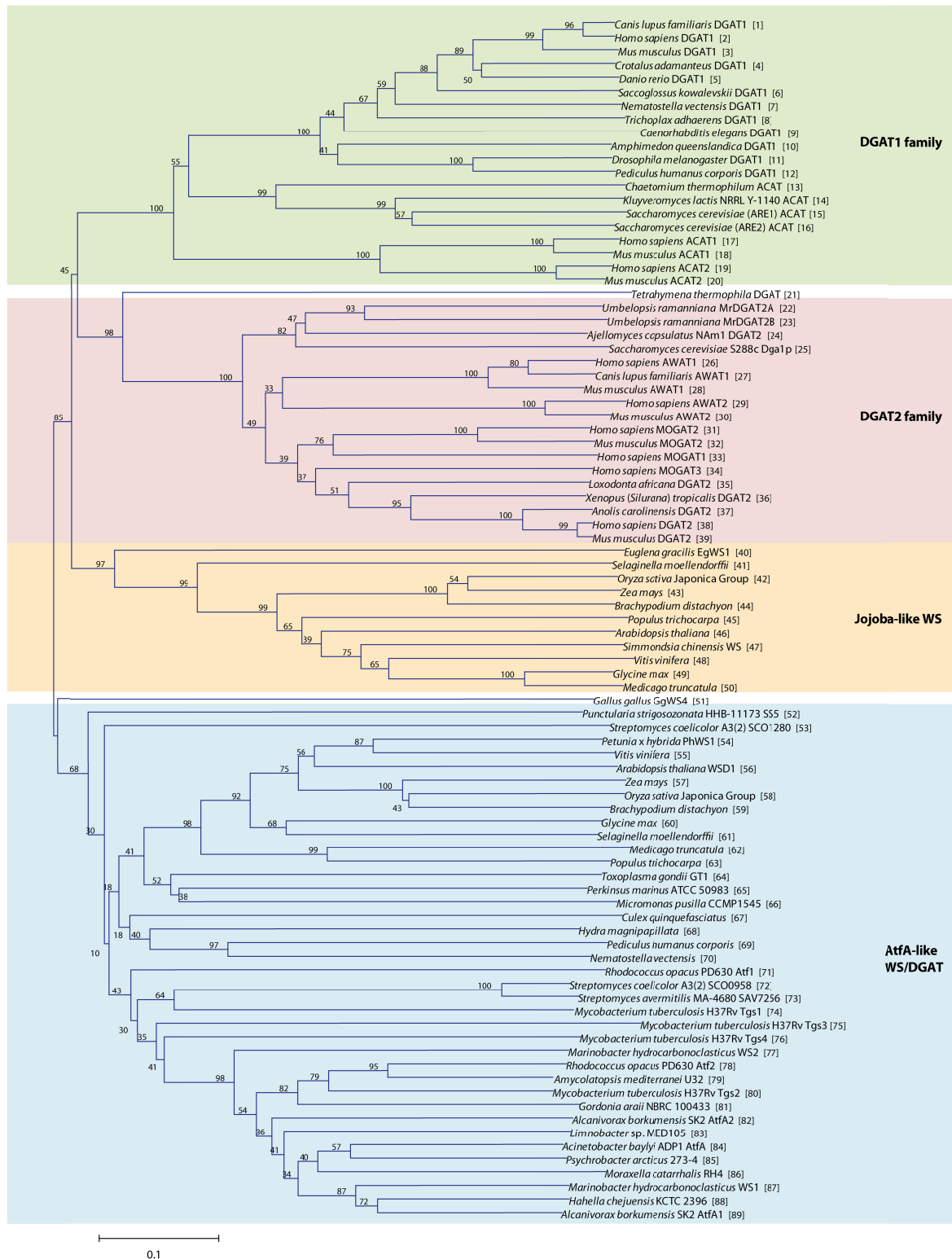


# Acyltransferases in Bacteria by Annika Röttig and Alexander Steinbüchel

## SUPPLEMENTARY MATERIAL



**Fig. S1** Phylogenetic tree of acyltransferases. Protein accession numbers: [1] XP 539214.2, [2] NP 036211.2, [3] NP 034176.1, [4] AFJ49921.1, [5] NP 956024.1, [6] XP 002736160.1, [7] XP 001639351.1, [8] XP 002112025.1, [9] NP 001256301.1, [10] XP 003389842.1, [11] NP

609813.1, [12] XP 002430154.1, [13] EGS17506.1, [14] XP 452607.1, [15] CAA42296.1, [16] CAA96298.1, [17] NP 003092.4, [18] NP 033256.2, [19] NP 003569.1, [20] NP 666176.1, [21] XP 001008104.1, [22] AAK84179.1, [23] AAK84180.1, [24] XP 001540241.1, [25] NP 014888.1, [26] NP 001013597.1, [27] XP 549058.2, [28] NP 001074605.1, [29] NP 001002254.1, [30] NP 808414.2, [31] NP 079374.2, [32] AAH52831.1, [33] NP 477513.2, [34] NP 835470.1, [35] XP 003412732.1, [36] XP 002934939.1, [37] XP 003225477.1, [38] NP 115953.2, [39] NP 080660.1, [40] ADI60058.1, [41] XP 002983828.1, [42] NP 001046772.1, [43] NP 001147171.1, [44] XP 003576211.1, [45] XP 002314065.1, [46] NP 200349.1, [47] AAD38041.1, [48] XP 002276902.1, [49] XP 003530771.1, [50] AFK35478.1, [51] XP 419207.1, [52] EIN09069.1, [53] NP 625567.1, [54] AAZ08051.1, [55] XP 002268615.1, [56] AED94163.1, [57] NP 001140997.1, [58] EEE55448.1, [59] XP 003571568.1, [60] ACU20370.1, [61] XP 002987493.1, [62] XP 003623995.1, [63] XP 002323706.1, [64] EEE25493.1, [65] XP 002765455.1, [66] XP 003059244.1, [67] XP 001847517.1, [68] XP 002155609.1, [69] XP 002429016.1, [70] XP 001632004.1, [71] ACX81314.1, [72] NP 625255.1, [73] NP 828432.1, [74] NP 217646.1, [75] NP 217751.1, [76] NP 217604.1, [77] ABO21021.1, [78] EHI41112.1, [79] YP 003769971.1, [80] NP 218251.1, [81] ZP 09211433.1, [82] YP 693524.1, [83] ZP 01914209.1, [84] AAO17391.1, [85] YP 263530.1, [86] YP 003627553.1, [87] ABO21020.1, [88] YP 436128.1, [89] YP 694462.1

**Table S1** Putative AtfA-like proteins in animals.

Organism	Phylum	Class	Accession №	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Hydra magnipapillata</i>	Cnidaria	Hydrozoa	XP_002155609.1	491	25% (44%)
<i>Nematostella vectensis</i>	Cnidaria	Anthozoa	XP_001632004.1	526	24% (41%)
			XP_001633379.1	490	23% (40%)
			XP_001632267.1	556	22% (39%)
			XP_002736281.1	751	23% (44%)
<i>Saccoglossus kowalevskii</i>	Hemichordata		XP_002736281.1	751	23% (44%)
<i>Pediculus humanus corporis</i>	Arthropoda	Insecta	XP_002429016.1	389	23% (41%)
<i>Metaseiulus occidentalis</i>	Arthropoda	Arachnida (mite)	XP_003742738.1	1198	20% (40%)
<i>Danaus plexippus</i>	Arthropoda	Insecta (butterfly)	EHJ69373.1	560	25% (45%)
<i>Culex quinquefasciatus</i>	Arthropoda	Insecta (mosquito)	XP_001847517.1	512	22% (42%)
			XP_001868729.1	657	23% (43%)
			XP_001847515.1	595	22% (42%)
<i>Ixodes scapularis</i>	Arthropoda	Arachnida (deer tick)	XP_002416346.1	411	19% (40%)

<sup>a</sup> Maximal percentage of identical or similar amino acids in comparison to the reference protein sequence of AtfA from *A. baylyi* strain ADP1.

**Table S2** Putative AtfA-like proteins in fungi.

Organism	Phylum	Class	Accession No	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Ustilago maydis</i> 521	Basidiomycota	Ustilaginomycetes	XP_758106.1	795	23% (39%)
<i>Ustilago hordei</i>	Basidiomycota	Ustilaginomycetes	CCF53109.1	763	24% (40%)
<i>Sporisorium reilianum</i> SRZ2	Basidiomycota	Microbotryomycetes	CBQ72199.1	774	24% (39%)
<i>Punctularia strigosozonata</i> HHB-11173 SS5		Agaricomycetes	EIN09069.1	539	21% (39%)
<i>Malassezia globosa</i> CBS 7966		Exobasidiomycetes	XP_001731626.1	725	19% (36%)

<sup>a</sup> Maximal percentage of identical or similar amino acids in comparison to the reference protein sequence of AtfA from *A. baylyi* strain ADP1.

**Table S3** Putative AtfA-like proteins in plants.

Organism	Family	Accession №	Size (amino acids)	Max. identity (similarity) <sup>a</sup>		
<i>Petunia hybrida</i>	Solanaceae	AAZ08051.1	521	22% (40%)		
<i>Arabidopsis thaliana</i>	Brassicaceae	NP_197139.1	488	22% (42%)		
		NP_190488.1	522	20% (40%)		
		NP_177356.1	479	21% (40%)		
		NP_197641.1	482	23% (38%)		
		BAB09801.1	485	21% (41%)		
		BAC42871.1	486	21% (41%)		
		NP_200151.2	486	21% (41%)		
		NP_200150.1	483	22% (40%)		
		BAB09102.1	499	22% (41%)		
		NP_568547.1	481	22% (41%)		
		NP_001185377.1	470	21% (39%)		
		NP_568275.1	480	22% (38%)		
		NP_190490.1	518	20% (39%)		
		<i>Arabidopsis lyrata</i> subsp. <i>lyrata</i>	Brassicaceae	XP_002871716.1	477	20% (42%)
				XP_002870738.1	467	23% (42%)
XP_002865972.1	488			20% (39%)		
XP_002873570.1	480			21% (40%)		
XP_002864239.1	481			22% (39%)		
XP_002877655.1	521			20% (39%)		
XP_002868506.1	500			21% (39%)		
XP_002879777.1	474			21% (40%)		
<i>Thellungiella halophila</i>	Brassicaceae	XP_002877657.1	519	21% (39%)		
		BAJ33896.1	467	19% (41%)		
<i>Brachypodium distachyon</i>	Poaceae	XP_003571568.1	507	23% (41%)		
		XP_003571567.1	506	24% (43%)		
		XP_003569567.1	516	22% (43%)		
		XP_003571438.1	427	22% (43%)		
		XP_003569566.1	519	22% (43%)		

**Table S3** (continued)

Organism	Family	Accession №	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Brachypodium distachyon</i>	Poaceae	XP_003567157.1	503	21% (38%)
		XP_003565936.1	534	19% (39%)
<i>Triticum aestivum</i>	Poaceae	CBH32551.1	515	22% (42%)
		CBH32550.1	489	23% (41%)
<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	Poaceae	BAJ97841.1	517	21% (43%)
		BAJ93204.1	517	21% (43%)
		BAJ93623.1	495	21% (41%)
		BAJ85619.1	500	21% (39%)
		BAK08349.1	504	20% (42%)
		BAK02325.1	571	20% (38%)
		BAJ84892.1	500	20% (38%)
		NP_001043877.1	531	22% (40%)
<i>Oryza sativa</i> Japonica Group	Poaceae	NP_001044374.1	518	20% (38%)
		EEE55448.1	437	21% (38%)
		EAY98969.1	565	20% (40%)
<i>Oryza sativa</i> Indica Group	Poaceae	EAY75974.1	507	20% (38%)
		EAY75973.1	518	20% (38%)
		NP_001140997.1	369	21% (39%)
<i>Zea mays</i>	Poaceae			
<i>Sorghum bicolor</i>	Poaceae	XP_002440221.1	554	20% (38%)
		XP_002458560.1	519	21% (38%)
<i>Medicago truncatula</i>	Fabaceae	XP_003623995.1	478	25% (41%)
		XP_003607481.1	469	24% (41%)
		XP_003588522.1	483	22% (40%)
		XP_003607478.1	455	23% (40%)
<i>Glycine max</i>	Fabaceae	ACU20370.1	461	21% (42%)
		XP_003529372.1	461	21% (42%)
		XP_003534230.1	479	22% (41%)
		XP_003534457.1	471	24% (40%)
		XP_003552517.1	467	23% (40%)

**Table S3** (continued)

Organism	Family	Accession №	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Glycine max</i>	Fabaceae	XP_003541905.1	468	20% (39%)
		NP_001241558.1	469	21% (38%)
		XP_003539933.1	470	22% (39%)
		XP_003527429.1	471	22% (39%)
		XP_003540916.1	478	20% (39%)
<i>Vitis vinifera</i>	Vitaceae	XP_002268615.1	490	23% (40%)
		CBI40540.3	531	24% (39%)
		XP_003633939.1	607	24% (39%)
		XP_002263196.1	477	23% (40%)
		CAN71951.1	513	23% (40%)
		XP_002263137.1	513	23% (40%)
		CBI40547.3	1045	23% (39%)
		XP_003633938.1	607	23% (39%)
		XP_002263252.1	508	23% (39%)
		CBI40536.3	479	23% (38%)
		XP_003633936.1	473	20% (41%)
		XP_002263409.1	514	23% (38%)
		XP_002278404.1	513	21% (41%)
		XP_003633940.1	617	22% (40%)
		CBI40544.3	531	23% (39%)
		XP_003633941.1	511	20% (38%)
		CBI21867.3	494	20% (38%)
<i>Populus trichocarpa</i>	Salicaceae	XP_002274522.1	473	20% (38%)
		XP_002323706.1	473	22% (39%)
		XP_002318416.1	482	21% (39%)
		XP_002325937.1	496	20% (42%)
		XP_002323911.1	422	23% (41%)
		XP_002310400.1	474	20% (38%)
		XP_002323705.1	473	23% (39%)

**Table S3** (continued)

Organism	Family	Accession №	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Populus trichocarpa</i>	Salicaceae	XP_002328965.1	455	22% (37%)
<i>Ricinus communis</i>	Euphorbiaceae	XP_002523348.1	506	22% (40%)
		XP_002517893.1	483	22% (39%)
<i>Physcomitrella patens</i> subsp. <i>patens</i>	Funariaceae	XP_001780431.1	497	22% (40%)
<i>Selaginella moellendorffii</i>	Selaginellaceae	XP_002987493.1	452	23% (44%)
		XP_002992800.1	468	23% (44%)
		XP_002988280.1	512	22% (38%)
		XP_002963877.1	512	22% (38%)

<sup>a</sup> Maximal percentage of identical or similar amino acids in comparison to the reference protein sequence of AtfA from *A. baylyi* strain ADP1.



**Table S4** Putative AtfA-like proteins in protists.

Organism	Kingdom	Phylum	Accession No	Size (amino acids)	Max. identity (similarity) <sup>a</sup>
<i>Perkinsus marinus</i> ATCC 50983	Chromalveolata	Perkinsozoa	XP_002765455.1	486	27% (45%)
			XP_002785958.1	449	25% (41%)
			XP_002787542.1	495	25% (41%)
			XP_002767852.1	495	23% (41%)
			XP_002783220.1	494	22% (43%)
			XP_002766051.1	494	23% (43%)
			XP_002785645.1	517	23% (38%)
<i>Phaeodactylum tricornutum</i> CCAP 1055/1	Chromalveolata	Heterokontophyta	XP_002184474.1	504	20% (40%)
<i>Aureococcus anophagefferens</i>	Chromalveolata	Heterokontophyta	EGB03968.1	505	23% (41%)
<i>Phytophthora sojae</i>	Chromalveolata	Heterokontophyta	EGZ11598.1	496	21% (45%)
<i>Thalassiosira oceanica</i>	Chromalveolata	Heterokontophyta	EJK75121.1	630	23% (39%)
<i>Toxoplasma gondii</i> GT1	Chromalveolata	Apicomplexa	EEE25493.1	670	22% (40%)
<i>Toxoplasma gondii</i> ME49	Chromalveolata	Apicomplexa	XP_002364905.1	670	22% (40%)
<i>Toxoplasma gondii</i> VEG	Chromalveolata	Apicomplexa	EEE32548.1	670	22% (40%)
<i>Capsaspora owczarzaki</i> ATCC 30864			EFW44455.1	596	22% (45%)
			EFW44815.1	920	24% (40%)
<i>Naegleria gruberi</i>		Percolozoa	XP_002677788.1	710	22% (42%)
			XP_002671612.1	515	22% (37%)
<i>Ostreococcus lucimarinus</i> CCE9901			XP_001419779.1	345	22% (41%)
<i>Entamoeba histolytica</i> HM-1:IMSS		Amoebozoa	XP_001914129.1	437	20% (43%)
<i>Entamoeba dispar</i> SAW760		Amoebozoa	XP_001738032.1	493	19% (38%)
<i>Micromonas pusilla</i> CCMP1545	Viridiplantae	Mamiellaceae	XP_003059244.1	503	23% (42%)
<i>Micromonas</i> sp. RCC299	Viridiplantae	Mamiellaceae	XP_002502575.1	360	21% (42%)

<sup>a</sup> Maximal percentage of identical or similar amino acids in comparison to the reference protein sequence of AtfA from *A. baylyi* strain ADP1.