Metabolism and Biological Activity of Cibberellin A, in Vegetative Shoots of *Zea mays, Oryza sativa,* **and** *A rabidopsis thaliana* '

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11 7-'3C,3H]Gibberellin A, (CA,) was injected into the shoots of tal1 (W23/1317), dwarf-1 *(d7),* **and dwarf-5** *(d.5)* **Zea mays** *1.* **(maize); tal1 (cv Nipponbare), dwarf-x** *(dx),* **and dwarf-y** *(dy)* **Oryza** *sativa* **L. (rice); and tal1 (ecotype Landsberg erecta),** *ga4,* **and** *ga5* **Arabidopsis tbaliana (1.) Heynh. [13C]CA4 and its metabolites were identified from the shoots by full-scan gas chromatography-mass spectrometry and Kovats retention indices. CA, was metabolized** to GA₁ in all nine genotypes. GA₄ was also metabolized in some of the genotypes to 3-epi-GA₁, GA₂, 2 β -OH-GA₂, 3-epi-GA₂, endo-**CA,, 16a ,17-H2-16,17-(OH),-CA,, CA3,, endo-CA3,, CASs, 15-epi-**GA₆₃, GA₇₁, and 16-epi-GA₈₂. No evidence was found for the **metabolism of CA. to CA7 or of CA, to CA3. The bioactivities of GA, and CAI were determined using the six dwarf mutants for** assay. GA₄ and GA₁ had similar activities for the maize and rice **mutants. For the Arabidopsis mutants, CA, was more active than** GA₁ at low dosages; GA₄ was less active than GA₁ at higher dosages.

Information conceming the GA biosynthetic pathways is necessary for an understanding of the origin, identification, and regulation of bioactive GAs. Specific pathways, together with mutants that block specific steps in these pathway(s), have been described for severa1 plant systems (Reid, 1990). In this report we evaluate the role of GA, and GA, **in** the control of shoot elongation for *Zea* mays (maize), Oyza *sativa* (rice), and *Arabidopsis thaliana*. (The structures of the C₁₉-GAs relevant to this study are shown in Fig. 1).

The early 13-hydroxylation pathway is the major one present in vegetative shoots of maize. The evidence is based on the isolation of nine members of the pathway from vegetative shoots (Fujioka et al., 1988a, 1988b) and the demonstration of five metabolic steps in the pathway (Spray et al., 1984; Fujioka et al., 1990). The relative roles of GA_{20} and GA, in the control of growth are based on studies of the

two GA mutants, *dl* and *d5.* The *dl* mutant controls the late step, GA_{20} to GA_1 . In the $d1$ mutant, GA_1 is bioactive and GA_{20} has less than 1% of the activity of GA_1 (Phinney and Spray, 1982). The *d1* mutant accumulates endogenous GA₂₀, has trace amounts of GA, (Fujioka et al., 1988a), and does not metabolize GA₂₀ to GA₁ (Spray et al., 1984). The d5 mutant controls the early step, copalylpyrophosphate to *ent*kaurene (Hedden and Phinney, 1979). In the *d5* mutant, $GA₂₀$ and $GA₁$ have similar bioactivities (Phinney and Spray, 1982), endogenous GA_{20} and GA_1 are present in trace amounts (Fujioka et al., 1988a), and the mutant metabolizes GA_{20} to GA_1 (Spray et al., 1984). The data suggest that GA_{20} is bioactive in maize shoots only because of its metabolism to bioactive GA,.

GA₃ is also endogenous to tall maize shoots but is present in trace amounts only (Fujioka et al., 1988b). $GA₃$ originates from GA₂₀ via GA₅ (Fujioka et al., 1990). GA₄, GA₇, GA₉, $GA₁₅$, $GA₂₄$, and $GA₃₄$ (GAs that are not members of the early-13-hydroxylation pathway) are also present in trace amounts in tall maize (Fujioka et al., 1988b). Nothing is known about their biosynthetic origin or their biological role in the control of maize shoot growth.

Five endogenous GAs have been identified from vegetative shoots of rice (Kobayashi et al., 1988). A11 are members of the presumptive early 13-hydroxylation pathway. Studies of the two GA mutants, *dx* and *dy,* indicate that the *dy* mutant controls the step GA20 to GA,, and the *dx* mutant controls a step before GA_{53} . GA_1 has relatively high bioactivity and GA20 has low bioactivity when assayed on the *dy* dwarf mutant of rice (Murakami, 1972). The dy mutant accumulates $GA₂₀$ and has reduced levels of $GA₁$ (Kobayashi et al., 1989). $GA₂₀$ and $GA₁$ have similar bioactivities when assayed on the dx mutant (Murakami, 1972), and levels of endogenous $GA₂₀$ and $GA₁$ are low (Kobayashi et al., 1989). The data support the position that GA_{20} is bioactive because of its metabolism to $GA₁$.

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Abbreviations: AcOH, acetic acid; AE, acidic ethyl acetate-soluble fraction; endo, **15,16** double bond isomer; EtOAc, ethyl acetate; *iso-*GA₃, 19,2-isomeric lactone of GA₃; KRI, Kovats retention index; MeOH, methanol; NB, neutra1 butanol-soluble fraction; NBE, acidic ethyl acetate-soluble fraction recovered from hydrolyzed NB fraction; Rt, retention time.

Figure 1. The structures of the C₁₉-GAs relevant to this study.

In addition to the GAs identified from rice shoots, GA4, $GA₉$, $GA₁₂$, $GA₁₇$, $GA₂₄$, $GA₃₄$, $GA₄₄$, and $GA₅₁$ have been isolated from reproductive organs (Kobayashi et al., 1984, 1988). This is the only identification of $GA₄$ in rice. Metabolic steps have been defined from anthers only. They are GA_{12} to GA_{15} , GA_{53} to GA_{44} , and GA_{20} to GA_1 (Kobayashi et al., 1990).

Twenty GAs have been isolated from the early bolting stage of tall *Arabidopsis* (ecotypè Landsberg *erecta)* (Talon et al., 1990b). They are members of three biosynthetic pathways, the early 13-hydroxylation pathway (eight GAs), the early-3-hydroxylation pathway (seven GAs), and the early non 3,13-hydroxylation pathway (five GAs). The three hypothetical pathways originate from GA_{12} and converge to GA₁. The two dwarf mutants *ga*4 and *ga5* have been analyzed in terms of these three pathways (Talon et al., 1990b; Zeevaart and Talon, 1992). The *ga4* mutant blocks 3P-hydroxylation at three different steps, GA_{20} to GA_1 (late in the early 13-hydroxylation pathway), GA_9 to GA_4 (late in the early non-3,13-hydroxylation pathway), and probably GA_{12} to GA14 (early in the early 3-hydroxylation pathway). **GA** levels are relatively high before the blocks and relatively low after the blocks. GA_{20} had relatively low bioactivity, and GA_1 had high bioactivity on the *ga4* mutant.

The *ga5* mutant blocks the oxidative remova1 of carbon-20 and also, possibly, the oxidation of the carbon-20 methyl group to the alcohol. The mutant controls the steps $GA₅₃$ to GA_{44} and GA_{19} to GA_{20} (early 13-hydroxylation pathway), GA_{12} to GA_{15} and GA_{24} to GA_{9} (early non-3,13-hydroxylation pathway), and GA_{14} to GA_{37} and GA_{36} to GA_{4} (early 3hydroxylation pathway). GA levels are relatively high for GAs before the blocks and relatively low for GAs after the blocks. It has been concluded (Talon et al., 1990b; Zeevaart and Talon, 1992) that 3β -hydroxylation is the critical feature for stem elongation, not the per se activity of $GA₁$, and that both GA_4 and GA_1 are active per se.

Here, we demonstrate the metabolism of GA_4 to GA_1 in vegetative shoots of maize, rice, and *Arabidopsis.* We also show that GA_4 and GA_1 have similar bioactivities when assayed on the *dl* mutant of maize and on the *dx* and dy mutants of rice. For *d5,* maize GA, is more active than GA,. For both the *ga5* and *ga4 Arabidopsis* mutants, GA, is more active than GA_1 at low dosages and less active than GA_1 at higher dosages.

MATERIALS AND METHODS

CAs

 $[17^{-13}C, ^{3}H]GA_{4}$ (0.979 atoms of ¹³C molecule⁻¹, 0.52 GBq $mmol^{-1}$) was synthesized from unlabeled GA_4 by the method of Fujioka et al. (1988a) for the synthesis of $[17⁻¹³C₁³H]GA₁$. [17-¹³C,³H]GA₄ was purified by silica gel column chromatography (n -hexane:EtOAc:AcOH, 7:3:0.2), followed by silica gel TLC (EtOAc:CHCl₃:AcOH, 15:5:1); [17-¹³C,³H]GA₄ was recovered from the zone with R_F 0.6 to 0.7. No radioactive impurities were detected after HPLC analysis of the recovered $[17⁻¹³C₃³H]GA₄$, and GC-MS analysis showed its purity to be greater than 99.9%. The GA_4 and GA_1 samples used for the bioassays were also shown to be greater than 99.9% pure by GC-MS. [17-¹³C,³H]GA₄ was dissolved in ethanol:H₂O (1:1, v/v) for metabolic studies; GA_1 and GA_4 were dissolved in acetone: $H_2O(1:1, v/v)$ for bioassays.

Plant Material

The origin of the *Zea* mays L. (maize) seed of the tall phenotypes segregating for the *d2* and *d5* mutants is given by Fujioka et al. (1988a). The seed of the tall phenotype of *Oyza satiua* L. (rice) (cv Nipponbare, previously called Nihonbare) and the dwarf mutants *dx* (cv *Tan-ginbozu)* and *dy* (cv Waito-C) originated from Dr. Hitoshi Saka (National Institute of Agrobiological Resources, Tsukuba-shi, Ibaraki

305, Japan). The *Arabidopsis thaliana* (L.) Heynh. seed of the tall phenotype (ecotype Landsberg *erecta)* and dwarf mutants *ga4* and *ga5* originated from Dr. Maarten Koomneef (Agricultural University, Wageningen, the Netherlands) via Dr. Judy Brusslan (Department of Biology, University of California, Los Angeles, CA).

For bioassay and metabolic studies, maize and *Ara bidopsis* plants were grown in the University of California, Los Angeles, greenhouse under natural sunlight supplemented with Sylvania incandescent 300-W PS35 Excel bulbs to give a daylength of at least 12 h. The rice plants used for bioassay and metabolic studies were grown in an incubator chamber maintained at 28°C under continuous light supplied by General Electric F96PG17CW fluorescent bulbs.

Bioassays

The maize seedling bioassay was described by Phinney and Spray (1982), and the rice microdrop bioassay was discussed by Murakami (1968). For the *Arabidopsis* assay, seeds were soaked in 0.1% agarose at 4°C for 48 h and sown in **15-** X 10-cm plastic trays filled with soi1:vermiculite:perlite (l:l:l), 24 seeds per tray, and covered with a 3-mm layer of fine vermiculite. Before treatment, the plants were thinned to 10 per tray. The GA solution of 2 μ L was added to the base of the fully developed vegetative rosette just before bolting (plants were about 3 weeks old). Five dosage levels were used with 10 plants per dosage level. After shoot elongation (10-14 d after treatment), plant height was measured from the soil level to the top of the inflorescence. Response data were calculated from the averages of the 10 treatments at each dosage level.

Metabolic Studies: Treatment, Extraction, and Purification

 $[17¹³C₁³H]GA₄$ was injected into the coleoptilar node of maize and rice seedlings at the three- to four-leaf stage; for *Arabidopsis,* the labeled GA, was injected into the basal petiole of the uppermost leaf of the vegetative rosette just before bolting. For maize, five seedlings of each genotype were each injected with 1510 Bq of $[17^{-13}C, ^{3}H]GA_{4}$ (2 μL); for rice, 97 tall and 100 *dx* and dy seedlings were each injected with 152 Bq of [17-'3C,3H]GA, (1 pL); for *Arabidopsis,* 30 plants of each genotype were each injected with 215 Bq of $[17^{-13}C^{3}H]GA_{4}$ (0.5 μ L). Incubation times were 8 (rice), 12 (maize), and 24 h *(Arabidopsis).* After incubation, the shoots were harvested and immediately frozen in dry ice. The frozen plant material was homogenized and extracted twice at 4°C with MeOH: H_2O (4:1, v/v). After filtration and removal of the MeOH, the aqueous residue was solvent fractionated to give the AEs as described by Fujioka et al. (1988a) and the NBs, as described by Yokota et al. (1980; see fig. 2.8, **p.** 126). The AEs and NBs were evaporated to dryness in vacuo and purified further (see below).

A€

The AE in H₂O (1 mL) was loaded onto a Bond Elut C_{18} column (1 g; Analytichem Intemational, Harbor City, CA). The column was washed with H₂O (2 mL) and then eluted with MeOH (2×2 mL). The MeOH eluates were combined, evaporated to dryness redissolved in MeOH (1 mL), and loaded onto a Bond Elut DEA column (500 mg) that had a head of DEAE-Sephadex A-25 (1 mL of gel suspended in MeOH). The column was washed with MeOH (1 mL) and then eluted with 1 N AcOH in MeOH (5 **X** 1 mL). The fractions containing radioactivity (usually fractions 2-4) were combined and dried under a stream of N_2 . This combined fraction was dissolved in 40% MeOH (aqueous) (200-250 μ L) and injected onto a HPLC column of Nucleosil 5 C₁₈ (10) cm X *6* mm, i.d.). The column was eluted as described by Kobayashi et al. (1990). Fractions were collected at 1-min intervals, and an aliquot of each fraction was analyzed by liquid scintillation spectrometry. Radioactive fractions were combined according to their Rt, and each of the combined fractions was purified further by HPLC on a column of Nucleosil 5 $N(CH_3)_2$ (10 cm \times 6 mm, i.d.). The column was eluted with 0.05% AcOH in MeOH at a flow rate of 1.5 mL min-', and fractions were collected at I-min intervals. The radioactivity in each fraction was determined by liquid scintillation spectrometry, and radioactive fractions were combined according to their Rt, concentrated, and derivatized for GC-MS analysis (Gaskin and MacMillan, 1991).

NB

The NB was passed through the two Bond Elut columns as described for the AE, and the recovered radioactive fraction was hydrolyzed with cellulase **(30** mg, type I; Sigma) in acetate buffer (1 μ , pH 4.5, 1 mL) at 30°C. After 24 h, the solution was acidified with 6 N HCl and extracted with EtOAc. The EtOAc extract (NBE) was dried, redissolved in MeOH (1 mL), and purified using a Bond Elut DEA column, followed by HPLC as described for the AE. The fractions containing radioactivity were combined according to their Rt values and dried. Each dried fraction was redissolved in MeOH and methylated with excess diazomethane, dried, and trimethylsilylated with N-methyl-N-trimethylsilyltifluoroacetamide, to give methyl ester, trimethylsilyl ether derivatives for GC-MS analysis (Gaskin and MacMillan, 1991).

Control Experiment for Metabolic Studies

['3C,3H]GA4 was injected into *dl* maize seedlings, and the seedlings were frozen immediately after injection, extracted, purified, and analyzed as described in 'Metabolic Studies: Treatment, Extraction, and Purification."

CC-MS

Mass spectra were obtained using a computerized VG 7050 mass spectrometer (VG Analytical, Manchester, UK) fitted with a DANI 3800 GC (Kontron Instruments, St. Albans, UK) equipped with a WCOT vitreous silica column (25 m **X** 0.2 mm, i.d.; GC^2 Chromatography, Altrincham, UK) coated with a 0.25 - μ m layer of bonded OV-1. The initial GC column temperature was 50°C. After injection, the temperature was held at 50°C for 2 min, followed by temperature programming at 10° C min⁻¹ to 150° C and then 3° C min⁻¹ to 300° C. The use of the GC-MS instrument and GC column was described by Gaskin et al. (1984).

~ ~ ~~~ **Table 1.** "C-Labeled metabolites identified by GC-MS after injection of ['3C,3H]CA4 *into* tall, dl, and d5 maize (4.85 *pg,* 7.55 *X* 103 *Bq* each), *tal1* (9.44 *pg,* 14.7 *X* 103 *Bq),* dx, and dy rice (9.76 *pg,* 15.2 x 103 *Bq* each), *and tal/,* ga4, and ga5 Arabidopsis (4.14 *pg,* 6.45 **x** !O3 *Bq* each)

^a Metabolites identified by comparison of GC-MS data and KRIs with published values (Gaskin and MacMillan, 1991). Representative data are presented in Table II. b Unusual Rt due to a lower concentration of AcOH in the so ^b Unusual Rt due to a lower concentration of AcOH in the solvent system.

RESULTS

The fractions from each genotype that were analyzed for $13C$ -metabolites are shown in Table I. The $13C$ -metabolites were identified by comparison of the full-scan GC-MS and KRI data with those of reference compounds (Kovats, 1958; Gaskin and MacMillan, 1991); typical characterizing data are given in Table 11.

In the free GA fraction, $[^{13}C]GA_1$ was identified as a metabolite of $[^{13}C, ^{3}H]GA_4$ from all nine kinds of plant material. Eleven additional ¹³C-labeled products were identified from other radioactive fractions. They were GA_{2} , GA_{34} , GA_{58} , 15-epi-GA $_{63}$, and 16-epi-GA $_{82}$ from maize, rice, and Arabi*dopsis;* **16a,17-H2-16,17-(OH)2-GA,** from maize and rice; endo-GA₄ from rice and Arabidopsis; 3 -epi-GA₁ from maize; and 2β -OH-GA₂, endo-GA₃₄, and GA₇₁ from Arabidopsis.

In the hydrolyzed fraction (NBE) of the presumptive bound GAs, $[{}^{13}C]GA_1$ was identified from maize and rice. Other ${}^{13}C$ labeled products also identified were GA_2 and GA_4 from maize, rice, and Arabidopsis; 2β -OH-GA₂, 16α , 17-H₂-16, 17- $(OH)_2$ -GA₄, and GA₃₄ from maize and rice; 3-epi-GA₁ and 3epi-GA₂ from maize; and 15-epi-GA $_{63}$ and 16-epi-GA $_{82}$ from rice .

A control experiment was designed to determine whether any of the identified GAs were artifacts of extraction and purification rather than metabolites of the added $[^{13}C, ^{3}H]GA_4$ (see "Materials and Methods"). Six HPLC fractions contained radioactivity; one had the Rt corresponding to GA_4 ; it was not analyzed further. The second fraction was shown by GC-MS to contain $[^{13}C]GA_2$. The other four fractions had only traces of radioactivity, and they were not analyzed chemically .

The dosage-response curves for GA_4 and GA_1 are shown

in Figure 2. For the d_1 maize and dx and dy rice mutants, GA_4 and GA_1 have similar bioactivities. For d5 maize, GA_1 is more active than GA_4 . For ga5 and ga4 Arabidopsis mutants, $GA₄$ is more active than $GA₁$ at low dosages and less active at high dosages.

DISCUSSION

The metabolism of $[{}^{3}H]GA_4$ to presumptive GA_1 has been reported for seedlings of rice (Durley and Pharis, 1973) and Phaseolus *coccineus* (Turnbull et al., 1986), maturing seeds of maize (Rood et al., 1983), germinating seeds of bean (Phas*eolus vulgaris*) (Yamane et al., 1975), germinating pollen of knobcone pine (Pinus attenuata) (Kamienska et al., 1976), and cell cultures of anise (Pimpinella anisum) (Koshioka et al., 1983a) and carrot (Daucus carota) (Koshioka et al., 1983b). However, in all of these examples, the presence of GA_1 was based on HPLC and/or GC Rt values. GC-MS-single ioncurrent monitoring has been used to identify $[{}^{2}H]GA_1$ as a metabolite of [²H]GA₄ from cell cultures of rice (Koshioka et al., 1991). For Arabidopsis there have been two preliminary reports of the metabolism of GA_4 to GA_1 with GC -MS identification (Kobayashi et al., 1991; Zeevaart and Talon, 1992). The results of the study reported here establish the metabolism of $[^{13}C, ^{3}H]GA_4$ to $[^{13}C]GA_1$ in shoots of maize, rice, and Arabidopsis using full-scan GC-MS and KRIs.

The amounts of $[{}^{13}C]GA_1$ formed from $[{}^{13}C,{}^{3}H]GA_4$ can be estimated from the radioactivities of the fractions from which $[^{13}C]GA_1$ was identified (Table I). For example, for tall plants of maize, rice, and Arabidopsis, the amounts of $[^{13}C]GA_1$ formed are 0.93, 0.39, and 0.71 ng g^{-1} fresh weight of tissue, respectively. These values are comparable to the reported endogenous levels of 0.12 ng g^{-1} fresh weight for maize

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GA from Purified Fractions/ Reference Compound ^a	KRI lons (mass/intensity [lnt.])														
$[^{13}C]CA$	2674	Mass	131	168	181	194	208	236	239	314	377	417	449	492	507
GA ₁ reference	2673	Int. Mass Int.	21 131 9	18 167 6	16 180 7	18 193 6	38 207 23	14 235 6	11 238 5	14 313 9	19 376 14	5 416 5	21 448 18	10 491 9	100 506 100
$[$ ¹³ C]3-epi-GA ₁	2793	Mass Int.	181 14	208 28	236 10	314 10	377 28	417 8	432 9	449 31	460 9	479 3	492 8	507 100	
3-epi-GA, reference	2793	Mass Int.	180 11	207 55	235 6	313 7	376 29	416 6	431 8	448 31	459 8	478 3	491 7	506 100	
$[^{13}C]GA2$	2761	Mass Int.	131 100	226 31	262 11	285 -15	290 24	329 14	387 -11	419 42	450 10	451 -13	493 10	494 9	509 22
GA ₂ reference	2762	Mass Int.	130 100	225 12	261 8	284 10	289 26	329 6	386 7	419 15	449 6	451 6	493 13		508 29
$[^{13}C]2\beta$ -OH-GA ₂	2906	Mass	131	147	217	262	284	290	373	417	449	507	539	582	597
2β -OH-GA ₂ reference	2905	Int. Mass Int.	100 130 94	37 147 10	24 217 16	14 261 13	21 283 15	22 289 25	11 372 13	10 416 7	14 449 19	22 506 18	6 539 8	5 581 12	61 596 100
$[$ ¹³ C]3-epi-GA ₂ (putative)		Mass Int.	131 100	226 24	262 18	290 41	329 25	344 16	372 25	387 13	419 30	451 12	493 9	494 8	509 21
$[^{13}C]GA$	2511	Mass	129	202 37	225 92	226 92	234 47	262 31	285	290 57	329	359	387	391	419
GA4 reference	2510	int. Mass Int.	64 129 54	201 26	224 77	225 78	233 41	261 28	100 284 100	289 58	23 328 25	11 358 10	16 386 17	12 390 11	16 418 22
$[$ ¹³ C]endo-GA ₄	2481	Mass	129	202	226	230	234	262	285	290	301	359	387	391	419
endo-GA4 reference	2478	int. Mass Int.	45 129 25	34 201 25	47 225 41	34 229 30	26 233 19	49 261 46	29 284 39	100 289 100	19 300 22	13 358 12	10 386 10	6 390 10	48 418 75
$[^{13}C]16\alpha, 17-H_2-16, 17-(OH)_2-GA_4$	2932	Mass	147	239	269	299	359	433	493	507	582	597			
16α , 17-H ₂ -16, 17-(OH) ₂ -GA, reference	2932	Int. Mass Int.	14 147 6	11 239 $\overline{2}$	11 269 9	14 299 13	6 359 5	3 433 $\mathbf{2}$	100 493 100	$\mathbf{1}$ 506 3	2 581 2	$\mathbf{1}$ 596 1			
$[{}^{13}C]GA_{34}$	2670	Mass	147	202	217	224	230	262	289	314	388	417	432	460	507
GA ₃₄ reference	2669	Int. Mass Int.	55 147 13	23 201 22	36 217 28	26 223 30	23 229 23	16 261 14	17 288 24	12 313 12	7 387 7	8 416 9	5 431 5	4 459 4	100 506 100
$[^{13}C]$ endo-GA ₃₄	2644	Mass	147	211	230	262	284	314	373	417	460	507			
endo- GA_{34} reference	2642	Int. Mass Int.	15 147 18	33 211 44	10 229 8	11 261 6	100 284 100	11 314 9	6 372 3	3 416 2	5 459 9	49 506 57			
$[$ ¹³ C]CA ₅₈	2738	Mass	224	228	267	283	327	357	373	385	400	417	447	452	507
GA ₅₈ reference	2740	int. Mass Int.	100 223 92	44 227 48	61 266 67	67 282 90	27 326 42	55 356 100	29 372 40	55 384 94	10 399 20	60 416 93	7 446 10	16 451 8	17 506 35
$[^{13}C]15$ -epi-GA ₆₃	2786	Mass	157	224	283	288	358	373	385	417	447	475	492	507	
15-epi-GA63 reference		Int. Mass Int.	33 156 100	25 223 28	22 282 30	6 287 17	12 357 8	10 372 5	6 384 7	7 416 10	18 446 11	3 474 $\mathbf{1}$	9 491 24	100 506 76	
$[^{13}C]GA71$	2695	Mass	129	222	228	267	283	314	327	357	385	417	447	492	507
$GA71$ reference	2693	Int. Mass Int.	95 129 27	100 221 53	55 227 42	35 266 58	70 282 77	41 313 33	28 326 39	70 356 98	60 384 94	57 416 100	9 446 13	11 491 24	18 506 46
$[^{13}C]16$ -epi-GA ₈₂	2821	Mass	129	226	234	262	285	290	380	449	477	481	491	494	509
16-epi-GA ₈₂ reference	2822	int. Mass Int.	79 129 47	100 225 76	39 233 56	37 261 49	31 284 29	68 289 100	30 379 26	16 448 15	15 476 20	17 480 12	13 490 11	33 493 5	15 508 10

Table II. *CC-MS data used for the identification of CAs listed in Table I*

a AS methyl ester, trimethylsilyl ether derivatives.

 $\label{eq:2} \frac{1}{2} \sum_{i=1}^n \frac{1}{$

Figure 2. Dosage-response curves showing relative bioactivities of **GA4** and **CAI** assayed on d5 and dl mutants of maize **(A),** *dx* and dy mutants of rice (B), and ga5 and *ga4* mutants of Arabidopsis (C). Each point represents the mean of 10 to 20 measurements. Vertical bars represent SE.

(Fujioka et al., 1988a), 0.16 to 0.25 ng g^{-1} fresh weight for rice (Kobayashi et al., 1989), and **0.34** ng g-I dry weight for Arabidopsis (Talon et al., 1990b).

In addition to $[^{13}C]GA_1$, 12 other ¹³C-labeled metabolites were identified. Of these, GA_{34} (2 β -OH-GA₄) is a bioinactive metabolite from GA₄ (Yamane et al., 1973). 16 α ,17-H₂-16,17- $(OH)_2$ -GA₄, GA₅₈, 15-epi-GA₆₃, GA₇₁, and 16-epi-GA₈₂ are metabolites from GA₄, unrelated to the biosynthesis of GA₁. GAss has been identified as a natural product from seeds of *Cucurbita maxima* (Beale et al., 1984), GA₇₁ from sporophytes of Cyathea australis (Yamane et al., 1985) and from the gai mutant of Arabidopsis (Talon et al., 1990a), and 16α , 17-H₂-16,17-(OH)z-GA4, and 16-epi-GAs2 from seeds of *Lupinus* albus (Gaskin et al., 1992). 15-epi-GA₆₃ has not been identified as a natural product. $[13C]GA_2$ is an artifact because of its identification from a control experiment using $[{}^{13}C, {}^{3}H]GA_4$ and d1 seedlings. $[{}^{13}C]3$ -epi-GA₁ has been shown to be an artifact from $[{}^{13}C]GA_1$ in maize (our unpublished data).

There was no evidence in any of the experiments for the metabolism of $[^{13}C, ^{3}H]GA_4$ to $[^{13}C]GA_7$ or to $[^{13}C]GA_3$ (Table I). By contrast, GA_4 is metabolized to GA_1 and to GA_3 via **GA7** in the fungus *Gibberella* fujikuroi (Bearder et al., 1975).

The data concerning the bioassays from all six mutants can be interpreted to mean that both GA_4 and GA_1 are active per se. Our metabolic studies show that at least some of the GA4 bioactivity could be due to its metabolism to $GA₁$. Although the question of per se activity for GA_4 and GA_1 can be discussed at length from these kinds of data, the question will probably not be resolved from bioassay and metabolic studies alone. The answer could come from bioassay and metabolic studies conducted in conjunction with the use of mutants and/or chemicals that block 13-hydroxylation (Zeevaart and Talon, 1992). The answer could also come from the isolation of a GA receptor followed by receptor-hormone interaction studies.

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