Judd, Shen and Kaufman (in press) have derived 116 lethal and semi-lethal recessive point mutations that map between z (3A3) and w (3C2) on the X chromosome of Drosophila melanogaster. These zw (zeste-white) mutations have been arranged into 12 complementation groups which correspond on a one to one basis to the 12 salivary gland chromosome arms in this region. The genetic sequence from z to w of the complementation groups (designated by number in the order of discovery) is zw1, zw8, zw4, zw10, zw2, zw3, zw6, zw2, zw7, zw5, zw11, zw9. By use of mutant males marked with the gene y, we have determined the lethality patterns of 42 mutants representing all zw complementation groups. (The lethality pattern of a mutant includes both its effective lethal phase (see Hadorn, 1955) and observations on its rate of growth and longevity.)

Mutants within a given complementation group have similar lethality patterns, as would be expected for members of an allelic series. The zw mutants are primarily post-embryonic in time of death, with the highest concentration of mortality occurring in the larval period (cf. Oster, 1952, 1954; Rizki, 1952; Seto, 1954). One group (zw2) is characterized by late embryonic-early larval "boundary lethality" (Hadorn, 1951). Three groups (zw6, zw12, zw5) show monophasic first instar lethality, and one group (zw7) shows diphasic first and second instar lethality. The remaining groups exhibit varying degrees of polyphasic lethality.

Semi-lethal mutants show polyphasic lethality, even if lethal mutants within the same complementation group are monophasic in time of death. Our observations generally support the concept of the phase specificity of lethal factors (Hadorn, 1948, 1951, 1955); i.e., critical (lethal) phases are interspersed with relatively insensitive periods when deaths rarely occur. The zw mutants resemble other lethal Drosophila mutants in that they usually live for a considerable time after development has ceased (cf. Hadorn, 1955).

Phenogenetic studies (Kaufman, 1970) reveal that members of each zw complementation group also have similar morphological and cellular autonomy characteristics. We infer that the mutations in any one complementation group are quite specific in action, apparently affecting the same developmental processes.