In many environments denitrifying bacteria are a major source of the potent greenhouse gas nitrous oxide (N$_2$O). These bacteria produce and consume the gas when carrying out the reduction of nitrates and/or nitrites to dinitrogen, this process being denitrification. In the environment N$_2$O becomes a problem when the net production of the gas exceeds that of the net consumption. However there is little known about what leads to this environmentally damaging situation.

The denitrification pathway in Paracoccus denitrificans has been well characterized, it consists of a variety of metalloproteins, one of which is a Cu containing enzyme N$_2$O reductase. In other denitrifying bacteria, such as Achromobacter xylosoxidans, the denitrification pathway consists of two Cu containing enzymes, N$_2$O reductase and also a Cu NO$_2^-$ reductase. The concentration of Cu is therefore vital in the complete reduction of NO$_3^-$ to N$_2$, however it is unknown how exactly Cu concentration affects the growth of denitrifying bacteria and the processes that reduce NO$_3^-$ to N$_2$. Cu depletion has been found in many agricultural soils, which are high in NO$_3^-$, and therefore this is potentially a major source of N$_2$O, this research is therefore to investigate into the affects that Cu has on various denitrifying bacteria. In understanding the metabolic processes in denitrifying bacteria we can have more of an insight into how we can suppress N$_2$O mitigation from agricultural soils.