

## Genetic Markers for Bovine Tuberculosis in African Zebu Cattle

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Bovine tuberculosis (BTB) is a considerable threat to livestock, wildlife and public health in many countries. Chadian zebu cattle were used to investigate relationship between microsatellite genetic markers and three ante and post-mortem diagnostic tests for BTB. A total of 248 animals were examined by comparative cervical tuberculin test (CCT), presence of lesions, and 102 animals for Mycobacterium culture, all were recorded as binary data (i.e., 1= phenotype present, 0= phenotype absent). Further details can be found in (Ngandolo et al., 2009). Animals were genotyped for 23 microsatellites markers and the NRAMP1 candidate gene. These microsatellites, distributed over 18 chromosomes were selected from the Food and Agriculture Organisation panel recommended for livestock biodiversity studies (<http://dad.fao.org/>). We included them in the association analyses to test if an association exist between markers and the phenotypes considered. A logistic regression analysis was performed. One marker at a time was tested by means of deviance difference test comparing full and reduced models. Threshold significant was set at  $P = 0.05$ . This was implemented using GenStat version 12.0.

Table 1 shows marker, chromosome (BTA) and  $P$ -values for CCT, lesion and culture phenotypes. Overall, 12 markers were identified as significant association with the three phenotypes we assessed (Table 1). The following markers were consistent significant across at least two phenotypes: BM1818 on BTA 23 ( $P = 0.05$ ; 0.04) for lesion and culture; BM2113 on BTA 2 ( $P = 0.01$ ; 0.04) for CCT and culture; INRA35 on BTA 16 ( $P = 0.05$ ; 0.01) for CCT and lesion respectively, hence, genomic regions around these markers should be investigated further. These are highlighted by bold type in the table. A statistical model that fits allele substitution effects would have advantages over the genotypic effect model developed here. This approach is currently being investigated.

**Table 1.  $P$ -values for tests for association between genetic markers and comparative cervical tuberculin test (CCT), lesion and bacterial culture of naturally infected BTB in African zebu cattle**

Marker	BTA	CCT	Lesion	Culture	Marker	BTA	CCT	Lesion	Culture
		N = 248	N = 248	N = 102			N = 248	N = 248	N = 102
BM1824	1	0.09	0.04	0.88	CSSM66	14	0.36	0.50	0.18
BM2113	2	<b>0.01</b>	0.18	<b>0.04</b>	SPS115	15	0.19	0.38	0.45
NRAMP1	2	0.31	0.15	0.47	INRA35	16	<b>0.05</b>	<b>0.01</b>	0.35
INRA23	3	0.46	0.55	0.06	TGLA53	16	0.03	0.10	0.26
ETH10	5	0.24	0.02	0.17	ETH185	17	0.25	0.01	0.21
ETH152	5	0.20	0.14	0.51	TGLA227	18	0.05	0.31	0.27
ILSTS006	7	0.03	0.06	0.72	ETH3	19	0.66	0.03	0.12
ETH225	9	0.69	0.38	0.33	TGLA126	20	0.11	0.06	0.38
MM12	9	0.17	0.15	0.09	HEL5	21	0.20	0.75	0.31
CSRM60	10	0.26	0.24	0.73	TGLA122	21	0.25	0.24	0.44
ILSTS005	10	0.05	0.17	0.18	BM1818	23	0.06	<b>0.05</b>	<b>0.04</b>
INRA32	11	0.86	0.95	0.59	HAUT27	26	0.02	0.35	0.23

This study reports association between 3 phenotype indicators for BTB infection and some microsatellite markers previously used for genetic diversity studies in African zebu cattle population. These associations may serve as a basis for further investigations.

Ngandolo, B. N., Müller B., Diguimbaye C., Schiller C., Zinsstag J. (2009). *Prev Vet Med* **89**, 81.

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