

## Supplementary Materials:

**Table S1.** Further information on *T. benhamiae* isolates used during this study.

<i>T. benhamiae</i> isolate	source <sup>a</sup>	phenotypic appearance (Sabouraud agar, 15 d, 28 °C)		ITS type (NCBI acc. no.) <sup>a</sup>	mating type [27]
		obverse	reverse		
205848	hum	white with yellow rim, furrowed	yellow, furrowed	yellow (KU257464.1)	mt -
205815	hum	white with yellow rim, furrowed	yellow, furrowed		
205850	hum	white with yellow rim, furrowed	yellow, furrowed		
206139	hum	white, radial	beige, velvety		
207002	hum	white, powdery	beige-brown, velvety		
207413	hum	white, powdery	yellow, velvety		
205858	hum	white, radial	yellow with white rim		
206785	hum	white with yellow rim, furrowed, radial	yellow, furrowed		
207860	hum	white, powdery	yellow, velvety		
206494	hum	white, radial	yellow with white rim		
7A	Gp	white with yellow rim	yellow		
12A	Gp	white, powdery	white-beige, velvety		
15B	Gp	white with yellow rim	yellow, furrowed		
1A	Gp	white with yellow rim	yellow		
2A	Gp	white with yellow rim	yellow		
5A	Gp	white with yellow rim	yellow		
14A	Gp	white with yellow rim	yellow		
8A	Gp	white with yellow rim	yellow		
3A	Gp	white with yellow rim	yellow		
6A	Gp	white with yellow rim (white, radial)	yellow	white (LN874022.1)	

<sup>a</sup> Human-derived (hum) isolates were obtained from patients of the Laboratory of Medical Microbiology (Moelbis, Germany) with informed consent. Isolates of Guinea pig origin (Gp) were collected at a local zoological garden from feed animals as part of a previous project to develop a dermatophyte biobank. All samples were taken according to local ethical guidelines and state law.

**Table S2.** Name, sequence and further information on the primers used for PCR and qPCR during this study.

use	target gene	primer	sequence (5'-3')	Tm [C°]	amplicon [bp]	ref.
Identification	ITS 1, 5.8 S rRNA and ITS 2	LSU266	GCATTCCCAAACAACCTCGACTC	61.5	ca. 1000	[26]
		V9G	TTACGTCCCTGCCCTTTGTA	58.1		
Screening for mt+	HMG partial	MF1	ATGGCCACTACTTCTGGGACC	63.7	307	[27]
		MF2	CATTGGTAAAACAGCAGCCCC	61.5		
Screening for mt-	$\alpha$ -Box partial	MF3	AAAATGTCTGGCACC GAAGTCTC	62.2	380	
		MF4	TCTGGGAGAGATCGGGAAACGC	66.4		
expression rates of virulence factors	<i>isocitrate lyase</i>	isol-f	TGGAAAGATTCAAGATGGCGATA	58.6	103	[30]
		isol-rev	TCTGTGCATTTGATGGGTAATCA	58.7		
	<i>subtilisin 3</i>	sub3-f	CATGCTTGCCCAGGGTGTTAG	63.0	81	[5]
		sub3-rev	CCTGGGTTGCGGATAACG	58.7		
	<i>subtilisin 6</i>	sub6-f	GCGGCAGCACTGATACTCTCT	62.7	121	
		sub6-rev	TTGCCCAATCCGATGAGGTA	58.3		
	<i>metallocarbxy peptidase A</i>	mcpA-f	GCATTGAAGGCGGTGCAT	57.9	84	[30]
		mcpA-rev	GTCAACACTGTCTCCATTA ACTTGGT	61.4		
Reference gene for normalization	<i>ADP-ribosylation factor</i>	ADPrf-f	CAGAGAAGAGTTGCAAAAGATGCT	59.5	74	[30]
		ADPrf-rev	TGCTTGTTGGCGAAAACGA	57.8		

**Table S3.** The expression rates of the different virulence factors found in human derived *T. benhamiae* isolates were compared (P values; statistically significant differences are defined as  $P < 0.05$  and indicated in bold letters).

Sampling day	human derived <i>T. benhamiae</i> isolates					
	<i>sub 3</i> vs. <i>sub 6</i>	<i>sub 3</i> vs. <i>mcpA</i>	<i>sub 3</i> vs. <i>isol</i>	<i>sub 6</i> vs. <i>mcpA</i>	<i>sub 6</i> vs. <i>isol</i>	<i>mcpA</i> vs. <i>isol</i>
3 (n = 3)	1,000	0,4	1	0,4	0,7	0,7
5 (n = 5)	0,222	0,151	0,151	1	1	0,841
7 (n = 6)	<b>0,004</b>	0,065	<b>0,015</b>	0,937	0,589	0,937
10 (n = 4)	<b>0,029</b>	0,057	<b>0,029</b>	<b>0,029</b>	<b>0,019</b>	<b>0,029</b>

**Table S4.** The transcript numbers of the different virulence factors expressed by Gp derived *T. benhamiae* isolates were compared (P values; statistically significant differences are defined as  $P < 0.05$  and indicated in bold letters).

Sampling day	Gp derived <i>T. benhamiae</i> isolates					
	<i>sub 3</i> vs. <i>sub 6</i>	<i>sub 3</i> vs. <i>mcpA</i>	<i>sub 3</i> vs. <i>isol</i>	<i>sub 6</i> vs. <i>mcpA</i>	<i>sub 6</i> vs. <i>isol</i>	<i>mcpA</i> vs. <i>isol</i>
3 (n = 3)	0,700	0,1	0,1	1	1	1
5 (n = 6)	0,093	0,24	0,31	0,589	0,818	0,937
7 (n = 7)	<b>&lt;0,001</b>	<b>0,017</b>	<b>0,007</b>	<b>0,002</b>	0,209	0,165
10 (n = 7)	<b>&lt;0,001</b>	<b>&lt;0,001</b>	<b>&lt;0,001</b>	<b>&lt;0,001</b>	0,209	<b>&lt;0,001</b>

**Table S5.** The expression rates of the different virulence factors produced by *T. benhamiae* isolates were compared (P values; statistically significant differences are defined as P < 0.05 and indicated in bold letters).

Sampling day	<i>T. benhamiae</i> isolates (hum and Gp derived)					
	<i>sub 3</i> vs. <i>sub 6</i>	<i>sub 3</i> vs. <i>mcpA</i>	<i>sub 3</i> vs. <i>isol</i>	<i>sub 6</i> vs. <i>mcpA</i>	<i>sub 6</i> vs. <i>isol</i>	<i>mcpA</i> vs. <i>isol</i>
3 (n = 6)	0,94	0,18	0,132	0,485	0,937	0,937
5 (n = 11)	<b>0,02</b>	<b>0,049</b>	<b>0,049</b>	0,694	0,743	0,844
7 (n = 13)	<b>&lt;0,001</b>	<b>0,004</b>	<b>&lt;0,001</b>	<b>0,013</b>	0,182	0,218
10 (n = 11)	<b>&lt;0,001</b>	<b>&lt;0,001</b>	<b>&lt;0,001</b>	<b>&lt;0,001</b>	0,511	<b>&lt;0,001</b>