Table S1. Overall raw data of the comparative proficiency study over the two years of study [a].

			50 Tgg		10 Tgg		5 Tgg		2 Tgg		1 Tgg		0.5 Tgg		0.2 Tgg		0.1 Tgg		'0.2' score [g]		'0.1' score [g]	
Centre	**Year**	**DNA target and primers (Ref)**	**nb** [e]	**%** [f]	**nb**	**%**	**nb**	**%**	**nb**	**%**	**nb**	**%**	**nb**	**%**	**nb**	**%**	**nb**	**%**	**nb/28**	**%**	**nb/44**	**%**
A	**2006**	B1 gene (6)	2/2	*	2/2	*	4/4	*	4/4	*	7/8	87.5%	6/8	75%	3/8	37.5%	4/16	25%	20.5	73.2%	24.5	63.6%
		rep529 [b]	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	7/8	87.5%	9/16	56.25%	27	96.4%	36	81.8%
	2007	B1 gene (6)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	6/8	75%	4/8	50%	5/16	31.25%	22	78.6%	27	61.4%
		rep529 [b]	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	8/8	*	10/16	62.5%	28	100%	38	86.4%
B	**2006**	B1 gene PCR ELISA (29)	nd	nd	2/2	*	2/4	50%	2/4	50%	1/4	25%	1/8	12.5%	0/8	0%	0/16	0%	6	21.4%	6	13.6%
		rep529 LNA (38)	2/2	*	2/2	*	4/4	*	4/4	*	3/4	75%	1/4	25%	2/4	50%	1/8	12.5%	14/20 (17/28)	60.7%	15/28 (19/44)	43.2%
		rep529 MGB (33)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	1/4	25%	1/4	25%	2/8	25%	14/20 (16/28)	57.1%	16/28 (20/44)	45.5%
	2007	B1 gene PCR ELISA (29)	2/2	*	2/2	*	3/4	75%	2/4	50%	2/4	50%	2/8	25%	0/8	0%	0/16	0%	9	32.1%	9	20.4%
		rep529 LNA (38)	2/2	*	2/2	*	4/4	*	4/4	*	3/4	75%	7/8	87.5%	2/8	25%	4/18	22.2%	20	71.4%	24/46 (24/44)	54.5%
		rep529 MGB (33)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	6/8	75%	2/8	25%	3/17	17.7%	20	71.4%	23/45 (23/44)	52.3%
C	**2006**	B1 gene (13)	2/2	*	2/2	*	4/4	*	2/4	50%	0/4	0%	3/8	37.5%	1/8	12.5%	0/16	0%	10	35.7%	10	22.7%
		rep529 (8)	2/2	*	2/2	*	4/4	*	4/4	*	3/4	75%	2/8	25%	4/8	50%	3/16	18.75%	17	60.7%	20	45.4%
	2007	B1 gene (13)	2/2	*	2/2	*	4/4	*	4/4	*	3/4	75%	3/8	37.5%	0/8	0%	0/16	0%	14	50%	14	31.8%
		rep529 (8)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	4/8	50%	nd	Nd	24	85.7%	nd	nd
D	**2006**	B1 gene (7) [c]	2/2	*	2/2	*	4/4	*	3/4	75%	0/4	0%	2/8	25%	2/8	25%	1/16	12.5%	11	39.3%	12	27.3%
		rep529 (20)	2/2	*	2/2	*	4/4	*	4/4	*	1/4	25%	4/8	50%	2/8	25%	0/16	0%	15	53.6%	15	34.1%
	2007	B1 gene (7) [c]	2/2	*	2/2	*	4/4	*	4/4	*	3/4	75%	5/8	62.5%	2/8	25%	5/16	31.25%	18	64.3%	23	52.3%
		rep529 (20)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	5/8	62.5%	9/16	56.25%	25	89.3%	34	77.3%
E	**2006**	B1 gene (26)	4/4	*	4/4	*	4/4	*	4/4	*	4/4	*	1/8	12.5%	1/8	12.5%	3/8	37.5%	14	50%	17/36 (20/44)	45.4%
	2007	B1 gene (26)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	5/8	62.5%	1/8	12.5%	1/8	12.5%	18	64.3%	19/36 (20/44)	45.4%
F	**2006**	B1 gene (15)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	7/8	87.5%	6/8	75%	8/16	50%	25	89.3%	33	75%
		rep529 (15)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	8/8	*	12/16	75%	28	100%	40	92.9%
	2007	B1 gene (15)	2/2	*	2/2	*	3/4	75%	4/4	*	4/4	*	8/8	*	5/8	62.5%	5/16	31.25%	24	85.7%	29	65.9%
		rep529 (15)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	6/8	75%	11/16	68.75%	26	92.9%	37	84.1%
G	**2006**	B1 gene (13)	1/2	50%	2/2	*	2/4	50%	0/4	0%	0/8	0%	0/8	0%	0/8	0%	0/16	0%	2	7.1%	2	4.5%
		rep529 (27)	2/2	*	2/2	*	4/4	*	4/4	*	8/8	*	8/8	*	2/8	25%	3/16	18.75%	22	78.6%	25	56.8%
	2007	B1 gene (13)	2/2	*	2/2	*	3/4	75%	3/4	75%	0/4	0%	1/8	12.5%	1/8	12.5%	1/16	6.25%	8	28.6%	9	20.4%
		rep529 (27)	2/2	*	2/2	*	4/4	*	4/4	*	8/8	*	8/8	*	2/8	25%	3/16	18.75%	26	92.9%	29	65.9%
H	**2006**	rep529 (16) [d]	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	8/8	*	0/16	0%	28	100%	28	63.6%
		rep529 (27)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	7/8	87.5%	12/16	75%	27	96.4%	39	88.6%
	2007	rep529 (27)	2/2	*	2/2	*	4/4	*	4/4	*	4/4	*	8/8	*	8/8	*	14/16	87.5%	28	100%	42	95.4%

[a] The results from both years were not summed up, as variations inherent to the microscopic counting of the cells could not be excluded. However, the Chi² test did not show any statistically significant variation between both years for each laboratory, except for participant D which showed an improvement in sensitivity that could not be attributed solely to a slight parasite concentration variation (Chi² test, p = 0.03 for the B1 gene assay, and p = 0.005 for the rep529 assay); this laboratory reported technical difficulties in 2006 which explain a decrease in sensitivity. [b]unpublished primers H1-H2 from Bastien *et al.*; [c] primers 1 and 4; [d] primers used in Laboratory H (27) are the Tox4 and Tox5 primers from Homan *et al.* (20), each without the dinucleotide CG, which is not contained in the rep529 (AF 146527) sequence, in the 5' position; [e,f] number (nb) or percentage (%) of positive reactions over number of reactions performed. * = 100% of positive reactions; [g] for the definition and use of '0.2' and '0.1' scores, see Materials and Methods and Results (the shaded cells at the top represent the concentrations used to calculate the '0.2' scores); an example of calculation of the scores is given here: the maximum hit for score 0.2 is 28 reactions (4 at concentration 5 Tgg, + 4 at concentration 2 Tgg, + 4 at concentration 1 Tgg, + 8 at concentration 0.5 Tgg, + 8 at concentration 0.2 Tgg) and it is 44 reactions for score 0.1 (28 from the concentrations included in score 0.2, + 16 reactions at concentration 0.1 Tgg); for centre A, year 2006, DNA target rep529, the 0.2 score is 96.4% (27/28=4+4+4+8+7/28) and the 0.1 score is 81.8% (36/44= 27+ 9/28+16).

Table S2. Comparison of the methods using the B1 gene and rep529 DNA targets in 2007, according to PCR protocols and DNA primers

Centre	B1 gene				rep529			
	PCR technology [a]	primers	'0.2' score	'0.1' score	PCR technology	primers	'0.2' score	'0.1' score
A	cnPCR-gel	(6)	78.6	61.4	cnPCR-gel	H1-H2 (unpublished)	100	86.4
B	cnPCR-ELISA	(29)	32.1	20.4	rtPCR-TaqMan	(33, 38)	71.4	53.4
C	rtPCR-FRET	(13)	50	31.8	rtPCR-FRET	(8)	85.7	-
D	rtPCR-SybrGreen	1-4 from (7)	64.3	52.3	rtPCR-SybrGreen	(20)	89.3	77.3
E	rtPCR-FRET	(26)	64.3	45.4	-	-	-	-
F	rtPCR-Taqman	(15)	85.7	65.9	rtPCR-TaqMan	(15)	92.9	84.1
G	rtPCR-FRET	(13)	28.6	20.4	rtPCR-FRET	(27)	92.9	65.9
H	-	-	-	-	rtPCR-FRET	(27)	100	95.4

[a] cnPCR: conventional PCR; rtPCR: real time PCR; ELISA: enzyme-linked immunosorbent assay; FRET: Fluorescence Resonance Energy Transfer