In contrast, the mRNA for plastid leucyl-tRNA synthetase; P/T ratio, defines the proportion of poly-

mersome-associated in vitro translatable and hybridizable mRNAs, however, demonstrated a restriction of
translatable and hybridizable mRNAs, however, demonstrated a restriction of rbcS and cab transcripts to smaller polysomes in JaMe-

cab gene product (Weidhase et al., 1987b) designated jasmonate-induced proteins (JIPs). Abundant JIPs have been shown to be proteinase inhibitors in tomato (Farmer and Ryan, 1990) and vegetative storage proteins in soybean (Anderson et al., 1989; Mason and Mullet, 1990; Staswick, 1990). The function of most jasmonate-induced vegetative storage proteins is largely unknown. Recent findings indicate, however, that certain proteins from potato and Sophora japonica have hydrolytic activity (Andrews et al., 1988) and lectin-like properties (Herman et al., 1988), respectively. In barley, one prominent JIP has been reported to be a leaf thionin (Andreasen et al., 1992). For certain other barley and cotton JIPs, a relationship to late embryogenesis abundant proteins has been suggested (Reinbothe et al., 1992a, 1992b).

Another aspect of jasmonate action is the repression exerted by JaMe on the translation of most "control" mRNAs, i.e. mRNAs that are already present before jasmonate treatment. This phenomenon is indicated by the maintenance of almost all in vitro-translatable mRNAs for at least 24 h, in contrast to the drastic reduction of synthesis of the respective control proteins (Müller-Uri et al., 1988).

In the present paper, we reinvestigate the phenomenon of restriction of control protein synthesis by JaMe with particular reference to nuclear genes encoding chloroplast proteins. We demonstrate that the synthesis of the small subunits of ribulose-1,5-bisphosphate carboxylase/oxygenase and of a light-harvesting chlorophyll protein complex apoprotein (LHC(P)) is likely impaired at the level of translation initiation in JaMe-treated leaf tissues.

MATERIALS AND METHODS

Plant Material—Seeds of barley (Hordeum vulgare L. cv. Salome) were germinated on vermiculite at 25 °C under continuous illumination for 7 days (modified after Weidhase et al., 1987a, 1987b). Primary leaves were cut from the seedlings and placed onto either water or on an aqueous solution of JaMe (45 μM, Firmenich, Geneva, Switzerland) for the various periods of time indicated in the text. For inhibitor experiments, leaf tissues were incubated with cycloheximide (2 μg/ ml final concentration) in the 2 h before harvest (Perlman et al., 1972).

Preparation, in Vitro Translation, and Blot Hybridization of RNA—

Total RNAs were prepared from the leaf segments by phenol/chloroform/isosamyl alcohol extraction (Müller-Uri et al., 1988). After reprecipitation with lithium chloride (Reinbothe et al., 1990a), high

* This work was supported in part by a research project grant (to B. P.) from the "Volkswagenstiftung," Hannover, FRG. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

† To whom correspondence should be addressed: Dept. of Genetics, Institute for Plant Sciences, ETH Zentrum, Universitätstrasse 2, CH-8092 Zürich, Switzerland. Tel.: 1-256-59-71; Fax: 1-252-08-29.

The abbreviations used are: JaMe, jasmonic acid methyl ester (methyl jasmonate); JIPs, jasmonate-induced proteins(s); LHC(P), light harvesting chlorophyll protein complex (proteins); LRS1, plastid leucyl-tRNA synthetase; P/T ratio, defines the proportion of polysomes to the sum of polysomes, ribosomal subunits, and monosomes; LSU, large subunits; SSU, small subunits; rbcL, gene for the large subunits of ribulose-1,5-bisphosphate carboxylase/oxygenase.

© 1993 by The American Society for Biochemistry and Molecular Biology, Inc.

Methyl Jasmonate-regulated Translation of Nuclear-encoded Chloroplast Proteins in Barley (Hordeum vulgare L. cv. Salome)*

(Received for publication, December 28, 1992)
molecular mass RNAs were translated into polypeptides in a wheat germ system, prepared according to Erickson and Blobel (1983) as modified by Reinbothe et al. (1990a). Assays for one- and two-dimensional polyacrylamide gel electrophoresis contained 11.2 MBq \(^{14}C\) methionine (37 TBq/mmol, Amersham International PLC, United Kingdom). Immunoprecipitations were performed with anti-

“Methyl Jasmonate-regulated Chloroplast Protein Formation”

Weidhase et al., 1987b; Müller-Uri et al., 1988). In addition, this substance induced a pronounced accumulation of new proteins (Müller-Uri et al., 1988; Reinbothe et al., 1992a). Both aspects of jasmonate action can be discerned by comparing the patterns of Coomassie-stained and L-[\(^{35}S\)]methionine-labeled polypeptides from JaMe- and water-treated leaves. As documented in Fig. 1, the patterns of Coomassie-stained proteins from JaMe- and water-treated leaf segments (Fig. 1, A versus C) differ with respect to the disappearance of several control proteins (open circles in Fig. 1A) and the appearance of the previously identified JIPs of 66, 37, 30, 23, and 12 kDa (arrowheads in Fig. 1C, see Müller-Uri et al., 1988; Reinbothe et al., 1992a).

Distinct patterns of pulse-labeled proteins could be found for JaMe- and water-exposed leaf tissues (Fig. 1, D versus B). The most remarkable difference was the almost complete repression of control protein synthesis, which is evident for a large number of proteins (framed in the autoradiogram of Fig. 1B), and the formation of abundant JIPs (arrowheads in Fig. 1D). Only a few constitutively synthesized proteins could be observed (vertical bars in Fig. 1, B and D). The obvious discrepancy between the most constant rate of amino acid monospecifiction into total protein of JaMe- and water-treated leaf tissues (Müller-Uri et al., 1988) and the drastic reduction of labeling of polypeptides seen in the autoradiograms (Fig. 1, D versus B) may be explained by assuming that several JIPs were not well resolved in the pH gradients (pH 4.5–7.5) employed for isoelectric focusing (O’Farrell, 1975).

As suggested by the decreased amount (Fig. 1C) and, even more strongly, by the decreased rates of labeling of the large (LSU) and small subunits (SSU) of ribulose-1,5-bisphosphate carboxylase/oxygenase (Fig. 1D), JaMe influenced chloroplast protein formation. We have studied this phenomenon further by analyzing the protein patterns of isolated plastids from JaMe- and water-treated leaf segments. Methyl jasmonate did not influence plastid volume but lowered plastid protein levels, in comparison to water-control tissues (Fig. 2A, lane 2 versus 1). On an equal plastid number and thus plastid volume basis, several polypeptide species decreased or even disappeared. Among them were the LSU and SSU of ribulose-1,5-bisphosphate carboxylase/oxygenase, whose amounts were determined by Western blot analyses with monoclonal antibodies directed against the purified proteins (Fig. 2A, lanes 3–6). In contrast, the three immunologically related LHCs (Golmer and Apel, 1983) did not show a significant quantitative change in the Western blots (Fig. 2, lanes 7 and 8). A similar conclusion could be drawn for LRS1 (Fig. 2, lanes 9 and 10), which was detected with antibodies against the purified enzyme from E. gracilis (Kraupe et al., 1987; Reinbothe et al., 1990a). As previously found for this alga (Kraupe and Parthier, 1988; Reinbothe et al., 1990b), the 110-kDa enzyme of barley is extremely sensitive toward proteolytic attack and is rapidly converted into a pseudodimeric form of 55 kDa.

The JaMe-induced changes in LSU and SSU protein levels were caused by corresponding alterations in protein synthesis (Fig. 2B, lanes 3–6). For the LHCs, the almost complete repression of their synthesis in JaMe-treated leaf tissues (Fig. 2B, lane 8 versus 7), however, contrasted with the nearly unchanged protein levels, suggesting that protein stabilities were also influenced by JaMe. For LRS1, the rate of synthesis and the amount of protein were balanced both in JaMe- and water-treated leaf tissues (Fig. 2, lanes 9 and 10).

Ribosomal RNA, rSs, cah, and lrs1 mRNA Levels—In order to determine whether the differential changes in the abun-

S. Reinbothe, unpublished observation.
dence and rate of synthesis of particular plastid proteins were caused by corresponding alterations at the mRNA levels, the amounts of rbcS, cab, and lrsl transcripts were determined. Total RNAs were isolated from leaf segments that had been exposed to either water or JaMe for various periods of time. After electrophoresis, the ribosomal RNAs were visualized by ethidium bromide staining (Fig. 3A). On an equal leaf number basis, a gradual decrease of cytoplasmic and plastid rRNA species could be observed, which occurred primarily in JaMe-treated leaves (Fig. 3A). This result had to be taken into account when individual transcripts were quantified by hybridization of RNA gel blots containing equal amounts of total RNA from JaMe- and water-treated leaf segments. As indicated in Fig. 3B, three transcript species of about 1.2, 1.1, and 3.5 kilobases hybridized with the barley rbcS and cab gene, and the E. coli lrsl probe, respectively. The detected transcripts behaved differently in response to JaMe. The rbcS and cab transcript contents were almost constant for 24 h of either treatment, whereas the lrsl mRNA level began to increase in the Northern blots containing RNAs of JaMe-incubated leaves (Fig. 3B). At later stages of treatment, JaMe promoted a decline of the rbcS and cab transcripts, but further increased the lrsl mRNA content, in comparison to water-treated leaf tissues (Fig. 3B). Calculated on an equal leaf number basis, however, the lrsl mRNA level did not change significantly in either JaMe- or water-treated leaf tissues (data not shown). This result is particularly interesting, since the leaf content of rRNAs (Fig. 3A) as well as rbcS and cab transcripts (data not shown) had decreased in JaMe-treated tissues and to a lesser extent in water-treated tissues. Thus, the general decline of leaf RNAs in JaMe-treated tissues was superimposed on specific hormone effects on individual transcripts.

Analysis of Polysome-bound mRNAs—The large observed decrease in the synthesis of most control proteins, including...
the LSU and SSU of ribulose-1,5-bisphosphate carboxylase/oxygenase and the LHCPs (Figs. 1 and 2), was at variance with the almost constant levels of the corresponding control mRNAs, such as rbcL, rbcS, and cab (Fig. 3, see also Müller-Uri et al., 1988). Since the rbcS and cab transcripts were in vitro translatable, a translational mode of regulation was implied that might be exerted by JaMe at the ribosome level. In order to test this idea, polysomes were isolated from leaves that had been treated with either water or JaMe for 8 h. At this time, control protein synthesis has been shown to be reduced in JaMe-treated leaf tissues to a low level similar to that found after 24 h (Müller-Uri et al., 1988).

The absorbance readings shown in Fig. 4 illustrate similar polysome profiles for JaMe- and water-treated leaf segments. The two major peaks represent the 60 S and 40 S ribosomal subunits. The several lower peaks are comprised of polysomes consisting of two to six or more message-bound ribosomes (fractions 4–8). The P/T ratios (as a measure for the proportion of ribosomes in polysomes) of 0.57 and 0.55 were comparable for polysomes from water- and JaMe-exposed leaves, respectively. This result first seemed to be surprising, if one considers that the previously characterized JIPs have lower molecular masses than the average control proteins (cf. Fig. 1). Thus, one should expect a higher portion of ribosomes associated with small polysomes (Fig. 4A, fractions 4–6) in the ribonucleoprotein fraction analyzed from JaMe-treated tissues, and a general increase in monosomes and ribosomal subunits (Vassart et al., 1971; Lodish, 1976). Neither effect was observed, however (Fig. 4). Nevertheless, the polysome profiles can be reconciled with the almost constant overall rates of protein synthesis in JaMe- and water-treated leaf tissues (Müller-Uri et al., 1988), suggesting that the polysomal association of several other mRNAs was not affected by JaMe.

The association of the rbcS, cab, and lrsl mRNAs with polysomes was analyzed as follows. RNAs from the arbitrarily defined fractions (Fig. 4A) were recovered by phenol extraction and ethanol precipitation. Northern blots separating the recovered RNAs on an equal nucleic acid basis were hybridized with radioactively labeled rbcS, cab, and lrsl gene probes, and the nucleic acid hybrids were detected by autoradiography. Alternatively, the recovered RNAs were used for in vitro translation and immunoprecipitation, using the different antiseras described above.

As demonstrated in Fig. 4, both the hybridizable and in vitro translatable rbcS and cab mRNAs were found associated with polysomes from water- and JaMe-treated leaf segments. However, their relative content in polysomes of fractions 7 and 8 was significantly reduced in favor of smaller polysomes in JaMe- versus water-treated leaves. In contrast, no such bias toward smaller polysomes could be found for the lrsl mRNA of JaMe-exposed leaf tissue (Fig. 4).

Polysome profiles can be interpreted in terms of translation initiation, elongation, and termination (Vassart et al., 1971; Lodish, 1976). Repression at any step results in a unique polysome profile that allows the site of regulation to be determined (Vassart et al., 1971). Since the rate of translation initiation is assumed to be low under most physiological conditions, compared to the rate of elongation (Vassart et al., 1972; Lodish, 1976), the higher proportion of rbcS and cab transcripts associated with larger polysomes in water-exposed leaves is consistent with a continuation of translation initiation within these tissues and a repression of initiation in JaMe-treated tissues (Vassart et al., 1971; Lodish 1976; Ilan, 1987). If this is the case, one would expect that cycloheximide, a specific inhibitor of translation elongation (Perlman et al., 1972), should shift the repressed rbcS and cab transcripts toward larger polysomes in JaMe-treated leaf tissues.

As shown in Fig. 5, treatment of JaMe-incubated leaf tissues with cycloheximide prior to harvesting led to increased proportions of rbcS and cab transcripts associated with poly-

![Fig. 4. Polysomal association of rbcS, cab, and lrsl transcripts in JaMe- and water-treated leaf segments. Polysomes were isolated from an equal number of segments that had been treated for 8 h with either water or JaMe. Ribonucleoprotein material was fractionated in sucrose gradients, and the absorbance at 254 nm was monitored continuously during harvest of the fractions. The dashed lines represent the base lines. A 6-fold decrease in full scale absorbance is indicated by a break in the absorbance tracing of each profile. RNAs recovered by phenol extraction and ethanol precipitation from the indicated gradient fractions were separated in denaturing agarose gels, blotted onto nitrocellulose filters, and hybridized with an excess of the 32P-labeled rbcS, cab, and lrsl probes. Nucleic acid hybrids were detected by autoradiography. Alternatively, RNAs recovered from the gradient fractions were used for in vitro translation. The precursor forms of SSU (pSSU, 20 kDa), LHCPs (pLHCP, 31 kDa) and LRS1 (pLRS1, 115 kDa) were detected by immunoprecipitation and visualized by autoradiography.](image)

![Fig. 5. rbcS and cab transcript association with polysomes after treatment of JaMe-exposed leaves with (+) or without (−) cycloheximide (CHI). Polysomes were isolated from leaf tissues that had been incubated with JaMe for 8 h. Starting 2 h before harvest, cycloheximide was included in the incubations. rbcS, cab, and lrsl transcripts, hybridizing with RNAs of the indicated polysome fractions, were detected by autoradiography.](image)
some of fractions 7 and 8, in comparison to non-treated tissues. Thus, an impairment of translation initiation at rbcS and cab transcripts likely represses synthesis of the corresponding SSU and LHCP in JaMe-treated leaf tissues.

**DISCUSSION**

Obvious responses of excised barley leaf segments to methyl jasmonate are the repression of synthesis of most control proteins preexisting in non-treated tissue, on the one hand, and the induction of novel proteins, on the other (Müller-Uri et al., 1988). Nuclear and plastid-encoded chloroplast proteins belong to the group of control proteins whose formation is negatively influenced by JaMe (Figs. 1 and 2). Quantitative differences in protein synthesis were observed for individual nuclear-encoded chloroplast proteins that, in most cases, correlated with altered protein abundances (Fig. 2). The changes in LHCP synthesis, however, seemed to contrast with the almost constant protein levels (Fig. 2), demonstrating that protein stabilities were also affected by JaMe. The synthesis and amount of LRS1 were maintained both in JaMe- and water-treated leaf tissues (Fig. 2).

The changes in control protein synthesis, as seen for the LSU and SSU of ribulose-1,5-bisphosphate carboxylase/oxygenase and the LHCps, were not caused by equivalent quantitative alterations of the corresponding rbcL, rbcS, and cab transcripts (Fig. 3). We posed the question of which of the different steps in translation was controlled by JaMe. Since translation of mrRNA involves chain initiation, elongation, and termination, each of these steps might have been a site of control (Vassart et al., 1971; Lodish, 1976; Ilan, 1987). Potential sites of regulation were analyzed by comparing polysome profiles of JaMe- and water-treated leaf tissues. We expected that the arrest at a discrete step of translation would be mirrored in a characteristic polysome profile (Vassart et al., 1971; Lodish, 1976). If translation was selectively inhibited at the step of initiation, then transcripts would be largely restricted to small polysomes and non-polysomal fractions, provided that initiation events are rate-limiting for the overall rate of translation (Vassart et al., 1971; Lodish, 1976).

Indeed the rbcS and cab transcripts were found to be associated with smaller polysomes in JaMe-treated versus water-treated leaf tissues (Fig. 4). This observation suggested a lowering but not a complete repression of translation initiation for the rbcS and cab mrRNAs in JaMe-incubated leaf tissues, in contrast to the irs1 mrRNA, which was uniformly distributed across the polysome gradients of JaMe- and water-exposed leaves (Fig. 4). The idea of regulation at the level of translation initiation is further substantiated by the fact that cycloheximide treatment caused increased proportions of rbcS and cab transcripts to be associated with larger polysomes in JaMe-incubated leaf segments (Fig. 5). On the other hand, isolated polysomes from JaMe-treated leaf tissues preferentially translate JIP mrRNAs, whereas polysomes from water-treated leaves primarily translate control mrRNAs. The observed lowering of translation initiation can be regarded as a specific event insofar as other mrRNAs, such as irs1 (Fig. 4), actin, and tubulin were not affected by JaMe. Since the polysome-associated rbcS and cab transcripts were in vitro translatable (Fig. 4B), the observed impairment at the level of translation initiation probably arose from an alteration at the ribosomal level. In this respect, our results resemble those obtained for stress-induced alterations in gene expression in diverse plant species (Nover et al., 1990).

Cell suspension cultures of tomato, for example, respond to heat shock with the rapid and reversible decline of the phosphorylation level of the basic ribosomal protein S6, and simultaneous labeling of several acidic ribosomal proteins (Scharf and Nover, 1982). These changes have been assumed to be involved in the discrimination between heat shock-induced and control mrRNAs (Scharf and Nover, 1982; Nover and Scharf, 1984). Together with certain heat shock-induced proteins, control mrRNAs are stored in specialized subcellular organelles designated heat shock granules (Nover et al., 1983), from which they can be remobilized during recovery from heat shock (Nover et al., 1989). In this context, it is tempting to speculate on the existence of similar subcellular structures in JaMe-treated barley leaf tissues, in which control mrRNAs are preserved. If they exist, it will be interesting to analyze whether such stored control mrRNAs can be reutilized for protein synthesis after recovery of leaf tissues from JaMe, either applied exogenously or released endogenously in response to osmotic stress.

Superimposed on such sequestration/mRNA availability model, our results might imply a preferential recruitment of JIP mrRNAs into polysomes (Fig. 1), possibly due to an above average rate of translation initiation, in comparison to control mrRNAs. This first detailed description of negative translational control by a plant growth regulator such as JaMe can be compared and contrasted with the regulation of chloroplast protein synthesis under other conditions. In most cases studied so far, regulation of chloroplast protein formation occurs at the step of translational initiation. In amaranth seedlings, the rbcS and rbcL mrRNAs have been shown to be present in dark- and light-grown cotyledons, but they are mobilized onto polysomes only upon illumination (Berry et al., 1990). Similarly, a light-activated polysome association of several mrRNAs has been demonstrated for E. gracilis (see Reinhothe and Parthier, 1990; Reinhothe, 1992, for summary). Well known examples for translational control at the step of chain elongation are the synthesis of the 65- and 70-kDa chlorophyll a apoproteins of photosystem I, the psaA and psaB gene products, and of the 32-kDa protein of photosystem II, the psbA gene product, in illuminated barley seedlings (Klein et al., 1988).

We have also analyzed plastid gene expression in barley leaf segments in response to JaMe and find a rapid and selective inactivation of the rbcL mRNA. Likewise, we observed a delayed jasmonate effect on transcript abundance for the psaA-psaB, psbA, and rbcL transcripts, similar to the results obtained for the rbcS and cab mrRNAs in this work (Fig. 3). Since we do not know whether the changes in transcript levels mirror alterations in transcription of the plastid and nuclear genomes or in RNA stabilities, both possibilities should be kept in mind. Nevertheless, these phenomena are reminiscent of abscisic acid-responsive cab and rbcS gene expression, which are depressed at the level of transcript accumulation in wheat (Quatrano et al., 1983) and pea (Medford and Sussex, 1989), and of transcription in tomato (Bartholomew et al., 1991). Since we have recently noticed a similar impairment of chloroplast and other control protein synthesis by abscisic acid in excised barley leaves (Reinhothe et al., 1992a) as found for JaMe, common molecular mechanisms for translational regulation can be hypothesized.

Together, our results show clearly that nuclear gene expression of plastid proteins is controlled not only by light, but also by signals belonging to the plant growth regulator type.

**Acknowledgments**—We thank Drs. K. Apel (Zürich, Switzerland), L. Hansen (Copenhagen, Denmark), and J. Lehmann (Halle/Saale, Germany) for gifts of the plasmid clones and antibodies described in the text. Typing of the manuscript by Ch. Dietel (Halle/Saale, FRG).
and critical reading of the manuscript by Dr. G. Armstrong (Zürich, Switzerland) are gratefully acknowledged.

REFERENCES

Anderson, J. M., Spilatro, S. R., Klauser, S. P., and Franceschi, V. R. (1986) Plant Sci 62, 45-62
Andresen, I., Becker, W., Schlüter, K., Burgess, J., Parthier, B., and Apel, K. (1992) Plant Mol. Biol. 19, 193-204
Andrews, D. L., Beames, B., Summers, M. D., and Park, W. D. (1988) Biochem. J. 252, 199-206
Bartholomeu, D. M., Bartsley, G. E., and Sclonik, P. A. (1991) Plant Physiol. 96, 291-296
Berry, J. O., Breiding, D. E., and Klessig, D. F. (1990) Plant Cell 2, 795-803
Braun, A. H., and Blobel, G. (1983) Methods Enzymol. 96, 38-56
Farmer, E. E., and Ryan, C. A. (1987a) Ann. Rev. Plant Physiol. 38, 50-73
Farmer, E. E., and Ryan, C. A. (1989) Proc. Nat. Acad. Sci. U.S.A. 87, 7713-7716
Gollner, I., and Apel, K. (1985) Eur. J. Biochem. 133, 309-313
Hartlein, M., and Madern, D. (1987) Nucleic Acids Res. 15, 10199-10210
Herman, E. M., Hankins, C. N., and Shannon, L. M. (1988) Plant Physiol. 86, 1027-1031
Ilan, J. (1987) Translational Regulation of Gene Expression, Plenum Press, New York
Klein, R. R., Mason, H. S., and Mullet, J. E. (1988) J. Cell. Biol. 106, 299-301
Krauspe, R., and Parthier, B. (1986) Biochem. Physiol. Pflanzen 183, 477-485
Krauspe, R., Lerbs, S., Parthier, B., and Wollgarten, R. (1997) J. Plant Physiol. 150, 327-342
Laemmli, U. K. (1970) Nature 227, 680-686
Ledl, H. F. (1970) Ann. Rev. Biochem. 40, 39-73
Mason, H. S., and Mullet, J. E. (1990) Plant Cell 2, 569-579
Medford, J. I., and Susser, I. M. (1989) Planta 179, 309-315
Meyer, A., Miersch, O., Böttger, C., Darhe, W., and Sembdner, G. (1984) J. Plant Growth Regul. 3, 1-8
Müller-Uri, F., Parthier, B., and Nover, L. (1988) Planta 176, 241-247
Nover, L., Scharf, K.-D., and Neumann, D. (1983) Mol. Cell. Biol. 3, 1648-1655
Nover, L., Scharf, K.-D., and Neumann, D. (1989) Mol. Cell. Biol. 9, 1298-1308
Nover, L., Neumann, D., and Scharf, K.-D. (1990) Heat Shock and Other Stress Response Systems in Plants, Springer-Verlag, Berlin
O’Farrell, P. H. J. (1975) J. Biol. Chem. 250, 4007-4021
Parthier, B. (1980) J. Plant Growth Regul. 9, 57-63
Parthier, B. (1991) Bot. Acta 104, 446-454
Perlman, S., Hirsch, M., and Penman, S. (1972) Nature 235, 143-144
Quatrano, R. S., Ball, B. L., Williamson, J. D., Haehlin, M. T., and Mansfield, M. (1983) in Plant Molecular Biology (Goldberg, R. B., ed) pp. 343-353, Alan R. Liss, New York
Reinbothe, S. (1990) in Regulation of Chloroplast Biogenesis (Argyroudi-Akoyunoglou, J., ed) pp. 45-50, Plenum Press, New York
Reinbothe, S., and Parthier, B. (1990) FEBS Lett. 265, 7-11
Reinbothe, S., Krauspe, R., and Parthier, B. (1990a) Planta 181, 176-183
Reinbothe, S., Krauspe, R., and Parthier, B. (1990b) J. Plant Physiol. 137, 81-87
Reinbothe, S., Reinbothe, C., Lehmann, J., and Parthier, B. (1992a) Physiol. Plant. 86, 49-56
Reinbothe, S., Machmudowa, A., Westerneck, C., Reinbothe, C., and Parthier, B. (1992b) J. Plant Growth Regul. 11, 7-14
Sandstrom, J., Frisch, E. F., and Maniatis, T. (1989) Molecular Cloning: a Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY
Safier, S. O., and Thimann, K. V. (1981) Compt. Rend. Acad. Sci. (Paris) Ser III 293, 735-740
Scharf, K.-D., and Nover, L. (1982) Cell 30, 427-437
Sembdner, G., and Gross, D. (1986) in Plant Growth Substances (Bopp, M., ed) pp. 139-147, Springer-Verlag, Berlin
Staswick, P. (1990) Plant Cell 2, 1-6
Towbin, H., Staehelin, T., and Gordon, J. (1979) Proc. Natl. Acad. Sci. U.S.A. 76, 4350-4354
Ueda, J., and Kato, J. (1986) Plant Physiol. 66, 246-249
Ueda, J., and Kato, J. (1984) J. Plant Physiol. 116, 557-559
Vasrnat, G., Dumont, J. E., and Cantraine, F. R. L. (1971) Biochim. Biophys. Acta 247, 471-485
Weidhaas, R. A., Lehmann, J., Kramell, H., Sembdner, G., and Parthier, B. (1987a) Physiol. Plant. 69, 161-166
Weidhaas, R. A., Kramell, H., Lehmann, J., Liebiach, H. W., Lerbs, W., and Parthier, B. (1987b) Plant Sci. 51, 177-186
Wilen, R. W., van Rooijen, G. J. H., Pearce, D. W., Pitsiris, R. P., Holbrook, L. A., and Moloney, M. M. (1991) Plant Physiol. 99, 399-405