TABLE II

Fungi spp. encountered on the infected wooden pole. Results are average of six replicates

Specific layers	Fungi species	No. of individual fungal colonies/ gm dry wt./ wood
Inner	*Penicillium* sp.	Numerous*
	Paecilomyces fusisporus	200
	Alternaria alternater	700
	Cladosporium sp.	100
Middle	*Penicillium* sp.	Numerous*
	Cunninghamella echinulata	300
	Paecilomyces fusisporus	2000
	Rhizopus sp.	300
Outer	*Penicillium* sp.	Numerous*
	Cladosporium sp.	100
	Paecilomyces fusisporus	100

* Above five thousand counts.

have been isolated in the present investigation. Species of *Curvularia*, *Rhodotorula* and *Torula* were not recorded in our studies.

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ORIGIN OF TRISOMICS IN THE *SOLANUM NIGRUM* COMPLEX

THE present note deals with the origin and cyto-morphological characters of trisomics recorded in F_1 population of a cross between *Solanum nigrum* L. and *Solanum opacum* A. Br. and Bouche.

A comparison of morphological characters of natural Indian hexaploid *S. nigrum* and *S. opacum* showed that they differ mostly in habit and fruit character. The hexaploid *S. nigrum* was erect with purplish black fruits whereas *S. opacum* was prostrate with yellowish green fruits. Meiotic behaviour of chromosomes of hexaploid *S. nigrum* was normal with 36 bivalents at metaphase$_1$. At anaphase$_1$, there was 36 : 36 distribution of chromosomes at poles. In *S. opacum*, in about 75·00% of pollen mother cells, there were 36 bivalents at metaphase$_1$ while in 25·00% of the cells there was precocious separation of chromosomes of a bivalent resulting in formation of 35 bivalents and 2 univalents at metaphase$_1$, and at anaphase I, in about 62·00% of these cells, there was 37 : 35 distribution of chromosomes at poles.

About one hundred reciprocal cross pollinations were made between hexaploid *S. nigrum* and *S. opacum*. Sixty per cent of the crosses were successful producing several fruits with viable seeds.

The reciprocal hybrids (F_1) were alike in morphological characters. They were semi-prostrate and profusely branched with dark green leaves. The hybrids flowered profusely but produced a few fruits. The fruits were purplish black with several viable seeds. On the basis of the fruit size the F_1 plants were classified into two groups. The plants of group I produced large fruits whereas the plants of group II bore small fruits.

A preliminary cytological study of the plants of group I showed these to be hexaploids with $n = 36$ chromosomes. In about 90% of the cells $35_{II} + 2_I$ were observed while in about 10% of the cells $34_{II} + 1_{III} + 1_I$ were seen. The plants of group II were found to be trisomics with one extra chromosome ($2n = 73$). In about 65% of the cells $36_{II} + 1_I$

and in about 35% of the cells $35_{II} + 3_I$ were recorded. The percentage of pollen fertility of plants of groups I and II was 58·00 and 52·00 respectively.

These investigations show that the origin of trisomics in F_1 progeny of the cross between the natural Indian hexaploid *S. nigrum* and *S. opacum* might be due to fusion of the male gamete of *S. opacum* carrying 37 chromosomes with the female gamete of *S. nigrum* containing 36 chromosomes resulting plants with 73 chromosomes. The origin of male gametes in *S. opacum* with 37 chromosomes is likely due to the precocious separation of a bivalent at metaphase$_I$.

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DORMANCY REGULATION IN GROUNDNUT SEEDS (*ARACHIS HYPOGAEA* L.) C. VAR. TMV-3

DORMANCY phenomenon in plants has been attributed to many factors including hormonal, mechanical and maturity[1]. In groundnut seeds (Var. TMV–3) natural dormancy was attributed to the low levels of growth promoting substances (auxins and gibberellins) and high levels of inhibitory substances[2,3]. In the present investigation, an attempt has been made to study the changes in indoleacetic acid, gibberellic acid and β-inhibitor (ABA), taking into consideration the activities noticed in the bioassay tests, specific to these compounds, along with the changes in the two phenolic compounds (*p*-coumaric acid and coumarin) in relation to dormancy regulation in these seeds.

Growth substances were extracted (using 3 g of seed material, cotyledons and embryonic-axes, separately) according to the method of Villiers and Wareing[4]. Following the method of Gordin–Sharir and Wareing[5], the extracts were chromatographed and the activity assayed using the rice coleoptile straight growth technique[6]. Gibberellin-like substances were extracted following the method of Corcoran and Phinney[7] and assayed using cucumber hypocotyl extension bioassay[8]. Phenolic compounds were extracted and estimated following the method of Bate Smith[9] as modified by Das and Rao[10].

In the dormant (0-day) seed parts, high levels of β-inhibitor activity (ABA) with negligible amounts of IAA and GA_3 was evident (Fig. 1). During dry storage after-ripening, a steep rise in the amounts of IAA and GA_3 took place by 20-days, associated with a fall in β-inhibitor activity. The 20-day after-ripened seeds exhibited 30% germination and the seedlings showed much stunted growth. The amounts of both the inhibitory phenolic compounds (coumarin and *p*-coumaric acid) were very high, in both the seed parts at 0-day (dormant) stage and decreased by 20 days (partially dormant), even though, their levels were much higher compared to 40-day (non-dormant) seeds (Table I). Apparently, the partial dormancy at 20-day stage, inspite of high levels of IAA and GA_3 (almost on par with non-dormant seeds), and very low level of β-inhibitor (ABA) could be due to the relatively high amounts of *p*-coumaric acid and coumarin which were shown to antagonise the IAA and GA_3 induced metabolic processes[11]. The second phase of after-ripening (between 20 and 40-days) was associated with very little change in IAA and GA_3 levels and the complete absence of β-inhibitor (ABA), in both the seed parts. However, the amounts of both the phenolic compounds had declined still further and were much lower than the 20-day seeds, especially in the embryonic axes. The quantum of reduction was much higher between 20 and 40 days than between 0 and 20 days. The seeds at 40 days were non-dormant and showed normal germination response. The lowered levels of these two phenolic compounds might have facilitated the expression of IAA and GA_3 mediated processes, preceding radicle emergence, leading to normal germination. Apparently, dormancy regulation in groundnut seeds is a complicated process, governed not only by an appropriate hormonal balance but also by certain other compounds like phenolics which seem to have a regulatory role either directly or indirectly[11]. Dormancy release in groundnut, seeds seem to be a two step process, the first 20 days of dry storage after-ripening facilitating normalisation of hormonal levels and the later 20 days resulting in the attainment of proper balance amongst different compounds influencing germination. The findings of Sengupta *et al.*,[12] as to the efficacy or otherwise of exogenous hormonal treatments at different intensities of dormancy in groundnut seeds also suggest the complexity of factors governing dormancy in groundnut seeds.

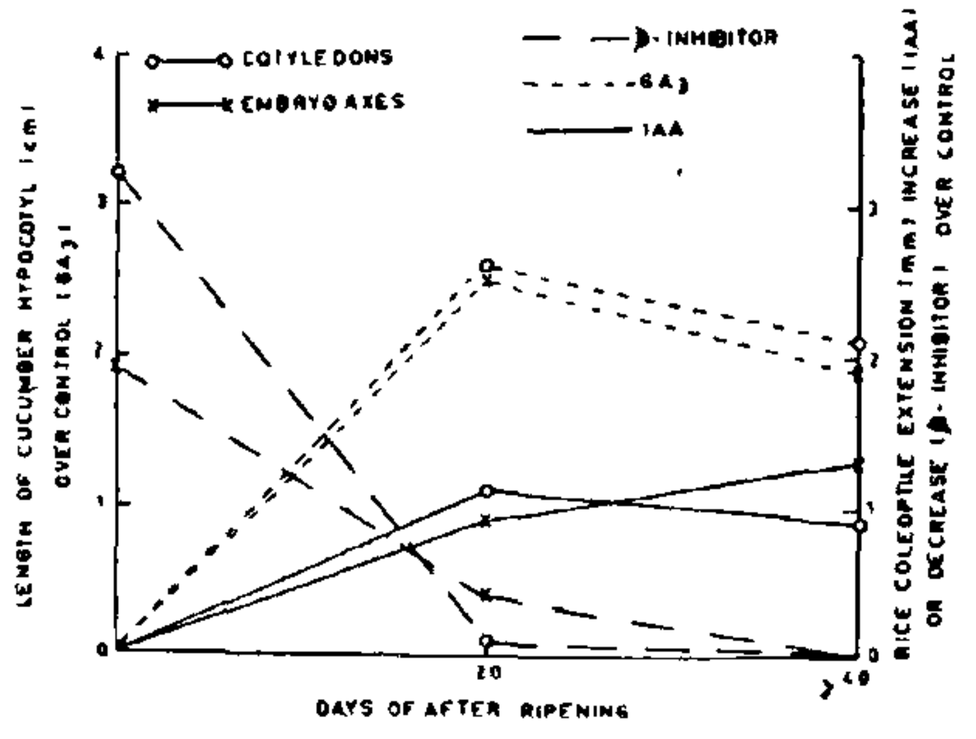

FIG. 1. Charges in the endogenous levels of IAA, GA_3 and β-inhibitor in seed parts during dry storage after ripening.