Supplement

Article title: ***Arabidopsis thaliana*** **accumulates DHEA after infection with phytopathogenic fungi – effects on plants and fungi.**

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The following Supporting Information is available for this article:

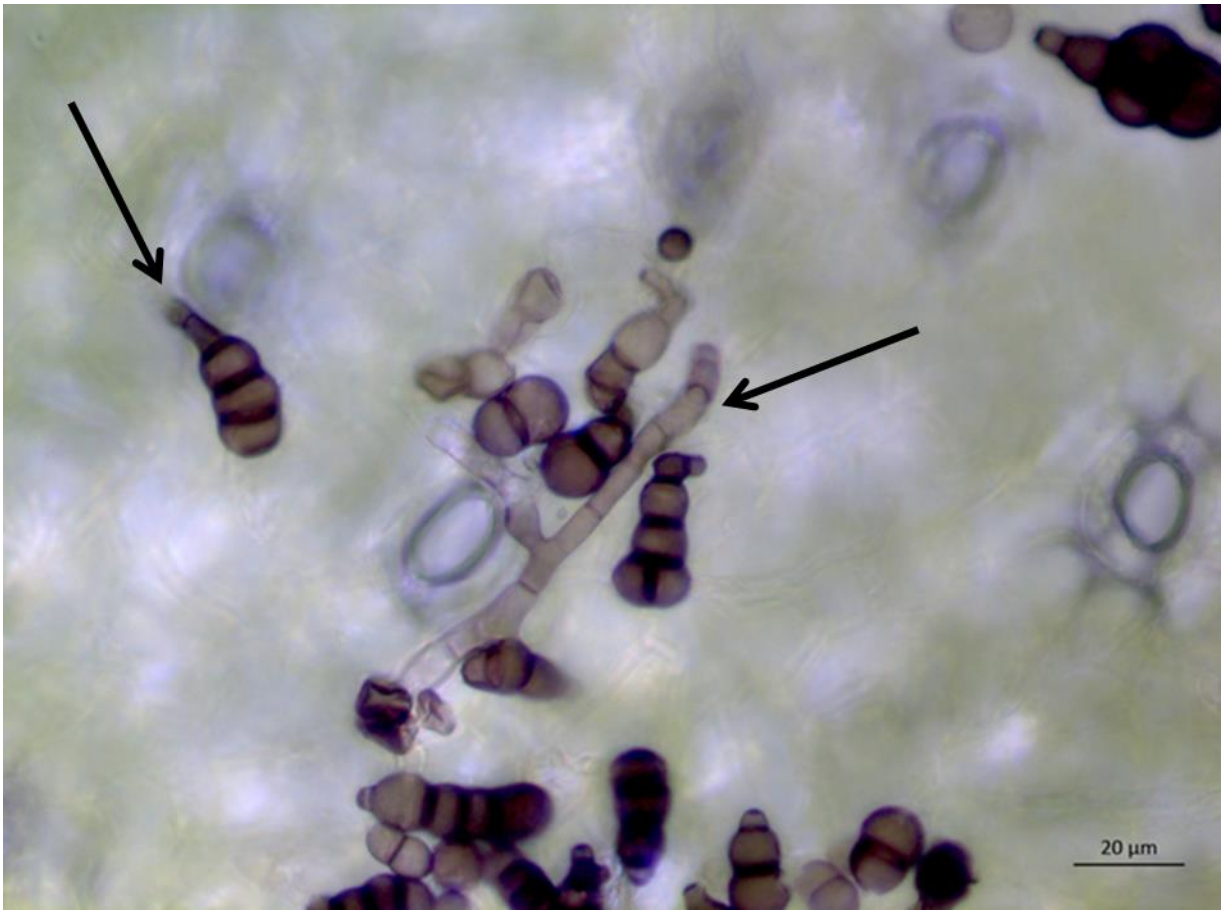

Figure S1: Germination of *Alternaria brassicicola* spores on *Spirodela polyrhiza*. To ensure that *A. brassicicola* is able to infect leaves of the Alismatales species *S. polyrhiza*, we treated leaves of *S. polyrhiza* with a spore solution of *A. brassicicola*. Plants were cultivated as described previously (Appenroth et al., 1996; Appenroth et al., 2018). 24 hours after infection leaves were analyzed using the bright-field of Axio Imager.M2 (Zeiss Microscopy GmbH, Jena, Germany). We could see the germination of *A. brassiciola* spores (black arrows shows hyphae material grown after spore germination) as well as the growth of hyphae through the stomata of *S. polyrhiza*.

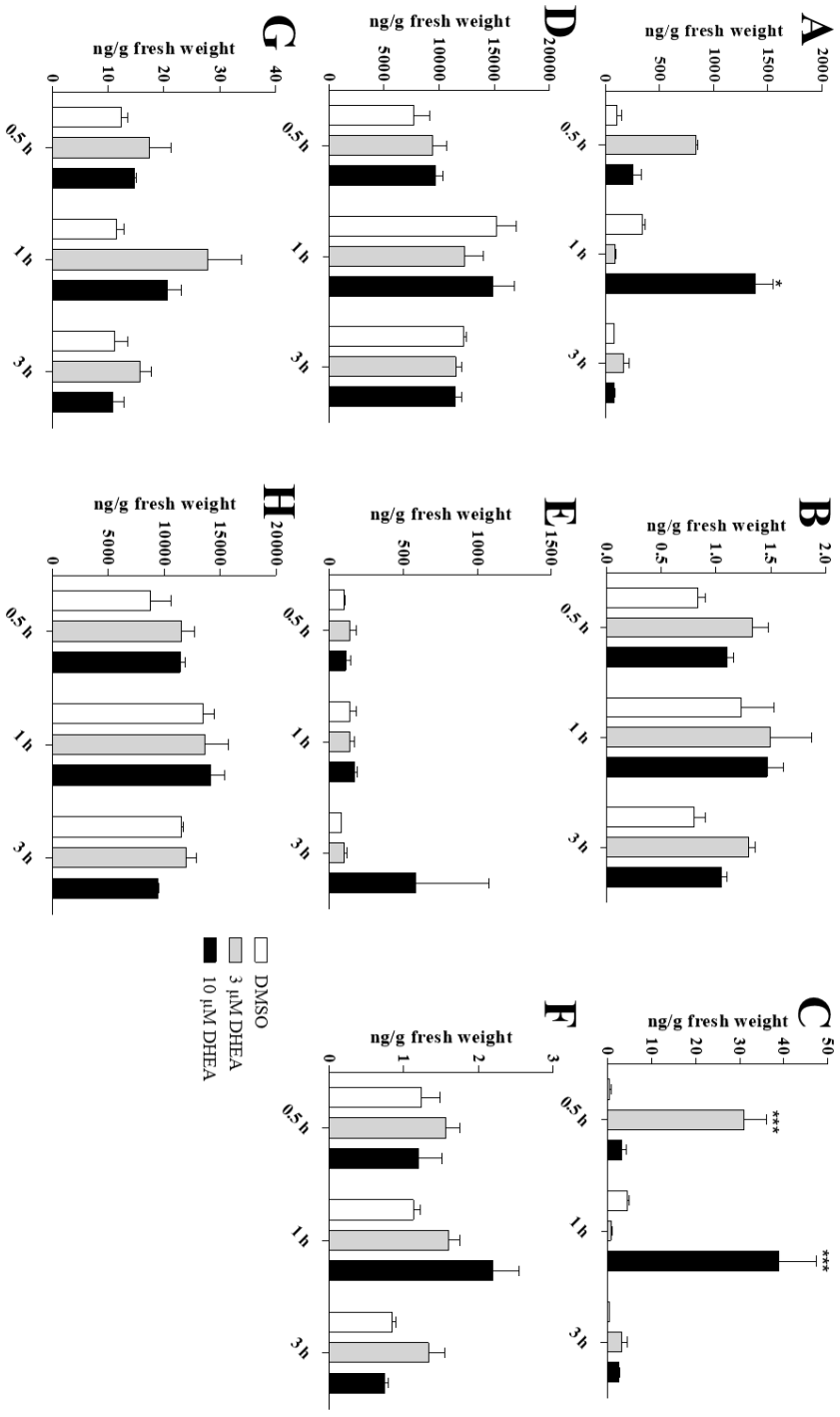

Figure S2: Phytohormone values in *A. thaliana* after DHEA-treatment. The graph depicts the phytohormone values in *A. thaliana* shoots after treatment with 3 (grey) or 10 µM (black) DHEA after 0.5, 1 and 3 h compared to the mock-treatment (DMSO; white). We analyzed the values of jasmonate (A), abscisic acid (B), jasmonate-isoleucin conjugates (C), *cis*-OPDA (D), hydroxyjasmonate (E), hydroxyjasmonate-isoleucin (F), carboxy-jasmonate-isoleucin conjugates (G) and dinor-OPDA (H). The graph shows mean ± SEM (n = 3).

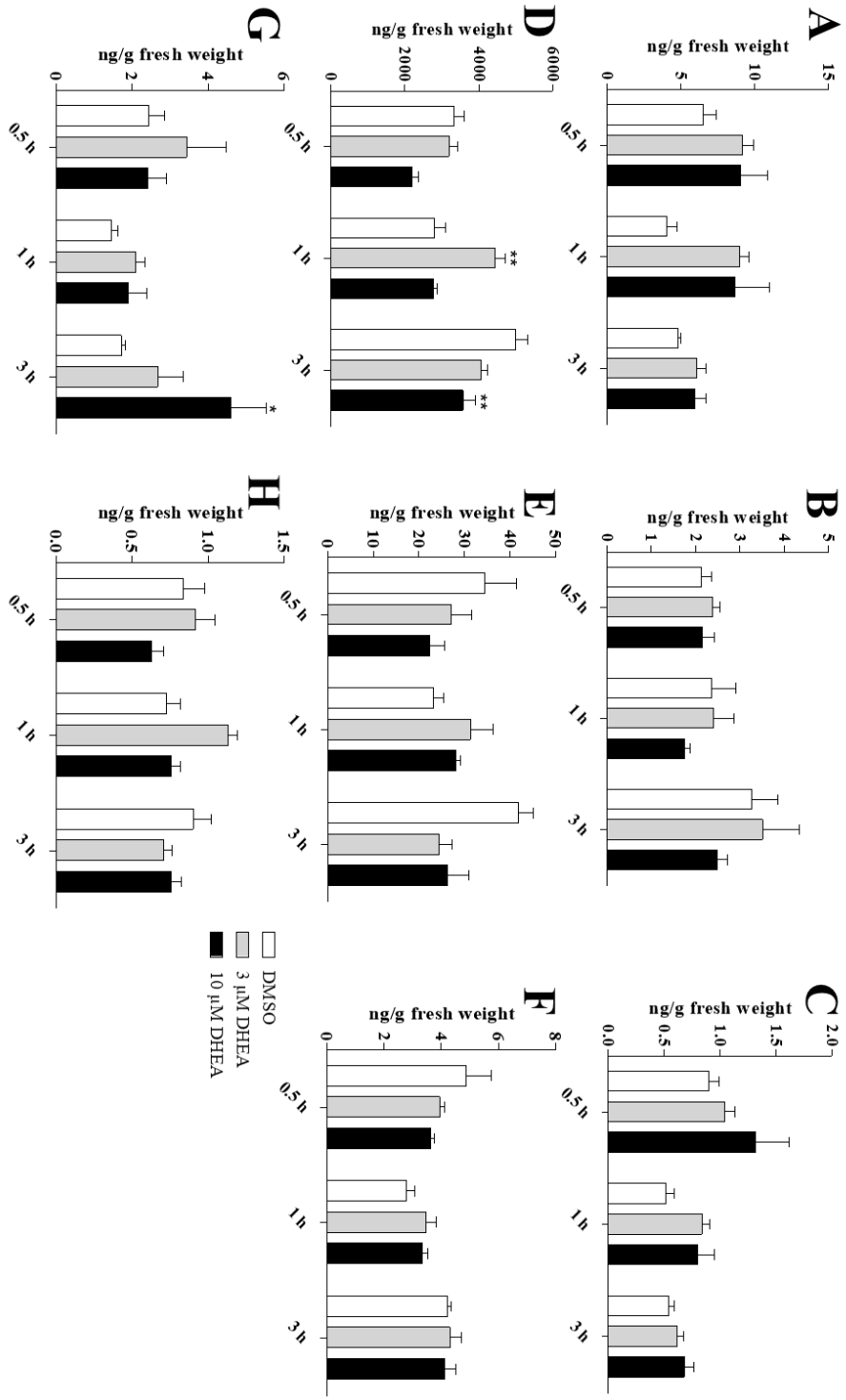

Figure S3: Phytohormone values in *H. vulgare* after DHEA-treatment. The graph depicts the phytohormone values in *H. vulgare* shoots after treatment with 3 (grey) or 10 µM (black) DHEA after 0.5, 1 and 3 h compared to the mock-treatment (DMSO; white). We analyzed the values of jasmonate (A), abscisic acid (B), jasmonate-isoleucin conjugates (C), *cis*-OPDA (D), hydroxyjasmonate (E), hydroxyjasmonate-isoleucin (F) and carboxy-jasmonate-isoleucin conjugates (G). The graph shows mean ± SEM (n = 5).

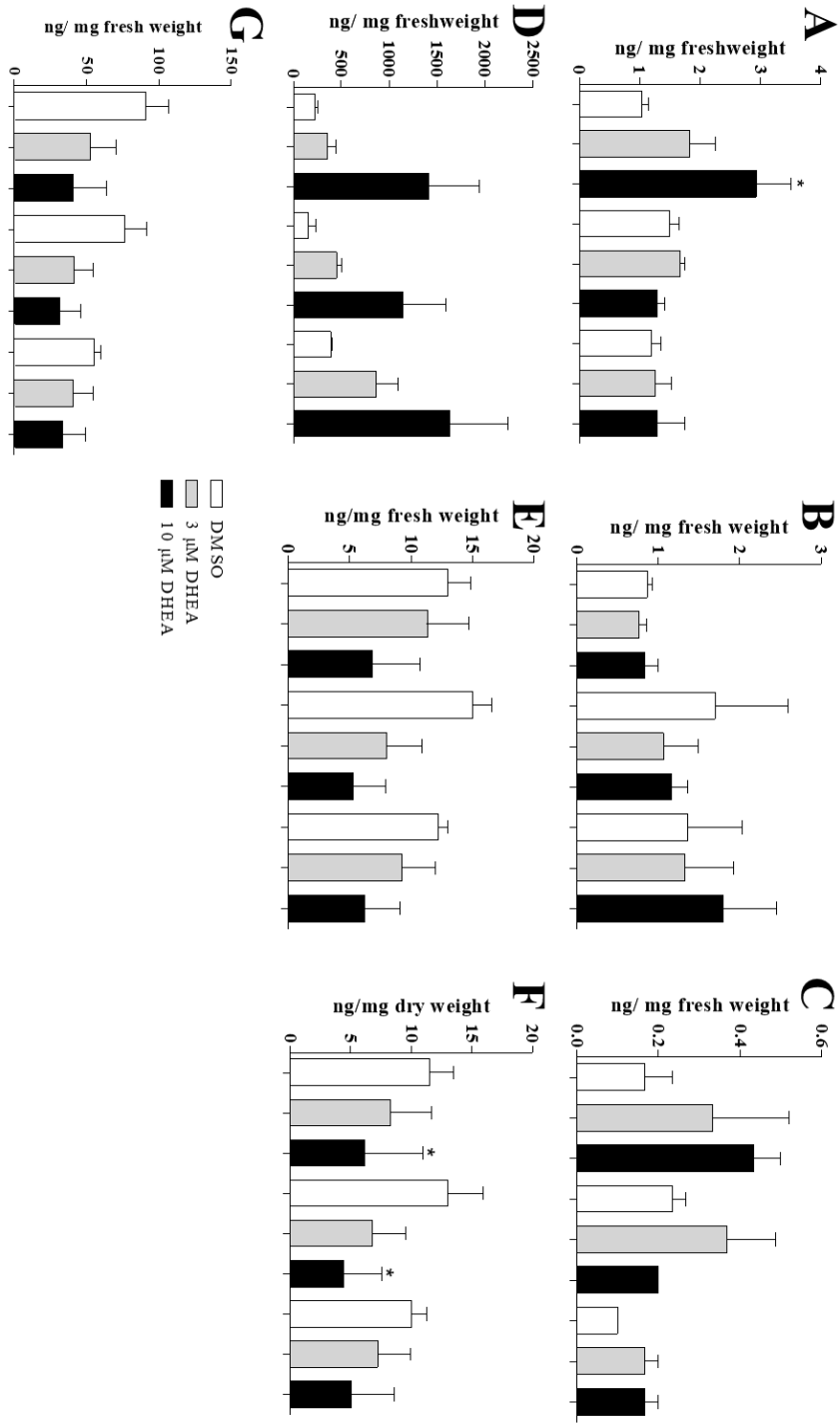

Figure S4: Phytohormone values in *S. polyrhiza* after DHEA-treatment. The graph depicts the phytohormone values in *S. polyrhiza* shoots after treatment with 3 (grey) or 10 µM (black) DHEA after 0.5, 1 and 3 h compared to the mock-treatment (DMSO; white). We analyzed the values of jasmonate (A), abscisic acid (B), jasmonate-isoleucin conjugates (C), *cis*-OPDA (D), hydroxyjasmonate (E), hydroxyjasmonate-isoleucin (F) and carboxy-jasmonate-isoleucin conjugates (G). The graph shows mean ± SEM (n = 5).

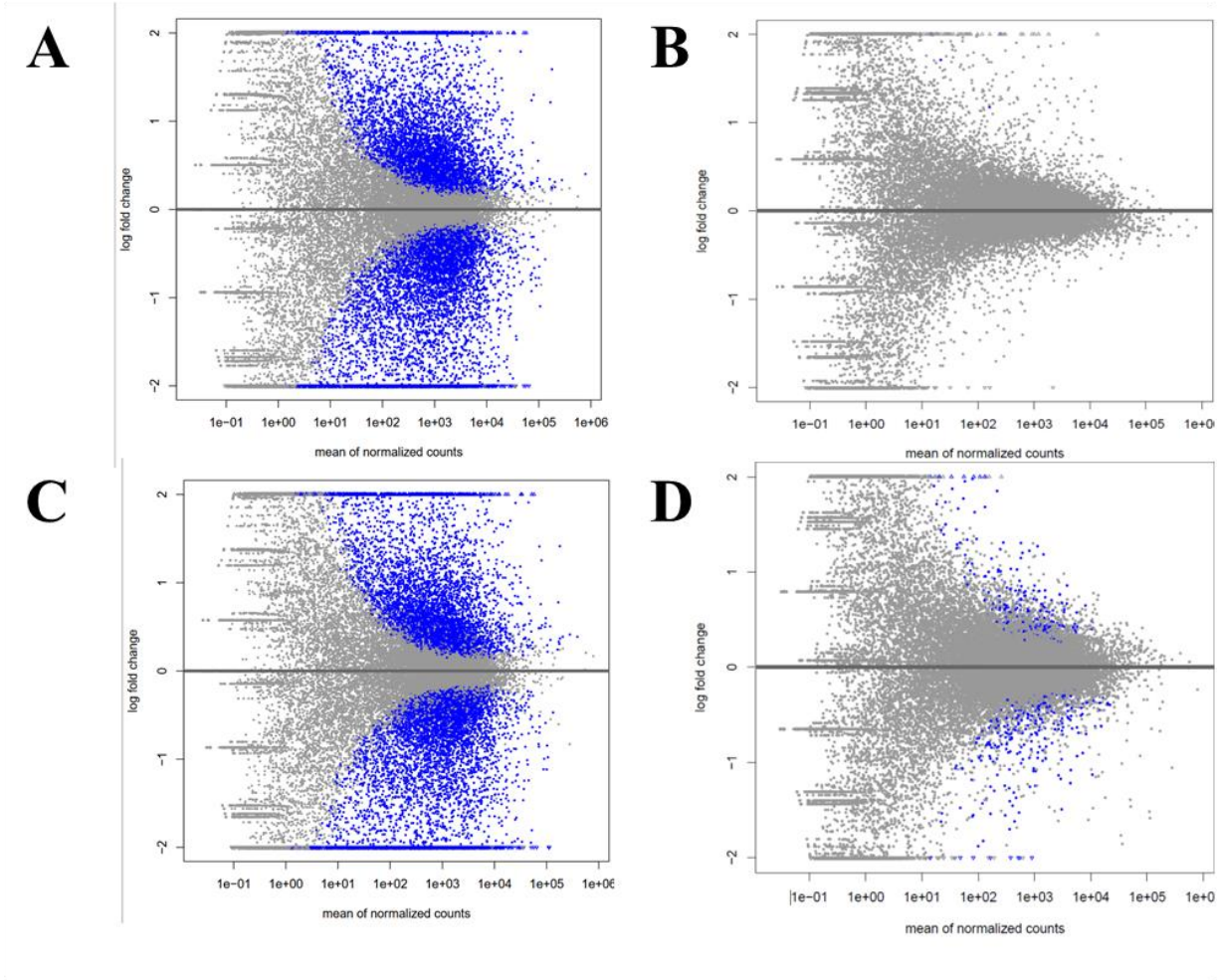

Figure S5: MA plots of RNAseq experiments. The graph depicts the MA plots for the RNAseq experiments within this study. The highest difference of transcripts can be found for infected plants compared to DMSO mock-treatment 24 h after infection (A), while DHEA-treatment compared to DMSO mock-treatment showed the smallest differences (B). Unsurprisingly, plants infected with DHEA-containing spore solution show a big difference compared to uninfected controls (C). Interestingly, infection vs. infection+DHEA-treatment showed stronger differences (D), than DHEA-treatment compared to the mock-treated control (D). The figure depicts MA plots for all conditions.

Table S01: Details of analysis of steroids by LC-MS/MS. A volume of 2 µL was injected into an Agilent 1260 infinity II LC system, consisting of a binary pump G7112B, an autosampler G7167A and a column thermostat G7116A (Agilent Technologies, Santa Clara, CA, USA) without preconcentration or filtering. Chromatographic separation was carried out on a ZORBAX Eclipse XDB-C18 column (50 × 4.6 mm, 1.8 µm) from Agilent Technologies (Santa Clara, CA, USA). A binary solvent system was used as mobile phase consisting of A) 0.05% formic acid in water and B) acetonitrile with a constant flow rate of 1.1 mL/min at 20 °C column temperature. The following gradient was applied: 0.00-0.50 min, 60% A; 0.50-5.00 min, 60-10% A; 5.00-5.05 min, 10-0% A; 5.05-6.50 min, 0% A; 6.50-6.55 min, 0-60% A; 6.55-9.00 min, 60% A. The column outlet was connected to a QTRAP 6500+ triple quadrupole mass spectrometer (AB Sciex LLC, Framingham, MA, USA). The Turbo Spray IonDrive ion source was running in positive ionization mode with 5500 V ion spray voltage and 650 °C turbo gas temperature. The curtain gas was set to 40 psi; the collision gas to 'medium' and both ion source gases 1 & 2 were set to 70 psi. Scheduled multiple reaction monitoring (scheduled MRM) was used to monitor analyte parent ion → product ion fragmentations. Q1 and Q3 quadrupoles were maintained at unit resolution. Analyst 1.6 software (Applied Biosystems) was used for data acquisition and processing. Nona-deuterated progesterone (PO-d_9) was used as internal standard (IS) for quantification. The response factors (analyte x standard^{-1}) of individual steroids relative to the internal standard have been experimentally determined. The table shows mass to charge ratio (*m/z*), retention time (RT), collision energy (CE) and the response factor to the used internal standard (*f*).

Compound	Usage:	*m/z:*	RT [min]	CE [V]	*f*
PR	Quantifier	299→ 281	4.29	15	0.49
	Qualifier	317→ 299		13	
PO	Quantifier	315→ 97	4.43	25	1.23
	Qualifier	315→ 109		30	
DHP	Quantifier	317→ 299	5.31	17	0.23
	Qualifier	317→ 281		19	
17α-OHPR-	Quantifier	315→ 297	2.80	13	0.11
	Qualifier	333→ 297		13	
DHEA	Quantifier	289→ 271	3.01	9	0.08
	Qualifier	289→ 253		15	
17α-OHPO	Quantifier	331→ 97	3.15	27	0.57
	Qualifier	331→ 109		30	
AD	Quantifier	287→ 211	3.07	27	0.09
	Qualifier	287→ 173		29	
TO	Quantifier	289→ 97	2.58	25	1.34
	Qualifier	289→ 109		30	
DHT	Quantifier	291→ 255	3.45	21	0.84
	Qualifier	291→ 273		19	
PO- D_9	Quantifier	324→ 100	4.43	29	-
	Qualifier	324→ 113		33	

Table S02: Steroid contents of *Alternaria brassicicola* infected *Arabidopsis thaliana* shoot material plants 4, 6 and 8 days post infection.

We here show the results of steroid measurement of *A. thaliana* plants infected with *A. brassiciola* compared to uninfected controls (control). We here show three independent experiments' mean and standard deviation (SD). All results are given in ng mg^{-1} dry weight.

	Day 4			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	6,02E-03	2,49E-03	2,03E-02	5,11E-03
Pregnenolone	0,00E+00	0,00E+00	5,05E-02	1,13E-02
Progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5a-pregnan-3,20-dione	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Dihydrotestosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

	Day 6			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	7,10E-03	8,53E-04	2,36E-02	7,45E-03
Pregnenolone	0,00E+00	0,00E+00	1,70E-02	2,94E-02
Progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5a-pregnan-3,20-dione	0,00E+00	0,00E+00	0,00E+00	0,00E+00
diOH-testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

	Day 8			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	1,13E-02	1,08E-02	3,36E-02	1,98E-02
Pregnenolone	0,00E+00	0,00E+00	5,51E-02	4,77E-02
Progesterone	0,00E+00	0,00E+00	1,12E-02	1,95E-02
5a-pregnan-3,20-dione	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Dihydrotestosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

Table S03: Steroid contents of *Alternaria brassicicola* infected *Arabidopsis thaliana* root material plants 4, 6 and 8 days post infection.

We here show the results of steroid measurement of *A. thaliana* plants infected with *A. brassiciola* compared to uninfected controls (control). We here show three independent experiments' mean and standard deviation (SD). All results are given in ng mg^{-1} dry weight.

	Day 4			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	9,75E-03	4,47E-03	9,50E-03	2,91E-03
Pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Progesterone	6,93E-03	6,04E-03	3,55E-03	3,12E-03
5a-pregnan-3,20-dione	4,52E-03	7,83E-03	1,05E-02	9,63E-03
Dihydrotestosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

	Day 6			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	1,35E-02	7,30E-03	1,34E-02	5,35E-03
Pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Progesterone	0,00E+00	0,00E+00	1,89E-03	3,27E-03
5a-pregnan-3,20-dione	1,52E-02	3,48E-03	8,89E-03	8,39E-03
Dihydrotestosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

	Day8			
	Control		Infected	
	Mean	SD	Mean	SD
DHEA	2,87E-03	1,12E-03	2,57E-02	1,87E-02
Pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
5a-pregnan-3,20-dione	0,00E+00	0,00E+00	2,01E-02	2,62E-02
Dihydrotestosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Testosterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-progesterone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
17α-OH-pregnenolone	0,00E+00	0,00E+00	0,00E+00	0,00E+00
Androstenedione	0,00E+00	0,00E+00	0,00E+00	0,00E+00

Table S04: Details of analysis of phytosterol pattern in *A. thaliana* by GC-MS. Phytosterols were quantified by GC-MS using 5 mg lypholized plant material. Extraction process and quantifications follows our previous protocols (Müller et al., 2017). The quantification was managed with six-point calibration curves ranged from 0-250 ng mL^{-1} for each analyte. The results were normalized to the dried fungal biomass and expressed as ng per mg dried biomass (Liebl et al., 2023).
The table shows retention time (RT), mass to charge ratio (Quantifier [m/z]) and relative retention time (RRT).

Compound	RT [min]	Quantifier [*m/z*]	RRT
Sterols			
5α-Cholestane	10.464	217,2	1.000
Squalene	10.003	137.1	0.956
Desmosterol-d6	13.603	447.4	1.300
Cholesterol	13.235	329.3	1.265
Cholesterol-d7	13.161	336.4	1.258
Cholestanol	13.338	215.1	1.275
Campesterol	14.498	459.5	1.374
Campestanol	14.378	382.3	1.386
Pregnenolone	10.185	386.2	0.990
Pregnenolone-2-C13-2d	10.168	390.3	0.989
Progesterone	11.024	372.3	1.072
Dehydroepiandrosterone	8.729	268.2	0.849
Allopregnanolone	9.551	388.3	0.929
5a-Cholestan-3-one	13.722	415.3	1.334
5b-Cholestan-3-one	13.115	384.3	1.275
Cholest-4-en-3-on	14.167	413.3	1.378
7a-Hydroxycholest-4-en-3-on	13.863	380.4	1.348
Sitosterol	15.353	357.4	1.467
Stigmasterol	14.699	394.4	1.405
Ergosterol	14.186	363.3	1.356

Table S05: Phytosterol contents of *Alternaria brassicicola* infected *Arabidopsis thaliana* plants 4 days post infection.

We here show the results of phytosterol measurement of *A. thaliana* plants infected with *A. brassiciola* compared to uninfected controls (control). We here show the individual results of three independent experiments. All results are given as mean ± SEM in ng mg^{-1} dry weight. n.q. = under limit of quantification.

Species	Condition	Tissue	Squalene	Cholesterol	Campesterol	Sitosterol	Stigmasterol
A. thaliana	Control	Shoot	77 ± 4	30 ± 6	218 ± 26	1171 ± 176	68 ± 28
A. thaliana	Infected	Shoot	69 ± 4	30 ± 4	141 ± 70	787 ± 333	132 ± 45
A. thaliana	Control	Root	173 ± 153	n.q. (<10 ng mL^{-1})	132 ± 15	548 ± 238	442 ± 150
A. thaliana	Infected	Root	78 ± 4	12 ± 2	139 ± 48	436 ± 57	382 ± 132

Table S06: Details of analysis of phytohormone. Phytohormone analysis was performed by LC-MS/MS as described by Heyer et al. (2018) on an Agilent 1260 series HPLC system (Agilent Technologies, Santa Clara, CA, USA) with the modification that a tandem mass spectrometer QTRAP 6500 (SCIEX, Darmstadt, Germany) was used. Chromatographic separation was achieved on a Zorbax Eclipse XDB-C18 column (50 × 4.6 mm, 1.8 µm, Agilent Technologies, Santa Clara, CA, USA). Water containing 0.05% formic acid and acetonitrile were employed as mobile phases A and B, respectively. The elution profile was: 0.00–0.50 min, 10% B; 0.50–4.00 min, 10–90% B; 4.00–4.02 min, 90–100% B; 4.02–4.50 min, 100% B and 4.51–7.00, min 10% B. Flow rate was kept at 1.1 mL min^{-1} and column temperature was maintained at 25 °C. The mass spectrometer was equipped with a Turbo spray ion source operated in negative ionization mode. The ion spray voltage was maintained at -4,500 eV. The turbo gas temperature was set at 650 °C. Nebulizing gas was set at 60 psi, curtain gas at 40 psi, heating gas at 60 psi, and collision gas was set to "medium". The mass spectrometer was operated in multiple reaction monitoring (MRM) mode. Since we observed that both, the d_6-labeled JA and $d_6$labeled JA-Ile standards (HPC Standards GmbH, Cunnersdorf, Germany) contained 40% of the corresponding d_5-labeled compounds, the sum of the peak areas of d_5- and d_6-compound was used for quantification. The table shows mass transition (Q1 and Q3), retention time (RT) the used internal standard, response factor to the used internal standard (*f*) and the collision energy (CE).

Compound	Q1	Q3	RT [min]	Internal std	*f*	CE [V]
SA	136.93	93.00	3.3	D4-SA	1.0	-24
ABA	263.00	153.20	3.4	D6-ABA	1.0	-22
JA	209.07	59.00	3.6	D5-JA+D6-JA	1.0	-24
JA-Ile	322.19	130.10	3.9	D5+D6-JA-Ile	1.0	-30
OPDA	290.90	165.10	4.6	D5-JA+D6-JA	1.0	-24
OH-JA-Ile	338.10	130.10	3	D5+D6-JA-Ile	1.0	-30
OH-JA	225.10	59.00	2.6	D5-JA+D6-JA	1.0	-24
COOH-JA-Ile	352.10	130.10	3	D5+D6-JA-Ile	1.0	-30
dinor-OPDA	263.00	165.10	4.2	D5-JA+D6-JA	0.7	-20
D4-SA	140.93	97.00	3.3			-24
D6-ABA	269.00	159.20	3.4			-22
D6-JA	215.00	59.00	3.6			-24
D5-JA	214.00	59.00	3.6			-24
D6-JA-Ile	328.19	130.10	3.9			-30
D5-JA-Ile	327.19	130.10	3.9			-30

Table S07: Comparism of RNAseq and qPCR results. The table lists the normalized Count Reads of PR1 obtained by RNAseq and the CT values of PR1 and RPS18B (reference gene) obtained by qPCR, as well as the calculated Log2 fold changes (RNAseq) and relative expression (qPCR). We can clearly see, that both methods show the strong expression changes within the DHEA treated samples, while expression differences in DMSO control were underestimated by qPCR. All in all our data ensure the reliability of the RNAseq experiment, which is even more sensitive and accurate compared to qPCR.

RNAseq				qPCR		
No	**Treatment**	**Normalized Count Reads PR1**	**Log2 Fold change**	**CT values PR1**	**CT values RPS18B**	**Relative Expression**
1	DMSO	**3.35**		**30.14**	**22.95**	
2	DMSO	**0.00**		**30.70**	**23.64**	**1.25**
3	DMSO	**2.10**		**30.92**	**22.5**	
4	DMSO	**45.21**		**30.28**	**23.17**	
1	DHEA	**3705.57**	**-7.12**	**23.16**	**22.63**	
2	DHEA	**7.26**		**30.36**	**22.44**	**62.3**
3	DHEA	**3365.53**		**22.93**	**22.46**	
4	DHEA	**1.78**		**29.18**	**22.33**	
1	Spores	**27.55**		**29.30**	**22.66**	
2	Spores	**71.74**		**28.20**	**23.29**	**1.70**
3	Spores	**91.93**		**24.96**	**22.27**	
4	Spores	**23.48**		**28.17**	**22.59**	
1	Spores+DHEA	**25.22**	**0.65**	**28.04**	**22.16**	
2	Spores+DHEA	**37.08**		**29.20**	**22.69**	**0.67**
3	Spores+DHEA	**39.82**		**26.33**	**21.89**	
4	Spores+DHEA	**35.02**		**28.57**	**22.35**	

Table S08: Details of analysis of sterol pattern in *A. brassicicola* by GC-MS. To determine the effect of DHEA treatment on the ergosterol biosynthesis pathway, the samples were analyzed by gas chromatography (GC) coupled to quadrupole mass spectrometry (MS). For analysis 2 × 5 mg lyophilized fungal biomass were used. The isoprenoid and the sterol pattern were determined by our previously described protocols (Müller et al., 2017; Liebl et al., 2023). Isoprenoid pyrophosphates were analyzed by GC-MS as their corresponding isoprenoid *tert*-butyldiphenylsilyl ether by GC-MS after enzymatic pyrophosphate cleavage to the free isoprenoid and subsequent derivatization with *tert*-butyldiphenylchlorosilane. As a positive control the azole antifungal ketoconazole was used in the post-lanosterol pathway of ergosterol biosynthesis. For The isoprenoid *t*BDPS ethers and squalene were identified by single ion monitoring (SIM) and their relative retention times (RRT) according to Liebl et al., 2023. The quantification was managed with six-point calibration curves ranged from 0-250 ng mL^{-1} for each analyte. The results were normalized to the dried fungal biomass and expressed as ng per mg dried biomass (Liebl et al., 2023). Additionally, the sum of all detected peak areas of each sample was set as 100% and the percentage of each analyte of the isoprenoid pathway of ergosterol biosynthesis was calculated. For the post-lanosterol pathway of ergosterol biosynthesis, the sterols were identified as their corresponding trimethylsilyl (TMS) ethers by mass spectra and RRT according to Müller et al., 2017 The quantification, managed with an external calibration with ergosterol, consists of six levels (0-10,000 ng mL^{-1}). The sum of all detected peak areas of each sample was set as 100% and the percentage of each sterol was calculated (Müller et al., 2018; Kühbacher et al., 2023).
The table shows retention time (RT), mass to charge ratio (Quantifier [m/z]) and relative retention time (RRT).

Compound	RT [min]	Quantifier [*m/z*]	RRT
Isoprenoids			
Isoprenol	9.787	225	0.71
Prenol	9.851	267	0.71
Geraniol	11.239	335	0.82
Squalen	11.912	69	0.86
Farnesol	12.580	69	0.91
Heptadecanol (I.S.- Isoprenoid)	13.779	437	1.00
Geranylgeraniol	14.980	69	1.09

Sterols			
Cholestan (I.S.-Sterol)	10.635	217	1.00
Ergosta-5,8,22,24-tetraen-ol	13.902	251	1.31
Lichesterol	14.033	363	1.32
Ergosterol	14.362	363	1.35
14-Methylfecosterol	14.556	469	1.37
Ergosta-5,7,22,24-tetraen-ol	14.685	466	1.38
Ergosta-7,22,24-trien-ol	15.155	343	1.43
Episterol	15.171	343	1.43
14-Methylergosta-8,24-dien-3,6-diol	15.490	467	1.46
Lanosterol	15.498	393	1.46
Eburicol	16.120	407	1.52

Table S09: Content and composition of intermediates of the isoprenoid and post-squalene pathway of ergosterol biosynthesis of *A. brassicicola* samples confronted with DHEA (10 µM) or ketoconazole (KC; 2 µg/mL) compared to untreated controls (ctrl). Cultures were grown for 12 h, 1 day, 3 d and 7 d under DHEA treatment and for 7 days under ketoconazole (KC) treatment. Isoprenoid pyrophosphates were analyzed by GC-MS as their corresponding isoprenoid *tert*-butyldiphenylsilyl ether by GC-MS after enzymatic pyrophosphate cleavage to the free isoprenoid and subsequent derivatization with *tert*-butyldiphenylchlorosilane. For the post-lanosterol pathway of ergosterol biosynthesis, the sterols were identified as their corresponding trimethylsilyl (TMS) ethers by mass spectra and RRT according to Müller et al., 2017. The results are presented as the average of three technical replicates. Intermediate content is expressed as ng intermediate per mg fungal biomass (dry weight) and the intermediate composition is given as the relative amount in % of all intermediates of the isoprenoid pathway or post-squalene pathway of ergosterol biosynthesis; n.d. not detected; i.t. in traces.

Compound			Treatment									
No	Name	Sample Time	DMSO 12 h	DMSO 1 d	DMSO 3 d	DMSO 7 d	DHEA 12 h	DHEA 1 d	DHEA 3 d	DHEA 7 d	MeOH 7 d	KC 7 d
1	isoprenol	**[ng/mg]**	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.
		[%]	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1
2	prenol	**[ng/mg]**	n.d.	n.d.	n.d.	n.d.	n.d.	i.t.	i.t.	i.t.	1	1
		[%]	0	0	0	0	0	<1	<1	<1	2	1
3	geraniol	**[ng/mg]**	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.	i.t.
		[%]	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1
4	squalene	**[ng/mg]**	162	106	73	186	132	200	86	147	62	151
		[%]	98	98	98	98	98	98	96	96	95	98
5	farnesol	**[ng/mg]**	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
		[%]	0	0	0	0	0	0	0	0	0	0
7	geranylgeraniol	**[ng/mg]**	i.t.	i.t.	i.t.	i.t.	i.t.	1	i.t.	i.t.	i.t.	i.t.
		[%]	<1	<1	<1	<1	<1	0	<1	<1	<1	<1
		∑ [ng/mg]	**164**	**108**	**75**	**188**	**135**	**204**	**89**	**150**	**66**	**154**
9	ergosta-5,8,22,24(28)-tetraen-3β-ol	**[ng/mg]**	105	155	75	140	135	147	141	169	51	43
		[%]	1	1	1	1	1	1	1	1	1	1
10	lichesterol (ergosta-5,8,22-trien-3β-ol)	**[ng/mg]**	414	500	485	431	458	553	469	439	539	108
		[%]	5	5	5	4	5	5	4	4	8	3
11	ergosterol (ergosta-5,7,22-trien-3β-ol)	**[ng/mg]**	6818	8536	8529	8499	7649	9748	8586	8402	6242	2224
		[%]	83	83	83	84	83	85	82	81	89	61
12	14-methylfecosterol (14-methylergosta-8,24(28)-dien-3β-ol)	**[ng/mg]**	1	1	7	3	3	2	21	7	1	91
		[%]	0	0	0	0	0	0	0	0	0	3
13	ergsta-5,7,22,24(28)-tetraen-3β-ol	**[ng/mg]**	44	51	44	47	47	51	36	36	23	19
		[%]	1	0	0	0	1	0	0	0	0	1
14	ergosta-7,22,24(28)-trien-3β-ol	**[ng/mg]**	360	460	492	409	402	387	479	578	49	22
		[%]	4	4	5	4	4	3	5	6	1	1
15	episterol (ergosta-7,24(28)-dien-3β-ol)	**[ng/mg]**	359	459	493	409	403	387	479	579	50	24
		[%]	4	4	5	4	4	3	5	6	1	1
16	14-methylergosta-8,24(28)-dien-3β,6α-diol	**[ng/mg]**	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	364
		[%]	0	0	0	0	0	0	0	0	0	10
17	lanosterol (4,4,14-trimethylcholesta-8,24-dien-3β-o)l	**[ng/mg]**	21	27	29	24	27	22	32	29	25	280
		[%]	0	0	0	0	0	0	0	0	0	8
18	eburicol (4,4,14-trimethylergosta-8,24(28)-dien-3β-ol)	**[ng/mg]**	101	149	147	127	124	141	171	114	52	454
		[%]	1	1	1	1	1	1	1	1	1	13
		∑ [ng/mg]	**8223**	**10,337**	**10,302**	**10,088**	**9246**	**11,438**	**10,415**	**10,353**	**7031**	**3629**

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