Supplemental data

Figure S1. Complementation of *Medicago truncatula hcl* mutants. (A) A B56 *hcl* mutant root that is transformed with the *MtLYK3* gene and a *DsRED* gene, allowing visual selection for transgenic red fluorescent roots. Six days after inoculation GFP expressing *S. meliloti* (green fluorescence) can be observed in infection threads (arrow) that are formed in transgenic tissue (red fluorescence). (B) A nodule (star) formed on a transgenic W1 *hcl* mutant root, the root nodule is pink indicating that it contains *S. meliloti* that fix nitrogen. (C) The root nodule and root shown in figure S1B visualized under a filter set allowing observation of red fluorescent light. Both nodule and root fluoresce red, which indicates that the tissue is expressing DsRED and thus transgenic. Plants containing 1 or more roots that fluoresce brightly red always contained root nodules. (D) The root nodule and root shown in figure S1B visualized under a filter set allowing observation of green fluorescent light. The central tissue of the root nodule fluoresces intensely green indicating that GFP expressing *S. meliloti* are present. (E) The root nodule shown in figure S1B dissected and visualized by confocal laser scanning microscopy. The central tissue contains cells filled with bacteroids (arrowhead) containing green fluorescent *S. meliloti*. Bars represent 250 micrometer, except in figure S1E where it represents 50 micrometer

Figure S2. Infection of *hcl-4* plants by wild type and *nod* mutant *S. meliloti*. In the upper row of pictures roots of *hcl-4* plants are visualized using bright field microscopy. The roots were co cultivated for 20 days with the *S. meliloti* indicated above. Arrows indicate root nodule primordia. In the lower row of pictures the same roots have been observed using a GFP filter set allowing the visualization of the GFP expressing *S. meliloti*. These infections resulted in the formation *S. meliloti* containing sac-like structures in root hairs. Arrowheads indicate micro colonies and sac-like structures formed within tightly curled root hairs. Bars represent 250 micrometer.

Figure S3. Phylogeny of LysM receptor kinases. The analyses was performed on the LysM receptor kinases from LysM cladeA as described by Zhu and coworkers (Zhu *et al.* 2006). We included the complete LYK2 sequence and repeated the analysis to see whether this would affect the topography of the tree. The topography of the tree does not differ from the one published by Zhu and coworkers except for the clade containing MtLYK2, MtLYK3 and LjNFR1 (shaded red). In our analyses MtLYK2 and MtLYK3 are more similar to each other, while in the analysis by Zhu *et al.*, using only a partial MtLYK2 sequence, MtLYK2 was more similar to LjNRF1 instead. Bootstrap values are represented as percentages. The bar represents the amount of changes per nucleotide. The mRNA sequence and the conceptually translated products of MtLYK2, MtLYK5, LjNFR1b, and LjNFR1c are deposited in the EMBL nucleotide database (BN001116 to BN001119, respectively).

Table S1.

Table shows the amount of identical (I) and similar (S) residues as well as gaps (G) between all LysM receptor kinases analyzed. The values are expressed as percentages as well as absolute values, above and under the diagonal (gray) respectively.

	MtLYK1	MtLYK5	MtLYK4	LjNFR1b	MtLYK6	LjNFR1c	MtLYK7	MtLYK3	MtLYK2	LjNFR1	AtLYK1	AtLYK2	
	624	72%	64%	60%	47%	48%	51%	64%	56%	54%	44%	24%	I
MtLYK1	0	81%	73%	74%	63%	64%	65%	73%	70%	68%	60%	42%	S
	0	1%	5%	2%	9%	6%	6%	5%	6%	6%	5%	7%	G
	454	625	71%	63%	52%	52%	56%	48%	49%	51%	47%	26%	I
MtLYK5	510	0	81%	76%	68%	67%	69%	62%	63%	64%	62%	44%	S
	9	0	6%	2%	9%	6%	6%	6%	7%	7%	6%	7%	G
	401	447	590	60%	56%	54%	55%	48%	48%	50%	46%	25%	I
MtLYK4	460	509	0	74%	68%	68%	69%	61%	63%	63%	61%	42%	S
	36	39	0	6%	12%	9%	9%	10%	10%	10%	9%	8%	G
	381	406	385	630	54%	56%	55%	51%	50%	51%	48%	24%	I
LjNFR1b	473	485	469	0	69%	70%	70%	66%	66%	66%	64%	42%	S
	16	15	44	0	10%	6%	5%	5%	6%	5%	5%	7%	G
	301	334	348	345	574	68%	60%	51%	49%	51%	50%	27%	I
MtLYK6	401	430	424	439	0	78%	73%	64%	64%	65%	65%	43%	S
	60	63	76	64	0	5%	9%	9%	10%	10%	9%	9%	G
	305	333	343	357	412	600	62%	52%	52%	53%	50%	27%	I
LjNFR1c	409	429	425	449	473	0	75%	67%	67%	67%	64%	44%	S
	42	43	58	44	32	0	5%	7%	8%	8%	7%	7%	G
	328	363	355	358	381	391	620	54%	53%	54%	53%	27%	I
MtLYK7	420	450	439	453	462	473	0	69%	69%	69%	69%	42%	S
	40	43	62	38	58	36	0	3%	5%	3%	4%	9%	G
	411	315	312	332	322	335	344	620	80%	77%	53%	25%	I
MtLYK3	473	404	396	427	408	429	440	0	90%	86%	69%	42%	S
	38	43	68	34	62	50	22	0	1%	1%	2%	8%	G
	361	316	309	325	311	331	336	503	612	77%	53%	26%	I
MtLYK2	449	411	399	426	406	429	440	561	0	86%	68%	44%	S
	44	49	64	40	66	54	32	10	0	2%	3%	7%	G
	350	330	322	334	323	340	345	483	486	621	53%	26%	I
LjNFR1	438	414	405	427	410	428	442	541	543	0	70%	45%	S
	39	46	69	37	63	51	23	7	17	0	2%	7%	G
	287	306	293	312	317	321	339	337	332	335	617	27%	I
AtLYK1	387	401	392	411	409	410	438	437	430	440	0	44%	S
	37	44	63	37	57	45	29	15	21	16	0	7%	G
	158	166	156	160	171	169	177	159	169	169	176	601	I
AtLYK2	268	282	266	273	269	277	275	273	281	290	283	0	S
	49	50	53	51	59	45	59	51	49	48	50	0	G

References

Zhu H, Riely BK, Burns NJ, Ane JM (2006) Tracing nonlegume orthologs of legume genes required for nodulation and arbuscular mycorrhizal symbioses. Genetics **172**: 2491-2499