1. *REVIEW OF LITERATURE*

1.1 *Magnaporthe oryzae*: Model organism to study host-pathogen interactions

Rice, wheat and maize contribute to approximately 40% of the available global cropland. Rice, staple food for more than three billion people, feeds almost half of the world's population. Over the past decade, rice production has doubled mainly due to improvements in cultivation practices and with the introduction of high yielding varieties and hybrids (Khush, 2005). The world population is predicted to increase to 9.6 billion by 2050, of which 86% of these populations is clustered in underdeveloped countries (Skamnioti and Gurr, 2009). There is a need to more than double global rice production by 2050; but it is constrained by farmland availability, soil fertility, climate change, water accessibility and plant diseases. Rice blast disease (Figure 1) has been found in more than 85 countries.

(Talbot, N.J., 2009)

Figure 1: Blast disease symptoms in rice. In rice seedling, small necrotic lesions appear initially which become larger and coalesce. The disease can also spread to neck and panicle. Neck blast can occur at nodes and neck region.

Between 10%-30% of the annual rice harvest is lost due to rice blast. Even a 10% loss is significant, as it is sufficient to feed approximately 60 million people for one year (Skamnioti

and Gurr, 2009). Since rice contributes about 23% of the calories consumed by the world population and is the most important food product in Asia, where 55% of the world's population lives and 92% of the rice is grown and consumed, it is crucial for food security (Wilson and Talbot, 2009). Hence, protection of rice from disease is of key importance for meeting the increased demands of global rice production. Considering the poor durability of many blast-resistant cultivars of rice, which have a typical field life of only 2-3 growing seasons before disease resistance is overcome, and increasing energy costs which affect fungicide and fertiliser prices, there is a need for better understanding of rice blast disease to combat this deadly crop destroyer (Ribot *et al.*, 2008). Increasing the efficiency of cereal cultivation through rice blast control programmes which can be set out as part of an environmentally sustainable plan are therefore urgently required (Wilson and Talbot, 2009).

Magnaporthe oryzae, a filamentous ascomycete fungus, is the causative organism for rice blast disease and has been defined as a new species, separate from *Magnaporthe grisea*, based on multilocus genealogy and mating experiments (Couch and Kohn, 2002).

Classification of *Magnaporthe oryzae*:

Domain	:	Eukaryota
Kingdom	:	Fungi
Phylum	:	Ascomycota
Subphylum	:	Pezizomycotina
Class	:	Sordariomycetes
Order	:	Sordariomycete sincertae
Family	:	Magnaporthaceae
Genus	:	*Magnaporthe*
Species	:	*oryzae*

Phylogenetic analysis divides *Magnaporthe* isolates into two clades, one that comprises *Digitaria* (crabgrass) infecting isolates of the fungus (*M. grisea*) and one that is associated with isolates capable of infecting rice, millets and other grasses, which was named *M. oryzae* (Couch and Kohn, 2002). The fungus is amenable to genetic and molecular manipulation (Jeon *et al.*, 2007; Talbot, 2003; Valent and Chumley, 1991) and consequently, as an outcome of its agronomic significance and tractability, it has emerged as a seminal model for the study of host-pathogen interactions (Dean *et al.*, 2005).

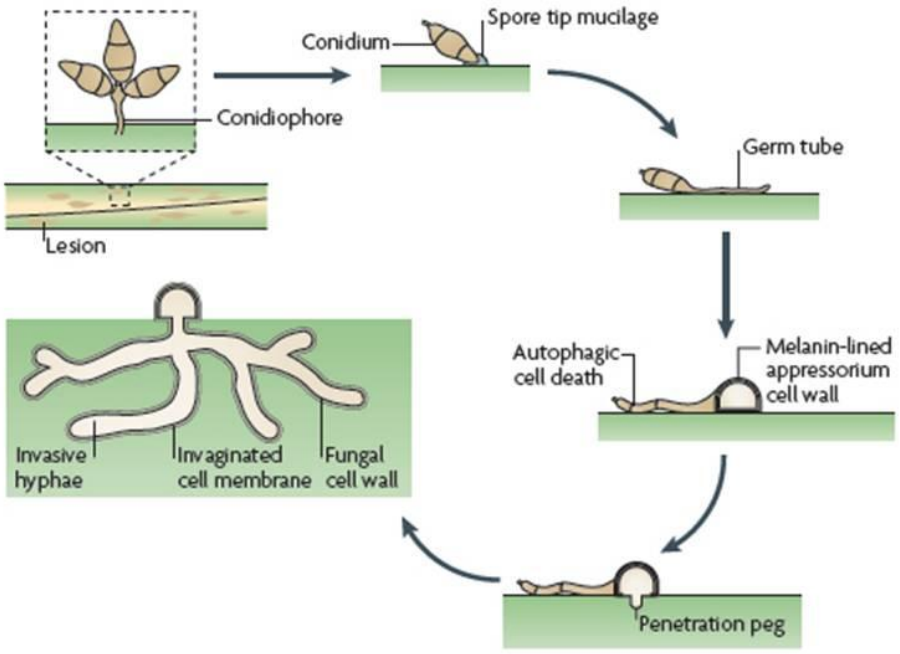
M. oryzae is a heterothallic fungus. There are two mating types of the fungus, *MAT1-1* and *MAT1-2*, and when sexually fertile isolates carrying opposite mating types are paired, they form sexual fruiting bodies called perithecia (Valent *et al.*, 1991). Perithecia are flask shaped bodies which carry ascospores, which are arranged as unordered octads. Carrying out crosses helps in following the segregation patterns of genetic markers and in the determination of the genetic basis of phenotypic traits (Valent *et al.*, 1991). The fungus can be readily transformed using a number of selectable markers or by introducing resistance to antibiotics such as Hygromycin B, Bleomycin, Bialophos, Sulphonylurea and Zeocin. Although transformation is not efficient (approximately 40 transformants are generated per microgram of transforming DNA), enhanced transformation frequencies can be obtained by using *Agrobacterium tumefaciens* Mediated Transformation (ATMT). The frequency of homologous recombination is only 20% of the total transformants, although the process is highly locus dependent (Talbot and Foster, 2001). Protein localisation is carried out with reporter genes and the cell biology of plant infection is well described.

M. oryzae reproduces asexually, using mitotically produced conidia that emerge from lesions on aerial plant parts. The fungus has a relatively small genome of ~40 Mb which is contained in 7 chromosomes (Dean *et al.*, 2005). In addition, the fungus is a non-obligate parasite and can be grown in a variety of culture formats away from the hosts. These features, of small

genome size and ease of growth in culture, have allowed the expansion of efficient technologies for mutagenesis and classical genetic analysis making *M. oryzae* one of the most genetically tractable plant pathogenic fungal species. Recently, *M. oryzae* topped the list among the top 10 fungal pathogens in plant pathology because of its economic significance and establishment as a model system for the study of host-pathogen interaction (Dean *et al.*, 2012). Also *M. oryzae*, shares many characteristics associated with other important cereal pathogens, such as appressorium formation and intracellular tissue invasion which opens up the possibility of finding disease determinants which can be targeted for broad spectrum crop disease intervention (Wilson and Talbot, 2009).

1.2 Infection cycle of *M. oryzae*

The conidia of *M. oryzae* initiate infection once they land on the hydrophobic leaf surface. These spores germinate upon contact with the host plant leaf, and adhere tightly to the leaf surface by means of spore tip mucilage that is released from the apex of the spore. Germination leads to the formation of a germ tube along the leaf surface which emerges from the conidium within an hour of its landing on the leaf surface. Within 4 hours, the germ tube starts to swell at its apex and develops into a swollen dome shaped structure, called the appressorium. Once formed, the appressorium matures and generates turgor (~8MP) by accumulating high concentrations of compatible solutes such as glycerol. The appressorium has a differentiated cell wall which is chitin-rich and contains a distinct layer of melanin between the cell wall and cell membrane, which acts as a barrier to the efflux of solute from the appressorium. Cellular turgor is translated into mechanical force, which is exerted by the emerging penetration peg, forcing it through the leaf cuticle (Figure 2).



(Talbot, N.J., 2009)

Figure 2: Infection disease cycle of *M. oryzae*. Infection cycle of *M. oryzae* is initiated when a three celled conidium lands on the rice leaf surface, produces a narrow germ tube following germination, which subsequently flattens and differentiates into appressorium. The appressorium develops substantial turgor which translates into mechanical force and a narrow penetration peg forms at the base, allowing the entry into the rice epidermis. Invasive hyphae forms which invaginate the rice plasma membrane and invade epidermal cells. Disease lesions occur between 72 and 96 hours after infection.

At the same time, the three-celled conidium undergoes autophagic programmed cell death, which is a pre-requisite for appressorium function and subsequent plant infection (Veneault-Fourrey *et al.*, 2006). *M. oryzae* enters plant tissue by direct penetration through the cuticle and cell wall using melanised appressoria. Inside the plant tissue, cell to cell invasion is accomplished by invasive hyphae (IH) (Giraldo and Valent, 2013). The host cells are initially invaded by narrow tubular primary hyphae which develop into bulbous IH. These bulbous IH are constricted at septal junctions (Giraldo *et al.*, 2013). During biotrophic invasion, *M. oryzae* secretes many low molecular weight biotrophy-associated secreted (Bas) proteins, including known effector proteins. These effector proteins fall into two categories, apoplastic effectors, which do not enter host cells and are retained within the extra-invasive hyphal membrane (EIHM) compartment, and cytoplasmic effectors which accumulate in the biotrophic interfacial complex (BIC), a membrane rich structure that initially appears close to

primary hyphal tips and later is positioned subapically as IH develop within the rice cells (Giraldo *et al.*, 2013).

Secondary infection hyphae subsequently develop and spread to adjacent epidermal cells, using plasmodesmata as a conduit for cell to cell movement. Up to this stage, the pathogen infection strategy is biotrophic. Lesion development ensues in the host once hyphal expansion spreads into mesophyll cells (typically 72 hours after infection) and as lesions become apparent, the fungus becomes more necrotrophic, and for this reason *M. oryzae* is a hemibiotroph. The fungus sporulates profusely from the lesions under conditions of high humidity, allowing the disease to spread rapidly to adjacent rice plants by wind and dewdrop splash. Single lesion caused by *M. oryzae* can produce 2,000 to 6,000 conidia per day for up to 24 days, resulting in multiple cycles of infection during a single growing season (Ou, 1987).

1.3 Signalling mechanisms contributing to infection related development

The ability of cells to receive and act on signals from beyond the plasma membrane is fundamental to life. In eukaryotic cells, Mitogen-activated protein kinases (MAPKs) bring together various cellular programmes in response to environmental signals. The *M. oryzae* genome encodes three MAPK cascades namely **P**athogenicity **MAPK** (***PMK1***), **MAP** kinase for **P**enetration and **S**porulation (***MPS1***) and **Os**moregulation **MAP kinase** (***OSM1***) which regulates appressorium development, penetration peg formation and adaptation to hyper osmotic stress (Figure 3). MAPKs are regulated by a MAPK Kinase or MEK (MAPK/ERK kinase), which in turn is activated by a third kinase termed as MAPKKK or MEKK (MEK kinase).

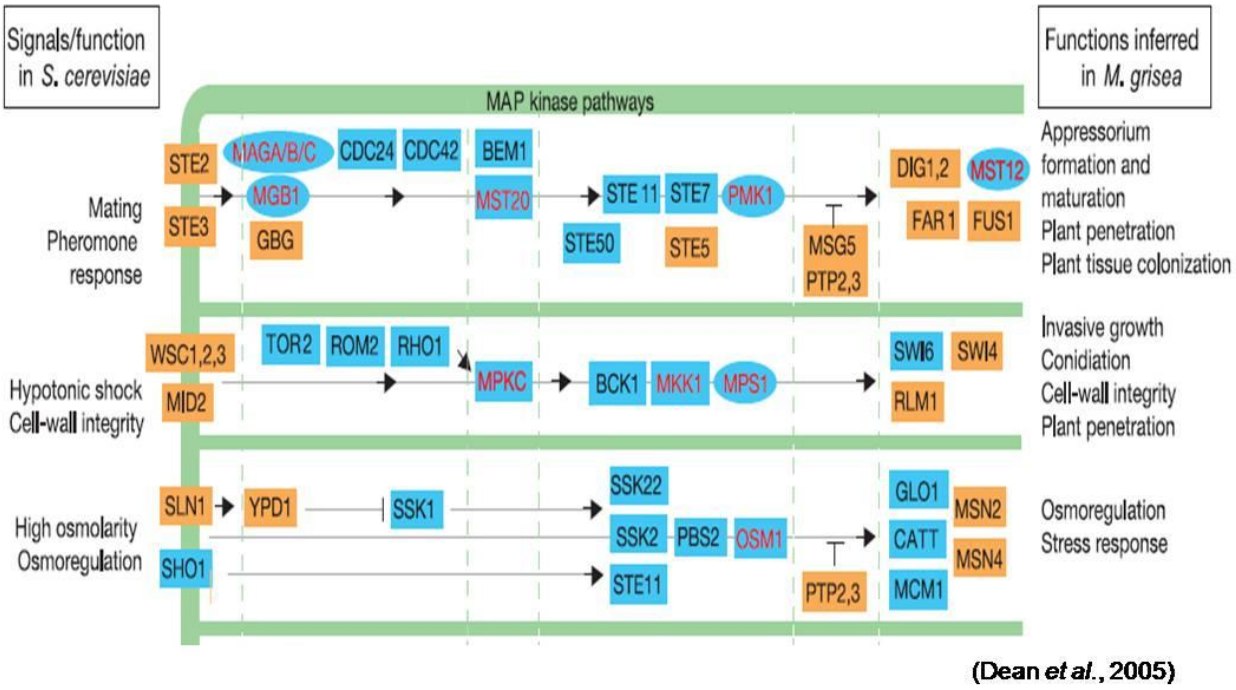


Figure 3: Comparison of major signalling pathways between *S. cerevisiae* and *M. oryzae*. The three core components of MAP Kinase which are *PMK1*, *MPS1* and *OSM1* pathways are conserved. Proteins names in red are previously identified *M. oryzae* homologues; names in black are *S. cerevisiae* proteins.

A cyclic AMP (cAMP) response pathway has been shown to be necessary for early stage of *M. oryzae* germ tube elongation. *MAC1* encodes adenylate cyclase and the mutants defective in *MAC1* gene are unable to form appressoria and hence are non pathogenic. Exogenous addition of cAMP restores appressorium development and pathogenicity in a *Δmac1* mutant (Choi and Dean, 1997). During germ tube extension, the hydrophobin gene, *MPG1*, is highly expressed and it provides a mean by which the fungus secures its attachment to the hydrophobic leaf surface (Talbot *et al.*, 1993). *Δmpg1* mutants are defective in appressorium formation and are poorly pathogenic because of absence of hydrophobins. Application of cAMP to *Δmpg1* mutants restores appressorium formation, which suggests that the *MPG1* gene is positively regulated by the cAMP dependent protein kinase A (PKA) pathway (Soanes *et al.*, 2002).

The Pmk1 MAPK pathway is a functional homologue of *FUS3*/*KSS1* in budding yeast, which is vital for pheromone signalling and pseudohyphal growth. This pathway has been explored

in great detail in *M. oryzae* and it has been shown to be essential for regulation of formation of the infection structure. Mutants lacking *PMK1* (*Δpmk1*) do not form appressoria, fail to cause blast lesions on rice plants and hence are non pathogenic. *Δpmk1* mutants respond to exogenous cAMP undergoing terminal swelling of the germ tube tip (Caracuel-Rios and Talbot, 2007). *PMK1* has been shown to be one of the major regulators controlling various targets which are essential for both the initiation of appressorium development and invasive growth.

In *S. cerevisiae* Protein kinase C activated MAPK, Slt2/Mpk1, controls cell growth in response to membrane stress. *Δslt2* mutants exhibit defects in cell wall integrity and an inability to grow at elevated temperatures in the absence of osmotic stabilisers (Costigan *et al.*, 1992; Davenport *et al.*, 1995). The homologous MAPK pathway in *S. pombe* also plays a role in the maintenance of cell wall integrity (Zaitsevskaya-Carter and Cooper, 1997). *MPS1* in *M. oryzae* is essential for plant infection; *Δmps1* mutant has a defect in appressorial penetration and is non-pathogenic, suggesting that penetration of the plant surface requires remodeling of the appressorium wall through a Mps1 dependent signalling pathway (Xu *et al.*, 1998).

1.4 Biochemistry of Mg^{2+}

The magnesium cation, Mg^{2+}, is fundamental for biological functions. Contribution of magnesium ions (Mg^{2+}) in various metabolic processes is governed not only by their relative amount in the cell but also by their physiochemical properties. The ionic radius of Mg^{2+} is much smaller than those of K^+, Na^+ and Ca^{2+}, while its hydrated radius is largest of all the cations. Mg^{2+} has higher affinity for oxygen donor ligands (negatively charged carboxylates and phosphates) in comparison to Ca^{2+}. Mg^{2+}-H_2O coordination (octahedral conformation) is

much bigger and more stable than Ca^{2+} in biological system. These properties make Mg^{2+} biochemically active.

Magnesium is not only one of the most abundant metal ions present in the earth's crust, but is also the most abundant divalent cation in sea water with a concentration of ~50 mM. Magnesium is the most abundant divalent cation in cells, where it is essential for a wide range of cellular functions. Mg^{2+} levels within the cell range from 15 to 25mM (Moomaw and Maguire, 2008). However, only 0.4 to 0.5mM ions are in the form of free cytosolic Mg^{2+} as most ions are bound or incorporated into cellular components. In plants, Mg^{2+} is particularly important for photosynthesis and approximately 15-20% of total leaf Mg is in chlorophyll.

Intracellular Mg^{2+} concentrations are regulated by various processes which involves Mg^{2+} uptake, movement of Mg^{2+} into cellular storage compartments and Mg^{2+} efflux (Figure 4).

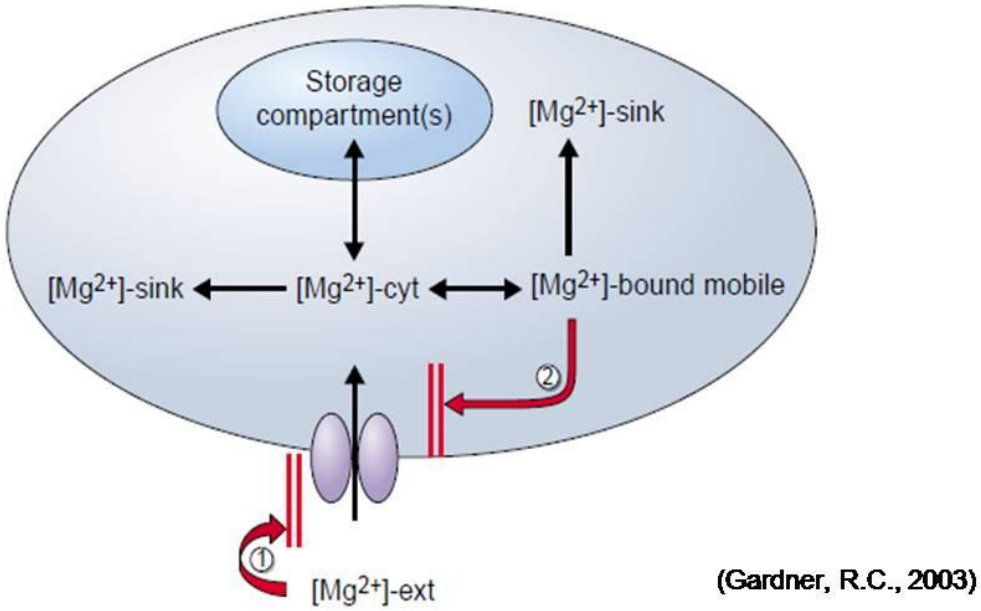


Figure 4: Control of Mg^{2+} homeostasis. (A) Model of cellular Mg^{2+} homeostasis. [Mg^{2+}]-ext is free Mg^{2+} outside the cell, [Mg^{2+}]-cyt is free Mg^{2+} inside the cell, [Mg^{2+}]-bound mobile is Mg^{2+} bound to ATP or GTP, and [Mg^{2+}]-sink is for cellular Mg^{2+}. Vacuole usually acts as storage compartment in the plant cells. In yeast (arrow 1), Mg^{2+} uptake is reduced by degradation of ALR1 uptake protein when external Mg^{2+} levels are high. In mammals (arrow 2), increased intracellular concentrations of Mg^{2+}-ATP inhibit Mg^{2+} uptake by Mg^{2+} channels (LTRPC7).

Magnesium is essential for maintenance of cellular integrity which includes structural stabilisation of nucleic acids, polynucleotides, chromosomes, polysaccharides and lipids.

Mg^{2+} governs adenylate cyclase activities and in turn regulates cAMP synthesis. Maintenance of intracellular levels of Mg^{2+} is critical considering Mg^{2+} is vital for DNA replication and protein synthesis, DNA repair proteins (as a cofactor), and maintenance of the anti-oxidative status of the cell. Its level has effects on cell cycle progression and apoptosis. It has been estimated that ~90% of Mg^{2+} within cells is bound to ribosomes and polynucleotides (Cowan, 1995). Mg^{2+} is an essential co-factor for multiple enzymatic reactions. Mg^{2+} is essential for the maintenance of membrane stability (Cowan, 1995). Mg^{2+} and Ca^{2+} form complexes with the phosphorylated and carboxylated head groups of the phospholipids and neutralise the charge.

In the fission yeast *Schizosaccharomyces pombe* and the budding yeast *Kluyveromyces fragilis*, the role of magnesium ions in cell division cycle control has been shown, where intracellular levels of Mg^{2+} regulate the timing of cell cycle progression (Walker and Duffus, 1980). In the human pathogen *Candida albicans*, Mg^{2+} is required for germ tube formation in vegetative cells, where germ tube formation coincides with a peak in the intracellular Mg^{2+} levels, consequently affecting its morphogenesis and pathogenicity (Walker *et al.*, 1984).

1.5 Regulation of genes by Mg^{2+}

Mg^{2+} has been shown to regulate gene expression in *Salmonella enterica* serovar Typhimurium, as well as in many other gram negative bacteria including *Escherichia coli*, where Mg^{2+} deprivation leads to expression of the PhoP/PhoQ two component regulatory system (Garcia-Vescovi *et al.*, 1996). *phoP* and *phoQ* encode the regulator and sensor proteins respectively and the PhoP/PhoQ regulon controls several pathogenic properties of *S. typhimurium*. It has been established that Mg^{2+} is a signal which controls the PhoP/PhoQ regulon that responds to extracellular Mg^{2+}; growth in the presence of millimolar levels of

Mg^{2+} down-regulates the expression of PhoP activated genes and also attenuates the virulence properties of *Salmonella* (Garcia-Vescovi *et al.*, 1996).

Mg^{2+} starvation in rats has been shown to lead to elevated expression of genes involved in oxygen stress in thymocytes (Petrault *et al.*, 2002). In *Saccharomyces cerevisiae*, genes responsive to Mg^{2+} deprivation include *ENA1* (encoding a P-type ATPase sodium pump) and *PHO89* (encoding a sodium/phosphate co-transporter), which are up-regulated under Mg^{2+} deprivation. This effect is mediated by induction of the transcription factor Crz1p, which leads to activation of the Crz1p/calcineurin pathway (Wiesenberger *et al.*, 2007).

1.6 CorA Mg^{2+} transporters

The molecular identity, function and regulation of Mg^{2+} transporters have been studied to understand the basis of Mg^{2+} homeostasis in eukaryotic cells. The CorA (or Metal Ion Transporter) superfamily is an important group of Mg^{2+} transporters in both prokaryotes and eukaryotes (Lim *et al.*, 2011). Mg^{2+} transporters were for the first time identified in bacteria in *E. coli* (Lusk and Kennedy, 1969) and it was established that Mg^{2+} transport could be inhibited by Co^{2+} (Nelson and Kennedy, 1971). Later it became evident that *E. coli* has two Mg^{2+} transport systems, one being repressed by high Mg^{2+} levels and unaffected by Co^{2+}, while the other was non-repressible and could mediate Co^{2+} uptake. This became evident by generation of $\underline{Co}^{2+}$ resistant (*cor*) mutants which survived lethal concentrations of Co^{2+} (Nelson and Kennedy, 1972).

CorA proteins which are integral membrane proteins constitute the major Mg^{2+} uptake system in *Eubacteria* and *Archea*. CorA proteins are unrelated to any other cation transporter family identified so far. They are characterised by two predicted transmembrane domains, which are separated by a short loop oriented to the outside of the membrane, and a GMN W/F motif at the end of the N-terminal of one of these two transmembrane domains, frequently followed by a MPEL motif in the loop sequence (Schweyen and Froschauer, 2007).

In bacteria, three proteins, CorA, MgtA and MgtB, have been shown to be involved in Mg^{2+} transport across the plasma membrane. The bacterial MgtA and MgtB Mg^{2+} transport systems belong to the P-type ATPases, which are regulated by the two component signal transduction system PhoPQ, which in turn is subject to regulation by Mg^{2+}. The MgtA and MgtB systems only transport Mg^{2+} and Ni^{2+} and extracellular Mg^{2+} down regulates the expression of these transporters (Snavely *et al.*, 1989).

Homologues of the bacterial CorA Mg^{2+} transporters have also been identified in eukaryotic systems and nearly all eukaryotic genomes encode distant relatives of CorA. Eukaryotic CorA proteins have diversified in function, facilitating both Mg^{2+} uptake and distribution between sub-cellular compartments. The **Al**uminium **R**esistance (***ALR1***) and *ALR2* genes in *S. cerevisiae* encode the Mg^{2+} transporters and were the first to be characterised in a eukaryotic system. The Alr proteins and their fungal counterparts show high similarity to CorA proteins in the region of the two TM domains, including the conserved GMN sequence. Loss of function of **Alr1** results in a dependence of yeast cells on high extracellular Mg^{2+} and leads to a reduction in intracellular levels of Mg^{2+}. These growth defects of Alr1 are restorable by Mg^{2+} supplementation (Graschopf *et al.*, 2001; MacDiarmid and Gardner, 1998). In *S. cerevisiae*, expression and turnover (via endocytosis and vacuolar decay) of Alr1 has been shown to be tightly controlled by Mg^{2+}. Disruption of ***ALR2*** does not affect the viability of *S. cerevisiae*, but its over-expression suppresses the growth phenotype of *Δalr1* mutant cells. *ALR2* is poorly expressed in yeast and makes only a minor contribution to Mg^{2+} homeostasis (Pasternak *et al.*, 2010).

A genetic screen for proteins affected in splicing of group II introns in *S. cerevisiae* mitochondria led to the identification of **Mrs2**, present in the inner membrane of mitochondria (Schindl *et al.*, 2007). Mrs2 has very low similarity to CorA proteins, but homologues of the yeast Mrs2 are found in most eukaryotic genomes. The human genome

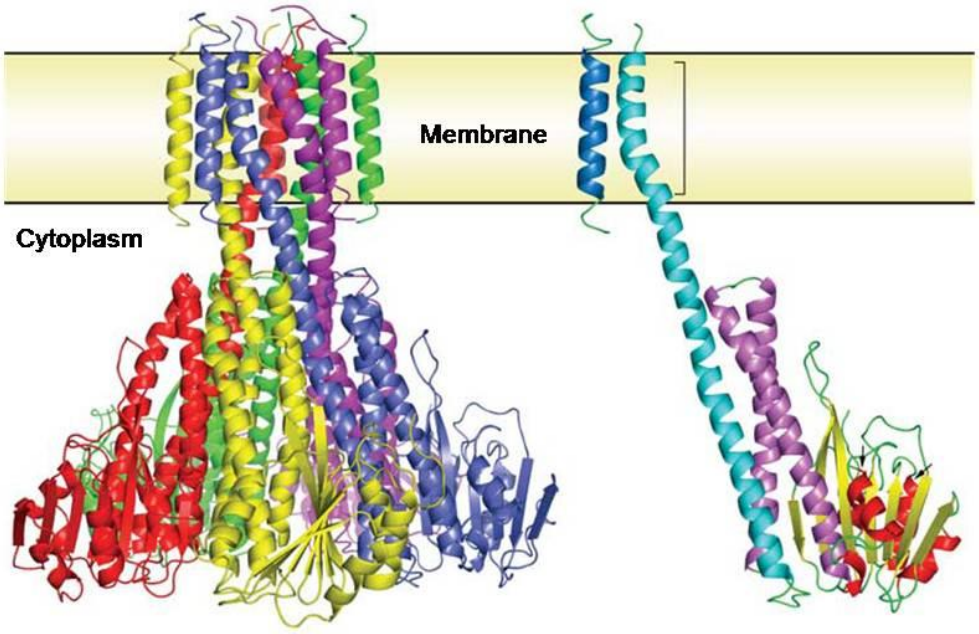
encodes a single functional Mrs2 which codes for a mitochondrial protein. The *Arabidopsis thaliana* genome encodes 15 CorA related genes, most of which are Mrs2-like and are present either in mitochondria, in the plasma membrane or in other cellular organelles (Li *et al.*, 2001). Mrs2 acts as a mitochondrial Mg^{2+} uptake system, as evident from *Δmrs2* mutant cells, which displayed defects of mitochondria associated with RNA splicing defects, and reduced Mg^{2+} levels in the mitochondria (Schindl *et al.*, 2007). These defects were restored with Mg^{2+} supplementation. The activity of the Mrs2 protein was also shown to be dependent on Mg^{2+} concentrations. In *S. cerevisiae* **Lpe10**, another homologue of Mrs2, is also present in the inner mitochondrial membrane. Deletion of *LPE10* results in a petite phenotype, exhibiting a respiratory growth defect on non-fermentable carbon sources. Both Lpe10 and Mrs2 have been shown to be crucial for the transport of Mg^{2+} into mitochondria of *S. cerevisiae*, as the proteins cannot substitute for each other (Sponder *et al.*, 2010).

Mnr2, a fifth CorA homologue in *S. cerevisiae*, is a vacuolar membrane protein which is required for access to intracellular Mg^{2+} stores (Pisat *et al.*, 2009). The protein shares the two predicted transmembrane domains and conserved GMN motif but has a tryptophan residue preceding the GMN motif in place of conserved phenylalanine.

All five of these proteins are members of the **M**etal **I**on **T**ransporter (**MIT**) superfamily, the founder member of which is CorA from *Salmonella typhimurium*. MIT proteins accomplish rapid, membrane potential-dependent transport, suggesting that they form Mg^{2+} selective channels. MIT proteins possess two conserved features: a pair of transmembrane domains close to the carboxy terminus and the conserved residues GMN that are essential for Mg^{2+} transport. Members of each of these subfamilies have been shown to form oligomeric membrane complexes mediating electrogenic uptake of Mg^{2+} (Schweyen and Froschauer, 2007). The first crystal structure of a CorA transporter from *Thermotoga maritime* was

determined (Lunin *et al.*, 2006) which showed that the transporter is a funnel shaped homopentamer with two transmembrane helices per monomer.

It has five fold symmetry about a central pore (Figure 5) and the cytoplasmic domain forms the funnel whose wide mouth points into the cell and whose walls are formed by five long helices (Lunin *et al.*, 2006).



(Lunin *et al.*, 2006)

Figure 5: Structure of CorA Mg^{2+} transporters. Ribbon diagram of the CorA pentameric complex. On the right is single unit of the CorA channel.

X-ray crystallographic studies have shown no conformational differences of CorA transporters between Mg^{2+}-bound and Mg^{2+}-free conditions, while **E**lectron **P**aramagnetic **R**esonance (**EPR**) spectroscopic studies show Mg^{2+}-driven quaternary conformational changes. Recently, 3D structures of CorA protein in its Mg^{2+}-bound and Mg^{2+}-free conditions showed closed and open conformations respectively through single particle cryo-EM (Matthies *et al.*, 2016) (Figure 6A).

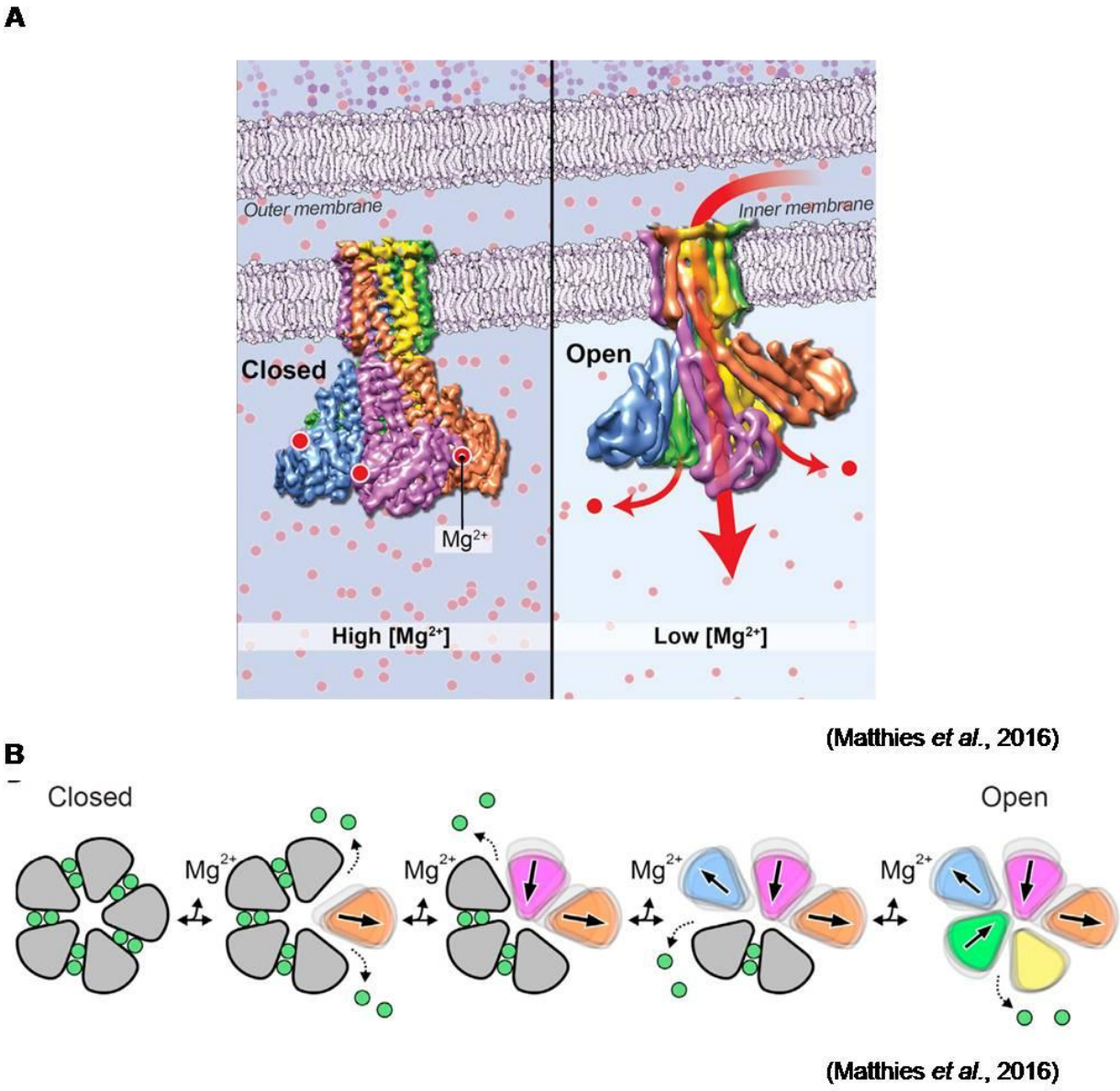


Figure 6: Cryo-EM structure and schematic model for the asymmetric opening of CorA Mg^{2+} transporter. (A) Cryo-EM structure of the closed and open state of Mg^{2+} channel CorA shows a loss of symmetry within the cytoplasmic domain under conditions of low concentrations of Mg^{2+}. (B) Mg^{2+} stabilizes neighboring subunits in the closed state. When Mg^{2+} level drops, Mg^{2+} ions between subunits are progressively and randomly removed. Once the first inter-protomer interface is disrupted, movements of the rest of the protomers are in a predictable sequence.

Cells and organelles have mechanisms to control intracellular and intraorganellar [Mg^{2+}] either through proteins involved in Mg^{2+} uptake processes or H^{+}/Mg^{2+} exchange or anion/Mg^{2+} co-transport (Beyenbach, 1990). Members of the CorA family appear to be capable of moving Mg^{2+} both into and out of the cell (Gardner, 2003). Experimental evidence suggests that Mg^{2+} homeostasis through CorA takes place via a negative feedback loop, where

Mg^{2+} binding leads to channel closure, whereas low Mg^{2+} concentrations tend to promote the transition to the open, conductive state (Dalmas *et al.*, 2014; Pfoh *et al.*, 2012) (Figure 6B).

As a divalent cation, Mg^{2+} neutralises charged residues to provide stability to cell membrane, DNA and ribosomes. It also acts as a co-factor for a number of enzymes, and therefore affects numerous biochemical reactions within the cell. The role of CorA transporters mediating Mg^{2+} transport and distribution are well studied in *S. cerevisiae* and recently have been documented in *Arabidopsis*. However, Mg^{2+} transporters in filamentous fungi have not been studied extensively. In filamentous fungus *Podospora anserina*, PaAlr1 Mg^{2+} transporter has been shown to be required for ascospores development (Grognet *et al.*, 2012). In *Aspergillus fumigatus*, role of MgtC (magnesium transporter), a homologue to bacterial virulence factor, was studied under magnesium limiting conditions (Gastebois *et al.*, 2011). In *M. oryzae*, studies of how metal ions affect signal transduction pathways regulating development and infection have been largely limited to calcium signalling. The role of CorA Mg^{2+} transporters in *M. oryzae* metabolism was unexplored. In the present work, we investigated the effect of depletion of CorA Mg^{2+} transporters on development and infection in *M. oryzae*.

Present Study: CorA Magnesium Transporters in growth and pathogenicity of the rice blast fungus *Magnaporthe oryzae*