smooth-surfaced pollen grains. The pollen grains lack the architectural pattern observed on the surface of *N. arbor-tristis* pollen.

These findings have revealed distinct micromorphological differences between the corolla tube and pollen grain surface of *N. arbor-tristis* and the morphological features of the trifid stigma and style of *C. sativus*. They may be of significant help in tackling the adulteration problem of commercial samples of saffron (especially with respect to corolla tubes of *N. arbor-tristis*).

The authors are indebted to the Director, Regional Sophisticated Instrumentation Centre, Punjab University, Chandigarh, for SEM photography. One of the authors (AG) is grateful to the Kurukshetra University authorities for a fellowship.

3 September 1988; Revised 11 November 1988

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SUGAR PHOSPHATES AND URIDINE NUCLEOTIDES IN DEVELOPING GRAINS OF LOW AND HIGH STARCH BARLEY GENOTYPES

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A high lysine and protein barley mutant Notch-2 has lower starch accumulation during grain development compared to its parent NP 113. The decreased starch synthesis in the mutant grain is not due to limitation of soluble sugar precursors[1]. Since sucrose is the primary precursor of starch biosynthesis in developing grain, the constraint in starch accumulation could be somewhere in the pathway of sucrose–starch conversion. Sugar phosphates and nucleotides are important metabolites in conversion of sucrose to starch[2]. This communication reports changes in the levels of some of these metabolites, viz. glucose 1-phosphate (G1-P), glucose 6-phosphate (G6-P), fructose 6-phosphate (F6-P), uridine triphosphate (UTP), uridine diphosphate (UDP) and uridine diphosphate glucose (UDP-glucose), in developing grains of NP 113 and Notch-2.

Barley plants of the two genotypes (NP 113 and Notch-2) were raised in pots under identical fertility and environmental conditions. The ears were harvested at weekly intervals beginning 10 days after anthesis, until maturity. The grains were dehusked and stored in liquid nitrogen until analysis.

The metabolites were extracted with ice-cold perchloric acid (0.8 N) by a slight modification of the method described by Rasi-Caldogno and DeMichelis[3]. The extracts were neutralized with potassium carbonate and diluted to suitable volume with Tris-HCl buffer (50 mM, pH 7.6).

G1-P, G6-P and F6-P[4]; UTP and UDP[5]; and UDP-glucose[6] were estimated by standard enzymatic methods, by coupling the corresponding enzyme reactions with reduction of nicotinamide adenine dinucleotide (phosphate) and monitoring the increase in absorbance at 340 nm.

Extracts were prepared in duplicate for each metabolite and duplicate estimations were carried out with each extract.

Developmental patterns and relative levels of sugar phosphates and uridine nucleotides in developing grains of NP 113 barley and the low starch mutant Notch-2 are presented in figure 1. Sugar phosphates estimated followed more or less similar developmental patterns in that the levels were higher during the early stages of development and declined during the later stages. These patterns resemble those reported earlier for developing wheat grains[7].

Sucrose is the primary precursor of starch biosynthesis in developing grains. There is evidence to suggest that sucrose-carbon enters the amyloplast (site of starch biosynthesis) in the form of triose phosphate[3], which is converted into starch via fructose 1,6-bisphosphate, F6-P, G6-P, and UDP-glucose and/or ADP-glucose (adenosine diphosphate glucose). Since developing grain is predominantly a biosynthetic tissue, all these metabolites and the accessory metabolites UDP and UTP are expected to be concentrated in the amyloplasts.

With the exception of G1-P average level per grain of all the metabolites reported here were higher in the mutant Notch-2 grain compared to those in normal NP 113 grain (figure 1); hence these metabolites are not expected to limit starch accumulation in the mutant grain. G1-P content was relatively lower in Notch-2 grain. In the amyloplast G1-P is formed from G6-P by the action of phosphoglucomutase and is utilized to produce ADP-

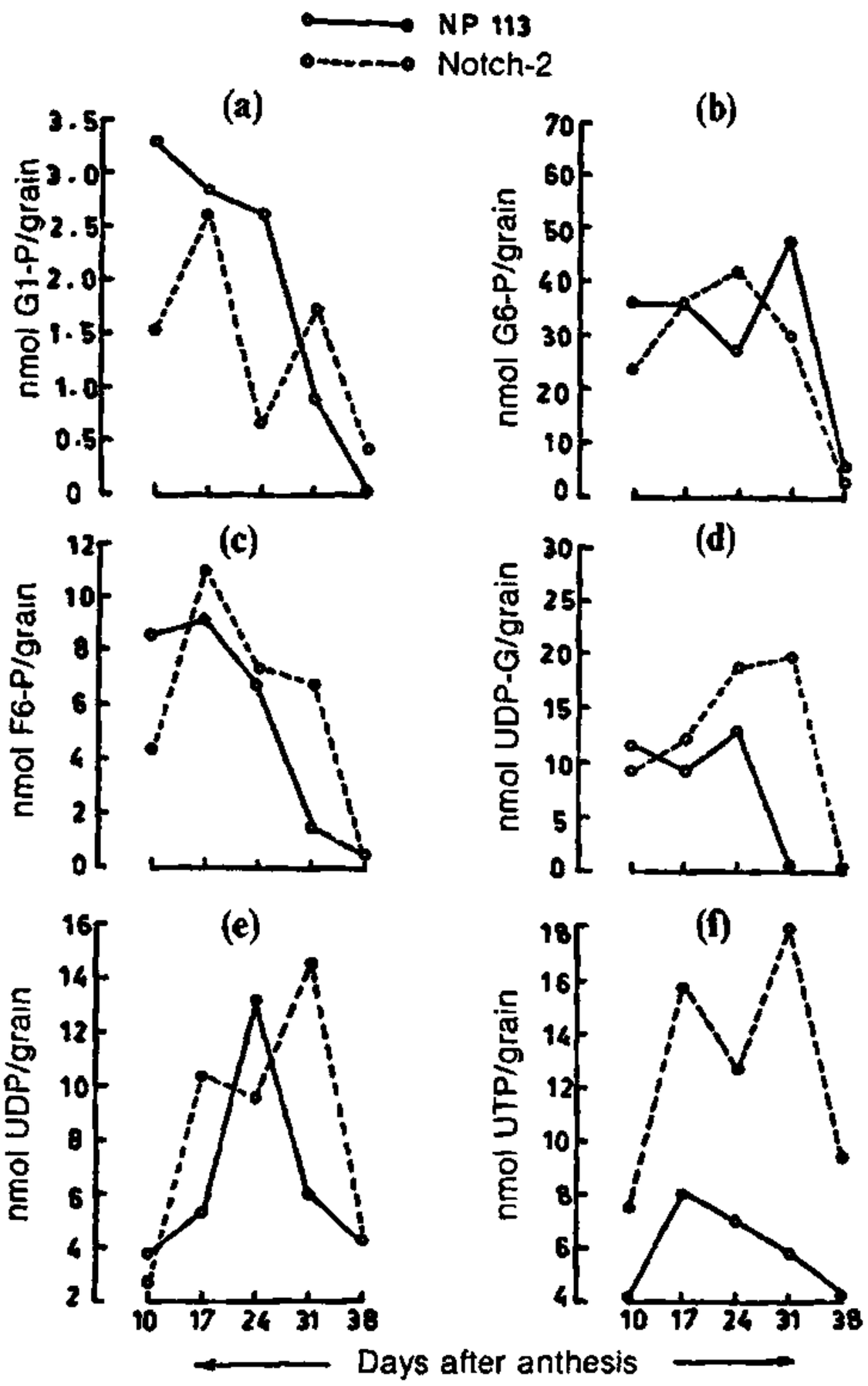

Figure 1. (a) Glucose 1-phosphate; (b) glucose 6-phosphate; (c) fructose 6-phosphate; (d) uridine diphosphate glucose; (e) uridine diphosphate; and (f) uridine triphosphate in developing grains of NP 113 and Notch-2 barley.

glucose (UDP-glucose) and amylose primer in reactions catalysed by ADP-glucose (UDP-glucose) pyrophosphorylase and starch phosphorylase[3]. The Notch-2 grain is known to have higher activities of phosphoglucomutase[8], UDP-glucose pyrophosphorylase and starch phosphorylase[9] compared to NP 113. The two genotypes had almost similar activities of ADP-glucose pyrophosphorylase[9]. It may therefore be inferred that the lower level of G1-P in Notch-2 mutant is not the result of reduced production; rather, it might be due to its higher utilization in Notch-2 amyloplasts compared to that in NP 113. Starch biosynthesis in Notch-2 is therefore also unlikely to be limited at the level of G1-P.

The authors thank Dr S. L. Mehta, IARI, New Delhi, for providing barley seeds and ICAR, New Delhi, for financial assistance.

24 October 1988

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OCCURRENCE OF VESICULAR-ARBUSCULAR MYCORRHIZAL FUNGI IN ROOTS OF *MORUS ALBA* L.

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VESICULAR-ARBUSCULAR mycorrhizal (VAM) fungi have been reported in several crop plants and ornamentals[1-4]. The anatomy and distribution of mycorrhizae and their influence on plant growth is well established[5,6]. In recent years studies on the ecophysiology of VAM associations have gained much attention[7]. This paper reports the occurrence of VAM in *Morus alba* L. K_2 variety. *Morus alba* L. is a cultivated plant and has great economic importance as the food of mulberry silkworms.

Roots of *Morus alba* L. K_2 were collected from mulberry plots in RRL campus. The roots were washed thoroughly with tap-water and distilled water, cleaned in 1 N KOH, bleached with 3% H_2O_2, and stained with trypan blue in lactophenol[4] and examined under a Leitz microscope. Spores, isolated from the infected roots and soil around the