The spliceosome is a large multi-megadalton RNA-protein machine which facilitates the removal of introns from eukaryotic nascent pre-mRNAs by two concerted transesterification reactions. The spliceosome is comprised of five UsnRNPs and several non snRNP components whose assembly and role in spliceosome catalytic activation have been well studied in budding yeast *S. cerevisiae* and mammalian systems. Spliceosome assembly involves formation of several ordered compositional and structural distinct complexes a process that is typified by the making and disruption of RNA-RNA, RNAprotein and protein-protein interactions. This pathway serves to define the splice-sites for each of the reactions, assist in catalysis and aids in fidelity of splice-site selection. *in vitro* studies with budding yeast *S. cerevisiae* (budding yeast) and mammalian cell free extracts together with experiments using plasmid expressed mini-transcripts elucidate discrete functions for DExD/H RNA helicases proteins in spliceosome assembly, catalytic center formation and disassembly (Staley and Guthrie, 1998). These splicing factors also ensure the fidelity of splice-site selection by kinetic proofreading of intronic *cis* elements- the 5'splice-site, the branch consensus sequence and the 3'splice site (Burgess and Guthrie, 1993; Mayas et al., 2006; Xu and Query, 2007; Yang et al., 2013). Thus the DExD/H proteins are indispensable for the generation of a functional transcriptome.
While the splicing reactions and nearly all factors of the spliceosome are conserved across eukaryotes, exon-intron architectures vary greatly in diverse species. The short intron length and degenerate intronic elements are features common to several other fungi and metazoans. Studies on *Schizosacharomyces pombe* (fission yeast) which bear such intronic features and splicing factors with greater sequence similarity to higher eukaryotes than *S. cerevisiae* offers the potential to understand a more common splicing mechanism (Kaufer and Potashkin, 2000; Kuhn and Kaufer, 2003). The spliceosome assembly pathway is presumably fine-tuned so as recognize and splice introns from pre-mRNAs with very diverse exon-intron architectures. In *S. cerevisiae* and humans the splicing factors Slu7 and Prp18, interact and act at the second splicing reaction for 3' splice site selection. While in *S. pombe* reports from our laboratory have found early splicing roles for SpSlu7 and SpPrp18, lack of mutual interaction and altered genetic interactions with other spliceosomal factors (Banerjee et al., 2013; Geetha Melangath, Thesis). Moreover, mutations of intronic *cis* elements like the 5'ss dinucleotide GU or in the 3'ss PyAG in at least a model *S. pombe* intron arrests splicing prior to first catalysis (Romfo et al, 2000; Romfo and Wise 1997; Alwarez and Wise 2001). Thus understanding functions for premRNA
splicing of fission yeast will allow for understanding splicing mechanisms relevant to many fungal introns and metazoans. The DExD/H helicases in the context of fission yeast splice-site recognition and spliceosomal interactions are largely unexplored. Here we probed into the role of fission yeast Prp16 by using a combination of molecular, genetic and biochemical approaches and our key findings are summarized below. We demonstrate its vital functions in the splicing of a vast majority of *S. pombe* introns, its interactions with intronic branch nucleotide and other splicing factors. We also provide compelling evidences of its influence on other cellular processes like cell cycle progression and heterochromatinisation.