known that plants of the temperate region often show a breakdown of their chromosomal mechanisms under conditions of high temperature[1].

Plants of the four species, taken at comparable stages, were subjected to a treatment of $37 \pm 1°$ C (relative humidity 70) for various durations of 2–96 h immediately before fixation of the flower buds for cytological analysis. The more important temperature effects were found to include degeneration of the chromatin material, partial asynapsis, chromosome breakage, disturbed arrangement at metaphase I, formation of micro-nuclei and induction of pollen sterility. The observations on each of the abnormalities showed that the chromosomes and the meiotic sequence in the diploid species *monococcum* were significantly more susceptible to high temperature conditions than those in the tetraploid *durum* and the hexaploid *aestivum*, the two latter species showing a comparable degree of resistance. *Triticum dicoccum* was found to approach the diploid species in its degree of susceptibility. These differences and similarities in the response of the four species are indicated in Table 1, in which observations on the degeneration of chromatin material, one of the abnormalities which paralleled other effects, are presented.

Table 1. PERCENTAGES OF *PMC*s SHOWING DEGENERATION OF CHROMATIN MATERIAL FOLLOWING TREATMENT

Duration of treatment (h)	*T. monococcum*	*T. dicoccum*	*T. durum*	*T. aestivum*	*C.D.* (5 per cent level)
0–4	0·00	0·00	0·00	0·00	—
6	1·40	1·02	0·00	0·00	2·14
12	5·86	3·82	2·53	0·00	3·82
24	8·74	6·66	3·98	2·56	3·42
36	15·17	12·05	6·13	4·74	4·23
48	24·78	19·86	11·62	9·03	5·41
72	45·16	38·62	20·46	16·43	5·86
96	—	48·95	30·24	22·16	7·26

It can be inferred from the foregoing observations that the addition of the *B* genome may have played an important part in extending the cultivation of the wheat plant by contributing to its adaptability to warmer conditions. There is little evidence of such adaptability at the diploid level[2,3]. It is also interesting to find that the *D* genome in *aestivum*, considered to be a poor combiner from the point of view of yield[4], does not appear to have contributed much to adaptability either. Shebaski[4] has proposed that it appears worth while to substitute the chromosomes of *D* genome in bread wheat with those of some other related species. The fact that *T. dicoccum* shows a behaviour different from that of *T. durum*, the more extensively cultivated tetraploid species, indicates that the *B* genome, cytologically indistinguishable, is genetically very different in these two species.

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SOIL SCIENCE

Hexosamines in Soil Aggregates

RECENT experiments at this Station on water-stable soil aggregates in a Bridgehampton silt loam have indicated that quantity of soil organic matter is not a reliable index of efficiency in the formation and stabilization of aggregates[1,2]. These investigations involved soils in frames that had been in redtop–potato and red clover–potato rotations for a long period of time—redtop I (1933), redtop II (1950), red clover (1950), continuous potatoes (1933). Crop yields were closely related to aggregation, and fresh additions of organic residues in the rotation systems enhanced aggregate formation.

Analyses to measure quality of organic matter as indicated by determinations for carbohydrates (hexose), polyuronides, and gums and mucilage, showed that, regardless of aggregate size, the organic matter composition within the various sizes was statistically similar for compounds measured. In effect, these chemical constituents were directly related to level of organic carbon rather than to their aggregating efficiency.

Investigations elsewhere have indicated that, in addition to the compounds measured at this Station, a considerable fraction of soil organic matter may be in the form of aminopolysaccharides or hexosamines[3,4]. These occur in a wide variety of biological tissue, and thus it is not surprising that they find their way into soil. In addition to outside sources a considerable portion may arise from microbial activity. The ability, particularly of such microbial, nitrogen-containing polysaccharides, to bind soil particles is well known, and unusual cohesive properties have been attributed to hexosamines.

To test this relationship an investigation was made of samples of the soil aggregates, previously reported, to ascertain the role of aminopolysaccharides in aggregate formation. Chemical methods proposed by Bremner[3] and Stevenson[5] for the determination of hexosamines in acid hydrolysates of soil were used.

The carbon, nitrogen and hexosamine contents of three sizes of aggregates in four rotations are presented in Table 1.

Table 1. CARBON–NITROGEN AND HEXOSAMINE IN SOIL AGGREGATES*

Aggregate diameter (mm)	Aggregates (%)	C (%)	N (%)	C/N (ratio)	Hexosamine-N (p.p.m.)	Hexosamine-N/total N (%)
Redtop I (since 1933)						
> 1	23	2·93	0·218	13·4	138	6·3
1–0·25	12	3·63	0·279	13·0	164	5·9
< 0·25	—	2·72	0·201	13·5	141	7·0
Redtop II (since 1950)						
> 1	20	2·87	0·215	13·3	134	6·2
1–0·25	11	3·37	0·258	13·0	168	6·5
< 0·25	—	2·47	0·188	13·1	145	7·7
Red clover (since 1950)						
> 1	13	2·98	0·236	12·6	164	6·9
1–0·25	15	3·51	0·280	12·5	200	7·1
< 0·25	—	2·57	0·199	12·9	146	7·3
Continuous potatoes (since 1933)						
> 1	8	2·70	0·214	12·6	131	6·1
1–0·25	13	3·45	0·269	12·8	159	5·9
< 0·25	—	2·46	0·187	13·1	123	6·6
$L.S.D._{.05}$	9	0·56	0·048	NS	21	NS

* Average of 9 frames, 0·001 acre each.

The concentration of hexosamines in soil aggregates although somewhat less than those reported by Stevenson emphasizes the considerable proportion of soil nitrogen found in this form. Although there was a significant difference in levels between aggregate sizes, the relationship was clearly in terms of proportionality with the carbon and nitrogen content rather than to aggregate size or to percentage aggregate distribution. These results suggest that there must be other factors that determine the size of aggregates and their distribution. The lack of variation in both carbon/nitrogen ratios and percentage of hexosamine nitrogen indicate clearly the similarity in the composition of acid hydrolysable soil organic matter independent of the origin of organic residues.

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