Zip1 M Region Phosphorylation Patterning: Implications for Effective Meiosis

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Understanding phosphorylation of Zip1's M region can elucidate required meiotic mechanisms. The study focused on understanding the phopsholitic importance of suspected critical serines: 512,514,515,546,593, and 678 via aspartic acid (D) and alanine (A) mutations and their effects on sporulation. Zip1 was deleted from Brockville (BR) strains: 1919-8D and 1373-6D; transformed strains were mated to form NH2225 diploids which were further transformed to possess the phosphomutations; tetrads, triads, and diads were counted as evidence of sporulation. Novel and desired alanine and aspartic acid mutations were present. NH2225::Zip1 Mutants were effectively selected via nutrient-deprivation-agar methods, suggesting an unrecorded recessive mutant allele in the BR1919-8D and BR1373-6D strains. Results indicate that time does not affect M region activity. The study pinpoints that serines 546 and 593 are likely substrates of the Mek1 and Cdc7 required pathways to ensure healthy meiosis. Thus, the study was novel as two new substrates of this pathway were suggested. Furthermore, the study suggets that serine 678 is not part of the meiotic segregation pathway, as its alanine mutants consistently had higher sporulation rates than the aspartic acid mutants ($p < .05$). The relevance of serines 512, 514, and 515, however, is still unclear as the aspartic acid and alanine mutants consistently had insignificantly differing sporulation rates ($p=.70$). Future investigations include performing antibodies and colocalization studies to determine whether Mek1 and Cdc7 are ever present near Zip1 S546 and S593 to further corroborate their phosphorylative potential. The study lays the required foundation to find more effective treatment to genetic and birth abnormalities.