or "something strange or foreign", and Schaden reported that "avati tupi" is said to be a type of maize obtained by the Guarani from their neighbors, the Caingangs, whom they call "tupis". However, at least two other hypotheses exist. Luccock (1820) translates "tupi" as "the excellent people" while Bertoni (1914) says that "tupi" signifies everything that is not civilized, everything that has not evolved from its inferior state; when applied to objects, plants, or animals, he says it always means the most rustic and primitive. Obviously the correct interpretation is important in the case at hand.

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1. Methylation of DNA as the molecular basis for paramutation in maize.

Several parallels can be drawn between the phenomenon of host-controlled modification of phage, and that of paramutation in maize. Recent evidence has established that the basis of the host-controlled modification process, at least in some instances, is a specific enzymatic alteration of DNA. This realization that alteration of DNA, by either glucosylation or methylation, has a specific biological effect prompts consideration of these processes as the possible molecular basis for paramutation in maize.

It is clear from recent reviews /Srinivasan and Borek, Prog. in Nucleic Acid Res. and Mol. Biol. 5: 157 (1966); Borek and Srinivasan, Ann. Rev. Biochem. 35: 275 (1966)/ that the enzymatic alteration of nucleic acids is a highly specific process. In particular, the process of methylation of DNA is apparently of universal biological distribution and has the specificity to reasonably accommodate the specific allelic interactions which occur in some paramutation systems. Moreover, the biological effects of methylation of DNA, as exemplified by host-controlled modification, suggest that certain of the properties distinguishing paramutation systems (invariability of occurrence, occurrence in somatic cells, reversibility of paramutant, and metastabilized states) could be expected as consequences of the process of specific methylation of DNA.

Although an hypothesis of paramutation based on specific methylation of preformed DNA is completely speculative, it may nevertheless be of interest to examine the principal postulates of such a hypothesis applied to the case of paramutation at the R locus:

1. Paramutation results from the effects of substitution of methyl groups on the DNA of a specific segment at or near the R gene. Paramutagenic alleles carry this DNA segment receptive to methyl groups, whereas non-paramutagenic alleles do not.

2. Methylation of the DNA segment is mediated by specific methylases, whose synthesis is controlled by a genetic region at or near the R gene

of paramutagenic alleles ($\underline{R}^{st}$, $\underline{R}^{mb}$, $\underline{R}^{sc}$, etc.).

3. Introduction of methyl groups produces an alteration in the structure of DNA. The biological consequence of this alteration is repression of R action, i.e., the paramutant phenotype, perhaps by interference with the transcription process.

4. The level of repression of R action is proportional to the extent of methylation of the DNA segment involved. This postulate is necessary to account for different levels of paramutation of the $\underline{R}^{r}$ gene. In host-controlled modification, there is evidence that T_1-DNA may be methylated to different extents, depending on its host specificity.

5. The reversion of paramutant $\underline{R}^{r:st}$ alleles has its basis in the specific but incomplete demethylation of the methylated DNA segment of the $\underline{R}^{r}$ allele. Chemically induced complete reversion may involve complete demethylation of the DNA segment.

6. Persistence of the paramutant state requires replication of the methylated form of DNA. This postulate is questionable, but is necessary to account for replication of the paramutant state following removal of the paramutagenic allele.

The hypothesis, as presented, bears many similarities to Brink's metamere hypothesis. Perhaps translation can be effected by substituting "methyl group" for "metamere" and the "process of specific methylation of DNA" for "under and over replication of metameres" in Brink's hypothesis.

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1. The effect of synaptic partner change on crossover frequency in adjacent regions of a trivalent.

Genetic markers B and sk flank the point of an interchange between maize chromosome 2 and a Tripsacum chromosome. In plants which carry a normal maize chromosome 2 as well as the reciprocal products of this interchange, synapsis is virtually limited to homologous maize segments so that a trivalent configuration is usually formed. Stocks were constructed to measure recombination in regions near the interchange point and beyond with the following results:

Region	% Recombination
B-interchange	8.8
interchange-sk	1.6
sk-v	40.9

Crossover frequency appears near normal or slightly increased in the vicinity of the region of partner exchange in trivalent configurations (in