ANALYSIS OF METALLO-B-LACTAMASES FROM *CHRYSEOBACTERIUM* SPP. OF SOIL ORIGIN

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World Health Organisation has announced antibiotic resistance as one of the biggest global health problems [1]. Antibiotics are substances naturally produced by microorganisms to combat bacteria, and have been used in clinical settings since 1941 to treat bacterial infections. Due to reckless use of antibiotics, many pathogenic bacteria are becoming more resistant to them, causing hardly treatable diseases. Most widely used antibiotic class is β-lactams, the compounds targeting bacterial cell wall synthesis by inhibiting transpeptidation of peptidoglycan, resulting in death of the cell. Resistant bacteria often have enzymes called β-lactamases that degrade these antibiotics. Genes of various β-lactamases can be easily transferred from one bacteria to the other, accelerating the spread of resistance [2].

Many soil microbes are naturally exposed to antibiotics and thus, have developed resistance to the compounds over millions of years. Some soil dwellers can also cause infections to patients with a suppressed immune system, thus becoming opportunistic pathogens. For example, *Chryseobacterium* genus consists of common soil bacteria, which can also cause urinary tract infections, sepsis or bacteraemia. *Chryseobacterium indologenes*, the most virulent species in the genus, have started to be associated with urinary tract infections in 1996 but nowadays more species are discovered to cause a variety of diseases, spreading from Taiwan, the primary source of *Chryseobacterium* infections [3]. *Chryseobacterium* are known to have a genus specific IND β-lactamase, responsible for their resistance to β-lactams [4].

In our previous study we have discovered two β-lactamases from *Chryseobacterium* spp.: IND-like and an unknown metallo-β-lactamase (MBL). Both of them gave significant resistance to β-lactam antibiotics when transferred to *Escherichia coli*. MBL gene homologues are found in almost half sequenced *Chryseobacterium* genomes and the proteins share ~40% similarity to IND β-lactamases, which are more common and found encoded in almost 60% of sequenced *Chryseobacterium* genomes. The aim of this study is to characterise these novel β-lactamases, as none of the MBL homologues have been characterised yet and less than a half of IND β-lactamases have their biochemical activities determined [5].

[1] https://www.who.int/news-room/detail/17-01-2020-lack-of-new-antibiotics-threatens-global-efforts-to-contain-drug-resistant-infections
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