

P1100 Genotypic differences in cc224, cc363, cc449 and cc446 of *Moraxella catarrhalis* isolates based on whole genome SNP typing, MLST and PFGEShu-Ying Yu¹, Liu Ya-Li², Yingchun Xu²¹ Department of Clinical Laboratory, Peking Union Medical College, Beijing, China, ² Department of Clinical Laboratory, Beijing, China**Background:** The better understanding of evolutionary path of the *Moraxella catarrhalis* from macrolide susceptible to resistant is crucial for controlling the spread of macrolide resistance.**Materials/methods:** A total of 472 *M. catarrhalis* isolates were collected from the adult and children patients (2010 to 2017). Macrolide resistance was detected by the Kirby-Bauer disk diffusion method. MLST were performed on all the 472 isolates. Specific clonal complexes were further analyzed by PFGE, *copB* typing, LOS typing, 16S rRNA typing and whole genome SNP typing (WGST).**Results:** A total 70 *M. catarrhalis* isolates were comprised of four main clonal complexes [CC224; CC363; CC446 (CCN08); CC449 (CCN10)] chosen for genetic differences study. Of which, 30 (42.9%) isolates were resistant to macrolide and only A2330T point mutation was detected. *CopB* I/III was detected in 55 isolates whilst *copB* II was in 15 isolates. All 70 isolates were in the lineage being 16S rRNA type 1. In each clonal complex, ST224 - B (LOS type) - I/III (*copB* type) - S (Macrolide susceptible), ST449-A-II-R, ST363-A-I/III-R, ST215-A-I/III-R, possessing 32% in CC224, 50% in CC449, 66.7% in CC363, and 53.8% in CC446, respectively. Furthermore, thirteen pairs or groups locate at 0.000 - 0.005 of evolutionary distance and 92.3% (12/13) of groups were considered as the same clones by using PFGE method and 100% (13/13) of groups have the same STs. Meanwhile, five groups locating at >0.005 - 0.010 of evolutionary distance correspond to 20.0% (1/5) and 80% (4/5) of groups having the same PFGE types and STs, respectively. In the evolutionary distance >0.010 - 0.015, 0.0% (0/6) and 66.7% (4/6) of groups having the same PFGE types and STs, respectively. The cut-off value for the four clonal complexes was very variable which varied with the group numbers.**Conclusions:** PFGE and WGST have a proper consistency of the same or closely related clones while MLST is less discriminative for different clones. All the four clonal complexes belonged to the *M. catarrhalis* lineage 1 which previously shown increased virulence potential and serum resistance. *CopB* II was highly related to CC449 and LOS type B was mainly gathered in CC224.