

## Report: Travel grant for training in a foreign institution

Carina Valente  
Laboratory of Molecular Genetics  
Instituto de Tecnologia Química e Biológica da Universidade Nova de Lisboa

### Background:

*Streptococcus pneumoniae* is an important pathogen and colonizer of the human nasopharynx. To date, there are 93 capsular types, or serotypes, described and since the complete sequence of all capsular types is available, a microarray-based method for capsular typing was developed, which includes the entire pneumococcal genome. Thus, this method is able to identify all capsular types and, more important, it is able to detect several serotypes in the same sample, as well as the relative proportions of each one of them.

### Objectives:

To learn the methodology and data analysis of microarray-based serotyping of *Streptococcus pneumoniae*

- To apply the method to Portuguese samples to detect multiple colonization in primary cultures of nasopharyngeal swabs taken from children in day care centers, as part of an
- ongoing collaboration between our group and the Bacterial Microarray Group at St. George's, University of London
- To discuss details related to a future publication, as the result of the collaboration mentioned above.

During the period that I worked at the Bacterial Microarray Group, St. George's, University of London I was able to learn how to perform microarray analysis for serotyping *Streptococcus pneumoniae*. First I was taught about the array design and its molecular basis for serotyping. Serotype determination was based on the homology group profile of the capsular genes present and on targeted discrimination of serotypes with identical homology group profiles. I was able to perform microarray analysis of 48 Portuguese nasopharyngeal samples suspected to be colonized by more than one pneumococcal strain.

Of the 48 samples suspected to be co-colonized, we identified more than one serotype in 43 of them (89.6%) and the number of strains in the samples ranged between 2 and 4. The array was able to assign a capsular type in all strains. The results obtained with the array were then confirmed by PCR serotyping or by the Quellung reaction when I returned to Portugal and the concordance of results was of 100%.

In the final days of my training we settled the details for a publication of the results of our collaboration and determined the lines for future work and future collaborations. Overall, I believe that this training was very important for me to understand a methodology that is an important component of the work I have been developing in the last few months and that will also be an important part of my PhD project.