During seed development DNA methylation is partially controlled by the small RNA-directed DNA methylation (RdDM) pathway. In RdDM, small interfering (si)RNAs, which are abundant in gametophytes and developing seeds, are produced by processing transcripts from RNA Polymerase IV. These siRNAs interact with Pol V transcripts via complementary base-pairing, thereby targeting methylation machinery to proximal regions of the genome, a process critical for proper expression of imprinted genes. *Arabidopsis thaliana* RdDM mutants show no obvious reproductive defects; however, *Brassica rapa* RdDM mutants show a significant reduction in seed set and seed weight. Two major differences between *A. thaliana* and *B. rapa* are breeding system and ploidy. *A. thaliana* is a primarily selfing species with a diploid genome, while *B. rapa* is an outcrosser whose genome reflects a mesohexaploid expansion. We hypothesized that RdDM may be more critical in *B. rapa* because methylation is mediating 1) conflicts between maternal and paternal genomes (imprinting), and/or 2) conflicts among subgenomes (genome dominance). To distinguish between these alternatives, we used a comparative evolutionary approach by characterizing RdDM mutants in three additional Brassicaceae species that vary in breeding system and genome copy number. We established mutant lines for each of these species for two genes critical to the RdDM pathway. Mutant plants exhibited significant differences in seed set and seed weight between the wildtype and mutant lines in our obligate outcrosser, *Capsella grandiflora*, but not in its self-compatible sister-species, *C. rubella*. These results indicate that RdDM is involved in mediating parental genome interactions in outcrossing species in Brassicaceae.