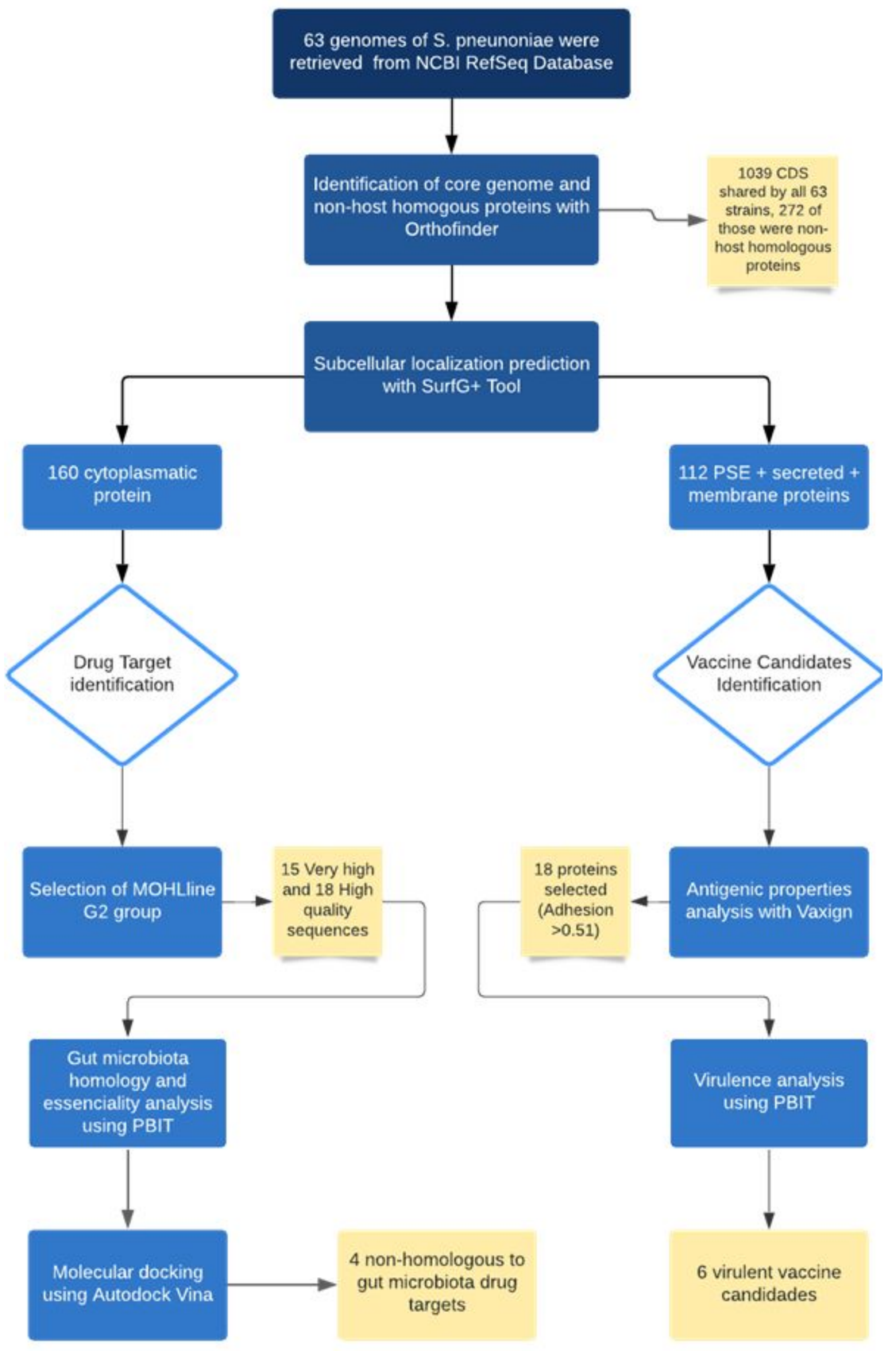

Figura 2: Structured workflow with the methodologies used and the total number of proteins identified in each step.

Conclusion

The present work brings up new perspectives to control the emerging and worldwide distributed S. pneumoniae infections in human. The 6 immunogenic proteins we screened are good candidates for a subunit vaccine against *S. pneumoniae* infections.

The structures of the 4 virulent cytoplasmic protein candidates will be used to screen potential drugs among a library of 5,000 natural plant compounds.