# Pathogenicity and Immunogenicity of a *Listeria monocytogenes* Strain That Requires D-Alanine for Growth

ROBERT J. THOMPSON,<sup>1</sup> H. G. ARCHIE BOUWER,<sup>2</sup> DANIEL A. PORTNOY,<sup>3</sup> AND FRED R. FRANKEL<sup>1\*</sup>

Department of Microbiology, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania 19104<sup>1</sup>; Immunology Research, VA Medical Center, Portland, Oregon 97207, and Earle A. Chiles Research Institute, Providence Medical Center, Portland, Oregon 97203<sup>2</sup>; and Department of Molecular and Cell Biology and School of Public Health, University of California, Berkeley, California 94720<sup>3</sup>

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Listeria monocytogenes is an intracellular bacterial pathogen that elicits a strong cellular immune response following infection and therefore has potential use as a vaccine vector. However, while infections by *L.* monocytogenes are fairly rare and can readily be controlled by a number of antibiotics, the organism can nevertheless cause meningitis and death, particularly in immunocompromised or pregnant patients. We therefore have endeavored to isolate a highly attenuated strain of this organism for use as a vaccine vector. p-Alanine is required for the synthesis of the mucopeptide component of the cell walls of virtually all bacteria and is found almost exclusively in the microbial world. We have found in *L. monocytogenes* two genes that control the synthesis of this compound, an alanine racemase gene (*dal*) and a p-amino acid aminotransferase gene (*dat*). By inactivating both genes, we produced an organism that could be grown in the laboratory when supplemented with p-alanine but was unable to grow outside the laboratory, particularly in the cytoplasm of eukaryotic host cells, the natural habitat of this organism during infection. In mice, the double-mutant strain was completely attenuated. Nevertheless, it showed the ability, particularly under conditions of transient suppression of the mutant phenotype, to induce cytotoxic T-lymphocyte responses and to generate protective immunity against lethal challenge by wild-type *L. monocytogenes* equivalent to that induced by the wild-type organism.

*Listeria monocytogenes* is a gram-positive facultative intracellular microorganism which has been used for decades as a model pathogen for the study of cell-mediated immunity (24). Immunization of mice with a sublethal *L. monocytogenes* infection results in the generation of immunity which is largely major histocompatibility complex (MHC) class I mediated. Such infections generate CD8<sup>+</sup> T cells, which can adoptively transfer immunity and specifically recognize and kill *Listeria*infected target cells (3, 6, 17, 19).

Recently, the cell biology of L. monocytogenes intracellular growth has been defined (47). Subsequent to internalization, the bacteria escape from a phagocytic vacuole and replicate in the host cell cytosol. Hence, secreted proteins of L. monocytogenes are delivered directly into the cytosol and into the MHC class I pathway of antigen processing and presentation (1, 5). Mutants of L. monocytogenes which are unable to enter the cytosol are absolutely avirulent and fail to immunize mice, and cells infected by such mutants are not recognized by L. monocytogenes-immune CD8<sup>+</sup> T cells (6, 28).

The natural properties of *L. monocytogenes* make it particularly attractive as a potential live vaccine vector for the induction of cell-mediated immunity to foreign antigens. Indeed, recombinant *L. monocytogenes* expressing such antigens successfully has been used to protect mice against lymphocytic choriomeningitis virus (15, 40) and influenza virus (22) infections and against lethal tumor cell challenge (32, 33). We have suggested the use of *L. monocytogenes* for the induction of

\* Corresponding author. Mailing address: Department of Microbiology, University of Pennsylvania School of Medicine, Philadelphia, PA 19104. Phone: (215) 898-8730. Fax: (215) 898-9557. E-mail: frankelf@mail.med.upenn.edu.

cytolytic T cells directed against human immunodeficiency virus (HIV) antigens and have shown that strong cell-mediated immune responses against HIV-1 Gag protein can be induced in mice infected with recombinant *L. monocytogenes* carrying a chromosomal copy of the HIV-1 gag gene (13).

Because of the potential broad use of this organism as a vaccine vector in infectious disease and cancer, the safety of *L. monocytogenes* becomes an important issue. While infections by *L. monocytogenes* are fairly rare and can readily be controlled by a number of antibiotics, the organism can nevertheless cause meningitis and death, particularly in immunocompromised or pregnant patients. An ideal vaccine strain of *L. monocytogenes* would be absolutely avirulent but fully immunogenic. We therefore sought to isolate a mutant which could enter the cytosol but have limited growth potential both in vivo and in the environment.

D-Alanine is required for the synthesis of the mucopeptide component of the cell walls of virtually all bacteria, including L. monocytogenes (21, 23, 43), and is also found in the lipoteichoic acids of this and some other gram-positive organisms (11, 37). However, it is present in only trace quantities and fails to accumulate in vertebrates; the likely origin of these trace quantities is the breakdown products of intestinal and food bacteria (16, 20, 25, 29). We hypothesized that a strain of L. monocytogenes that is unable to synthesize this compound could be grown in the laboratory when supplemented with D-alanine but should be unable to grow outside the laboratory, particularly in the cytoplasm of eukaryotic host cells, the natural habitat of this organism during infection. The isolation of such a mutant of L. monocytogenes required the identification and inactivation of two genes, dal and dat. dal encodes alanine racemase, which catalyzes the reaction: L-alanine↔D-alanine. dat encodes D-amino acid aminotransferase, which catalyzes the reaction D-glutamic acid + pyruvate $\leftrightarrow \alpha$ -ketoglutaric acid + Dalanine. The *dal dat* double-mutant strain had the anticipated phenotype and in addition showed the ability to induce cytotoxic T-lymphocyte (CTL) responses and to generate protective immunity against lethal challenge by wild-type *L. monocytogenes* in infected mice under restricted conditions.

## MATERIALS AND METHODS

**Bacteria and plasmids.** L. monocytogenes 10403S (34) was the wild-type organism used in most of these studies. It was grown in brain heart infusion medium (BHI; Difco Laboratories). Escherichia coli DH5 $\alpha$ , used for cloning, was grown in Luria broth (38). Plasmid pKSV7, used for allellic exchange reactions in L. monocytogenes, is a shuttle vector capable of replication in E. coli, where it is selected in the presence of 50 µg of ampicillin per ml of medium, and in L. monocytogenes, where its replication is temperature sensitive and selection is in the presence of 10 µg of chloramphenicol per ml of medium (42). Plasmid DNA from E. coli and total DNA (chromosomal and plasmid) from L. monocytogenes were isolated by standard methods (38).

Identification of genes in *L. monocytogenes* by homology. Based on sequences of alanine racemase (*dal*) genes in two gram-positive organisms, *Bacillus subtilis* (10) and *B. stearothermophilis* (46), we devised consensus oligonucleotide sequences from highly conserved regions at the 5' and 3' ends of the gene and then modified these sequences to reflect preferred codon usage in *L. monocytogenes*. These 5' and 3' consensus oligonucleotides, 5'-GGG-[AAGCTT(*Hind*III)]-AAA GC(A/T)AA(C/T)GC(A/T)TATGG(A/T)CATGG-3' and 5'-GGG-[AAGCTT (*Hind*III)]-GATCCAT(A/G)CAAAT(A/G)CG(A/G)CC-3', respectively, were used as primers in a PCR using chromosomal DNA from either *L. monocytogenes* or *B. subtilis* as the template. A product of about 850 nucleotides was obtained from each. Translation of the sequenced product from the *L. monocytogenes* template showed that it resembled the alanine racemases of the grampositive organisms.

A similar strategy was used to infer the presence and to sequence the central portion of a D-amino acid aminotransferase (*dat*) gene of *L. monocytogenes*, based on published sequences from *B. sphaericus* (12), *Bacillus* sp. strain YM-1 (45), and *Staphylococcus haemolyticus* (35). The 5' and 3' oligonucleotide primers were 5'-GGG-[AAGCTT(*Hind*III)]-GGTTATGT(A/T)TT(T/C)GGTGAT GG-3' and 5'-GGG-[AAGCTT(*Hind*III)]-TTTAATATCACA(A/G)CG(T/A)A A/GCC-3', respectively. In this case, we obtained a PCR product of about 400 nucleotides whose DNA sequence and translation showed significant homology with the aminotransferase genes of the other organisms.

Strategy for sequence determination of the complete genes. We determined the sequence of the remaining portions of the *L. monocytogenes dal* gene adjoined to the 5' and 3' ends of the original 850-bp PCR product by anchored PCRs (36). Briefly, this strategy used a *Bgl*II restriction digest (for the 5' portion of the gene) or an *XbaI* digest (for the 3' portion of the gene) of *Listeria* chromosomal DNA, onto the ends of which was then ligated a small fragment of DNA containing the T7 promoter. A 5'-portion PCR product and a 3'-portion PCR product were then synthesized and sequenced by using primers from within the central *dal* gene PCR product and a second primer homologous to the T7 promoter fragment. This procedure permitted determination of the entire sequence of the gene.

The sequence of the remainder of the *dat* gene was determined by use of an inverse PCR (8, 49). Briefly, a *HindIII* digest of *Listeria* chromosomal DNA was permitted to self-ligate under conditions of low DNA concentration so that mainly single circular molecules were produced. Outward-directing primers with homologies at the two ends of the original PCR segment of the gene were then used to make a new PCR product that began at the 5' end of the original PCR segment and continued to the 5' end of the gene, through the *Hin*dIII self-ligation site, and into the 3' end of the gene. Using this method, we obtained the sequence of the entire gene.

**Production of mutations in the** *dal* **and** *dat* **genes.** The *dal* gene was initially inactivated by means of a double-allelic exchange between the chromosomal gene and the temperature-sensitive shuttle plasmid pKSV7 (42) carrying an erythromycin resistance gene (39) between a 450-bp fragment from the 5' end of the original 850-bp *dal* gene PCR product and a 450-bp fragment from the 3' end of the *dal* gene PCR product, following the protocol of Camilli et al. (7). Subsequently a *dal* deletion mutant covering 82% of the gene was constructed by a similar exchange reaction with pKSV7 carrying homology regions from the 5' and 3' ends of the intact gene (including sequences upstream and downstream of the gene) surrounding the desired deletion. PCR analysis was used to confirm the structure of this chromosomal deletion.

The chromosomal *dat* gene of *L. monocytogenes* was inactivated by a similar allelic exchange reaction. pKSV7 was modified to carry 450-bp fragments derived by PCR from both the 5' and 3' ends of the intact *dat* gene (including sequences upstream and downstream of the gene). These two fragments were ligated by appropriate PCR. Exchange of this construct into the chromosome resulted in the deletion of 30% of the central bases of the *dat* gene, which was confirmed by PCR analysis.

**Infection of cells in culture.** To examine the intracellular growth of the attenuated strain of *L. monocytogenes* in cell culture, monolayers of J774 cells, a murine macrophage-like cell line, primary murine bone marrow-derived macrophages, and the human HeLa line were grown on glass coverslips and infected as described previously (34). To enhance the efficiency of infection of HeLa cells, a naturally nonphagocytic cell line, the added bacteria were centrifuged onto the HeLa cells at  $543 \times g$  for 15 min. At various times after infection, samples of the cultures were taken for differential staining, for the determination of viable intracellular bacteria, or for immunohistochemical analysis.

Immunohistochemistry. Coverslips with infected macrophages or HeLa cells were washed with phosphate-buffered saline, fixed in 3.2% formalin, and permeabilized with 0.05% Tween 20. Bacteria were detected with fluorescein isothiocyanate (FITC)-labeled rabbit anti-*Listeria* antiserum (Molecular Probes, Eugene, Oreg.) or with rabbit anti-*Listeria* antiserum (Listeria O Antiserum Poly; Difco Laboratories) followed by lissamine rhodamine sulfonyl chloride (LSRSC)-labeled donkey anti-rabbit antibodies or coumarin-labeled goat antirabbit antibodies. Actin was detected with FITC- or tetramethylrhodamine isothiocyanate (TRITC)-labeled phalloidin. To distinguish extracellular (or phagosomal) from intracytosolic bacteria, the former were stained prior to permeabilization.

**Induction of LLO-specific CTLs.** Female BALB/c mice, 6 to 8 weeks of age (Charles River Laboratories, Raleigh, N.C.), were immunized by intraperitoneal inoculation with either the wild-type or *dal dat* strain of *L. monocytogenes*. After 14 days, some of the mice were boosted with a second inoculation at the same number of microorganisms. Ten or more days after the last inoculation,  $6 \times 10^7$  splenocytes from a given animal were incubated in Iscove's modified Dulbecco modified Eagle medium with  $3 \times 10^7$  splenocytes from that same animal that had been loaded with 10  $\mu$ M LLO peptide 91-99 during a 60-min incubation at 37°C. After 5 days of in vitro stimulation, the resulting cultures were assayed for the presence of CTL activity capable of recognizing LLO peptide-labeled P815 cells as previously described (13, 53). Every determination of lytic activity was corrected for activity on unlabeled target cells, which showed between 1 and 10% lysis in different experiments.

Animal studies. Fifty percent lethal dose  $(LD_{50})$  assays were performed by injecting female BALB/c mice (Bantin-Klingman, Freemont, Calif.) at 8 weeks of age with 0.2 ml of three- to fivefold serial dilutions of bacteria as described previously (2). The LD<sub>50</sub> of wild-type *L. monocytogenes* strain 10403 in these animals is approximately 10<sup>4</sup>. The LD<sub>50</sub> of the *dal dat* double-mutant strain of *L. monocytogenes* was found to be  $>8 \times 10^8$  or, when injected in the presence of 20 mg of D-alanine in the 0.2-ml injection volume, approximately  $7 \times 10^7$ .

To examine the protection produced by immunization with the *dal dat* mutant, groups of four to five BALB/c mice were injected with viable wild-type or *dal dat* double-mutant bacteria (in the presence or absence of 20 mg of D-alanine) by tail vein injection. Three to four weeks following immunization, the mice were challenged with approximately 10  $\text{LD}_{50}$  of viable wild-type *L. monocytogenes* 10403 in 0.2 ml by tail vein injection. Spleens were removed 48 h later and homogenized individually in 4.5 ml of phosphate-buffered saline–1% proteose peptone in a tissue homogenizer (Tekmar). The homogenates were serially diluted and plated onto BHI agar. Log<sub>10</sub> protection was determined by subtracting the mean of the log<sub>10</sub> CFU/spleen values of the ust ontrol group.

**Nucleotide sequence accession numbers.** The nucleotide sequences of the *L. monocytogenes dal* and *dat* genes, shown in Fig. 1 and 3, respectively, have GenBank accession no. AF038438 and AF038439.

### RESULTS

Construction of a strain of L. monocytogenes defective in cell wall synthesis. We determined whether L. monocytogenes harbors genes expected to be required for the synthesis of Dalanine. The alanine racemase (dal) gene, used by many microorganisms for the synthesis of D-alanine, has been sequenced in Salmonella typhimurium (14, 51), B. subtilis (10), and B. stearothermophilis (46) but has not been found in L. monocytogenes. To search for evidence of the gene in this organism, we synthesized primers based on the sequences (adjusted for preferred codon usage in L. monocytogenes) of two highly conserved regions of the gene present in the two grampositive organisms and used these in a PCR on L. monocytogenes chromosomal DNA. A product that showed significant homology with the published *dal* gene sequences was obtained. The sequence of the remainder of the L. monocytogenes dal gene was determined (see Materials and Methods) and is shown in Fig. 1. The translated protein sequence showed 44 to 53% identity with the alanine racemase proteins of the grampositive microorganisms and is shown in comparison with these sequences in Fig. 2.

1	ATGGTGACA	GGCTGGCAT	CGTCCAACA	TGGATTGAA	ATAGACCGC	GCAGCAATT	CGCGAAAAT	АТАААААТ	GAACAAAAT	AAACTCCCG	GAAAGTGTC
	мут	G W H	RPT	WIE	IDR	AAI	REN	IKN	EQN	KLP	ESV>
100	GACTTATGG	GCAGTAGTĆ	AAAGCTAAT	GCATATGGT	CACGGAATT	ATCGAAGTT	GCTAGGACG	GCGAAAGAA	GCTGGAGCA	AAAGGTTTC	TGCGTAGCC
	DLW	A V V	KAN	AYG	HGI	IEV	ART	АКЕ	AGA	KGF	C V A>
199	ATTTTAGAT	GAGGCACTG	GCTCTTAGA	GAAGCTGGA	TTTCAAGAT	GACTTTATT	CTTGTGCTT	GGTGCAACC	AGAAAAGAA	GATGCTAAT	CTGGCAGCC
	TLD	EAL	ALR	EAG	FOD	DFI	LVL	GAT	RKE	DAN	L A A>
298	AAAAACCAC	ATTTCACTT	ACTGTTTTT	AGAGAAGAT	TGGCTAGAG	AATCTAACG	CTAGAAGCA	ACACTTCGA	ATTCATTTA	AAAGTAGAT	AGCGGTATG
	KNH	ISL	TVF	RED	WLE	NLT	LEA	TLR	IHL	K V D	SGM>
397	GGGCGTCTC	GGTATTCGT	ACGACTGAA	GAAGCACGG	CGAATTGAA	GCAACCAGT	ACTAATGAT	CACCAATTA	CAACTGGAA	GGTATTTAC	ACGCATTTT
	GRL	GIR	тте	EAR	RIE	ATS	TND	HOL	OLE	GIY	T H F>
496	GCAACAGCC	GACCAGCTA	GAAACTAGT	TATTTTGAA	CAACAATTA	GCTAAGTTC	CAAACGATT	TTAACGAGT	TTAAAAAAA	CGACCAACT	TATGTTCAT
	АТА	DOL	ETS	YFE	ООЬ	AKF	OTI	LTS	LKK	R P T	Y V H>
595	ACAGCCAAT	TCAGCTGCT	TCATTGTTA	CAGCCACAA	ÂTCĜGGTTT	GATGCGATT	CGCTTTGGT	ATTTCGATG	TATGGATTA	ACTCCCTCC	ACAGAAATC
000	TAN	SAA	SLL	O P O	TGF	DAT	RFG	ISM	YGL	TPS	T E I>
694	AAAACTAGC	TTGCCGTTT	GAGCTTAAA	CCTGCACTT	GCACTCTAT	ACCGAGATG	GTTCATGTG	AAAGAACTT	GCACCAGGC	GATAGCGTT	AGCTACGGA
091	KTS	L P F	ELK	PAL	ALY	ТЕМ	V H V	KEL	APG	DSV	S Y G>
793	GCAACTTAT	ACAGCAACA	GAGCGAGAA	TGGGTTGCG	ACATTACCA	ATTGGCTAT	GCGGATGGA	TTGATTCGT	CATTACAGT	GGTTTCCAT	GTTTTAGTA
	АТҮ	ТАТ	ERE	WVA	TLP	IGY	ADG	LIR	HYS	GFH	V L V>
892	GACGGTGAA	CCAGCTCCA	ATCATTGGT	CGAGTTTGT	ATGGATCAA	ACCATCATA	AAACTACCA	CGTGAATTT	CAAACTGGT	TCAAAAGTA	ACGATAATT
0.72	DGE	PAP	IIG	RVC	MDO	TII	KLP	REF	ОТG	з к v	T I I>
991	GGCAAAGAT	CATGGTAAC	ACGGTAACA	GCAGATGAT	GCCGCTCAA	TATTTAGAT	ACAATTAAT	TATGAGGTA	ACTTGTTTG	TTAAATGAG	CGCATACCT
	GKD	HGN	тут	ADD	AAO	YLD	TIN	YEV	TCL	LNE	R I P>
1090	AGAAAATAC	ATCCATTAG		_	~	_					
	RKY	I H *>									

FIG. 1. Nucleotide sequence and translation of the alanine racemase (*dal*) gene of *L. monocytogenes*. The gene was inactivated either by insertion of a 1.35-kb fragment of DNA encoding erythromycin resistance at a *SpeI* site at nucleotide 517 or by deletion of nucleotides 44 to 948.

The gene was inactivated by insertion of a 1.35-kb fragment of DNA encoding erythromycin resistance at a *Spe*I site near the center of the gene. The resulting *dal* bacteria were found to grow both in rich bacteriological medium (BHI) and in a synthetic medium (48) in the presence or absence of D-alanine (not shown). A mutation of the *dal* gene constructed by an in-frame deletion covering 82% of the gene (from nucleotides 44 to 949) had the same properties.

A second enzyme used by some bacteria for synthesis of D-alanine is D-amino acid aminotransferase, encoded by the

dat gene (12, 35, 45). Using a strategy similar to that used to detect the dal gene in L. monocytogenes, we obtained a PCR product that showed significant sequence homology with known dat genes and gene products. The sequence of the remainder of the dat gene was determined (see Materials and Methods) and is shown in Fig. 3. Its deduced protein sequence showed 49 to 51% identity with sequences of aminotransferases of other gram-positive organisms. Comparison of these dat gene products is shown in Fig. 4.

This gene was inactivated by in-frame deletion of 31% of its

LMDAL	1	- MV T GWH RPTWIE I DRAA IRENIKNE QNKLPESVDLWAVVKANA	43
BSTDAL	1	MNDFHRD TWAEVDLDA IYDNVENLRRLLPDD THIMAVVKANA	42
BSUBDAL	1	MS TKPEYRD TWAE I DLSA IKENVSNMKKH I GEHVHLMAVEKANA	44
LMDAL	44	YGHGIIEVARTAKEAGAKGFCVAILDEALALREAGFODDFILVL	87
BSTDAL	43	YGHGDVQVARTALERIGPPP-AVAFIDEALALREKGIEAP-ILVL	84
BSUBDAL	45	YGHGDAETAKAALDAGASCLAMAILDEAISLRKKGLKAP-ILVL	87
LMDAL	88	GATRKEDANLAAKNHISLTVFREDWLENL-TL-EATLRII-	124
BSTDAL	85	GASRPADAALAAQORIIALTVFRSDWLEEASALYSGPFPIHF	125
BSUBDAL	88	GAVPPEYVAIIAAEYDVTLTGYSVEWLQEA-AR-HTKKGSLHF	127
LMDAL	125	H L K V DSGMGR L GIRTTEEARRIEATS TNDHQLQLEGIY TH FATA	168
BSTDAL	126	H L K MD TGMGR L GV K DEEETKRIVAL IERHPH FVLEGLY TH FATA	169
BSUBDAL	128	H L K V D TGMNR L GV K TEEEV ON VMAIL DRNPRLK C K GV FTH FATA	171
LMDAL	169	DOLETSY FEQQLAKFQTILTSLKKRPTYVHTANSAASLLQPQI	211
BSTDAL	170	DEVNTDYFSYQYTRFLHMLEWLPSRPPLVHCANSAASLR-FPDR	212
BSUBDAL	172	DEKERGYFLMQFERFKELIAPLPLKNLMVHCANSAAGLRLKKGF	215
LMDAL	212	GFDAIRFGISMYGLTPSTEIKTSLPFELKPALALYTEMVHVKEL	255
BSTDAL	213	TFNMVRFGIAMYGLAPSPGIKPLLPYPLKEAFSLHSRLVHVKKL	256
BSUBDAL	216	- FNAVRFGIGMYGLRPSADMSDEIPFQLRPAFTLHSTLSHVKLI	258
LMDAL	256	AP GDS V S Y G A T Y T A T E REWVATLP I G Y A D GL I RH Y SG F H V L V D G	299
BSTDAL	257	QP G EKV S Y G A T Y T A Q T E E W I G T I P I G Y A D G - VRR L Q H F H V L V D G	299
BSUBDAL	259	R K G E S V S Y G A E Y T A E K D TW I G T V PVG Y A D GW L RK L K G T D I L V K G	302
LMDAL	300	EPAPIIGRVCMDQTIIKLPREFQTGSKVTIIGKDHGNTVTADDA	343
BSTDAL	300	QK <u>AP</u> IVGRICMDQCMIRLPGPLPVGTKVTLIGRQGDEVISIDDV	343
BSUBDAL	303	KRLKIJA <u>GRICMDQ</u> FMVELDQEYPP <u>GTKVTLIGRQGDE</u> VISMDEI	346
LMDAL	344	AQYLDTINYEVTOLLNERIPRKYIH	368
BSTDAL	344	ARHLETINYEVPCTISYRVPRIFFRHKRIMEVRNAIGRGESSA	386
BSUBDAL	347	AGRLETINYEVACTISSRVPRMFLENGSIMEVRNPLLQVNISN	389

FIG. 2. Linear alignment of deduced protein sequences of alanine racemases of L. monocytogenes (LMDAL), B. stearothermophilus (BSTDAL), and B. subtilis (BSUBDAL). Identical amino acids are boxed.

1	ATGAAAGTA TTAGTAAAT	AACCATTTA GTTGAAAGA	GAAGATGCC ACAGTTGAC	ATTGAAGAC CGCGGATAT	CAGTTTGGT GATGGTGTA TATGAAGTA
	MKV LVN	NHL VER	E D A T V D	IEDRGY	QFGDGVYEV>
100	GTTCGTCTA TATAATGGA	AAATTCTTT ACTTATAAT	GAACACATT GATCGCTTA	TATGCTAGT GCAGCAAAA	ATTGACTTA GTTATTCCT TATTCCAAA
	VRL YNG	KFF TYN	EHI DRL	Y A S A A K	IDL VIPYSK>
199	GAAGAGCTA CGTGAATTA	CTTGAAAAA TTAGTTGCC	GAAAATAAT ATCAATACA	GGGAATGTC TATTTACAA	GTGACTCGT GGTGTTCAA AACCCACGT
	EELREL	LEKLVA	ENNINT	G N V Y L Q	VTRGVQNPR>
298	AATCATGTA ATCCCTGAT	GATTTCCCT CTAGAAGGC	GTTTTAACA GCAGCAGCT	CGTGAAGTA CCTAGAAAC	GAGCGTCAA TTCGTTGAA GGTGGAACG
	NHV I PD	DFP LEG	VLTAAA	REV PRN	ERQFVEGGT>
397	GCGATTACA GAAGAAGAT	GTGCGCTGG TTACGCTGT	GATATTAAG AGCTTAAAC	CTTTTAGGA AATATTCTA	GCAAAAAAT AAAGCACAT CAACAAAAT
	AITEED	VRW LRC	DIKSLN	LLGNIL	AKN KAH QQN>
496	GCTTTGGAA GCTATTTTA	CATCGCGGG GAACAAGTA	ACAGAATGT TCTGCTTCA	AACGTTTCT ATTATTAAA	GATGGTGTA TTATGGACG CATGCGGCA
	A L E A I L	HRGEQV	TECSAS	N V S I I K	DGVLWTHAA>
595	GATAACTTA ATCTTAAAT	GGTATCACT CGTCAAGTT	ATCATTGAT GTTGCGAAA	AAGAATGGC ATTCCTGTT	AAAGAAGCG GATTTCACT TTAACAGAC
	DNLILN	GITRQV	IID VAK	K N G I P V	KEADFTLTD>
694	CTTCGTGAA GCGGATGAA	GTGTTCATT TCAAGTACA	ACTATTGAA ATTACACCT	ATTACGCAT ATTGACGGA	GTTCAAGTA GCTGACGGA AAACGTGGA
	LRE ADE	VFISST	TIEITP	I T H I D G	VQVADGKRG>
793	CCAATTACA GCGCAACTT	CATCAATAT TTTGTAGAA	GAAATCACT CGTGCATGT	GGCGAATTA GAGTTTGCA	AAATAA
	PITAQL	H Q Y F V E	EITRAC	GELEFA	K *>

FIG. 3. Nucleotide sequence and translation of the D-amino acid aminotransferase (*dat*) gene of *L. monocytogenes*. The gene was inactivated by deletion of nucleotides 370 to 636.

central region (from nucleotides 370 to 636). The growth of the resulting *dat* bacteria in broth and synthetic media was again found to be independent of the presence of D-alanine.

A *dal dat* double-mutant strain of *L. monocytogenes* was produced by a double-allelic exchange reaction between the erythromycin-resistant *dal* organism and the shuttle vector carrying the *dat* gene deletion. The growth of the resulting double mutant in bacteriological media was found to be completely dependent on the presence of D-alanine (Fig. 5). A double mutant containing deletions in both of the genes had the same phenotype. The growth defect of the double-deletion strain in the absence of D-alanine could be complemented by a plasmid carrying the *dal* gene of *B. subtilis* (not shown). All of the experiments reported used the single-deletion strain.

**Defective growth of the** *dal dat* **double mutant in eukaryotic cells.** Our original hypothesis was that a defect in the ability of *L. monocytogenes* to synthesize D-alanine would be expressed as an inability to replicate in the cytoplasm of eukaryotic cells due to the absence of the required substrate at that site. To test this hypothesis, several cell lines and primary cells in culture were examined after infection with the wild-type and mutant strains of the organism.

J774 cells are mouse macrophage-like cells that readily take up *L. monocytogenes* by phagocytosis and permit its cytoplasmic growth following escape of the bacteria from the phagolysosome (47). Figures 6A and B show typical cells seen at 5 h after infection with wild-type *L. monocytogenes* and with the *dal dat* double mutant, respectively. Whereas large numbers of

LMDAT	1	M - KVLVNNHLVEREDATVDIEDRGYQFGDGVYEVVRLYNGKFFT	43
Shaedat	1	MTKVFINGEFIDQNEAKVSYEDRGYVFGDGIYEYIRAYDGKLFT	44
BSPHDAT	1	MAYSLWNDQIVEEGSITISPEDRGYQFGDGIYEVIKVYNGHMFT	44
BSPDAT	1	MGYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFT	44
LMDAT	44	Y NEH I DRILYASAAK I DLVI PYSKE ELRELLE KLVAENNIN TGNV	87
SHAEDAT	45	V TEHEERFIRSASEI QLDLGYTVEELII DVVRELLKVNNI QNGGI	88
BSPHDAT	45	A QEH I DRFYASAEKIRLVI PYTKDVLHKLLHDLIEKNNLN TGHV	88
BSPDAT	45	V NEH I DRLYASAEKIRI TIPYTKDKFHQLLHELVEKNELN TGHI	88
LMDAT	88	YLQVTRGVQNPRNHVIPDDFPLEGVLTAAAREVPRNERQFVEGG	131
Shaedat	89	YIQATRGV-APRNHSFPT-PEVKPVIMAFAKSYDRPYDDLENGI	130
BSPHDAT	89	YFQITRGT-TSRNHIFPD-ASVPAVLTGNVKTGERSIENFEKGV	130
BSPDAT	89	YFQVTRGT-SPRAHQFPEN-TVKPVIIGYTKENPRPLENLEKGV	130
LMDAT	132	TAITTEEDVRWLRCDIKSLNLLGNILAKNKAHQQNALEAILHRGE	175
SHAEDAT	131	NAATVEDIRWLRCDIKSLNLLGNVLAKEYAVKYNAGEAIQHRGE	174
BSPHDAT	131	KATLVEDVRWLRCDIKSLNLLGAVLAKQEASEKGCYEAILHRGD	174
BSPDAT	131	KATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNN	174
LMDAT SHAEDAT BSPHDAT BSPDAT	176 175 175 175	QV TECSASNVSIIKDGVLMTHAADNLILNGITRQVIIDVAKKNG TV TEGASSNVYAIKDGA JYTHPVNNYILNGITRKVIKWISEDED IJTECSSANVYGIKDGKLYTHPANNYILNGITRQVILKCAAEIN TV TEGSSSNVFGIKDGILYTHPANNMILKGITRDVVIACANEIN	219 218 218 218 218
LMDAT Shaedat BSPHDAT BSPDAT	220 219 219 219 219	IPVKEADFTLTDLREADEVFISSTTIEITPLTHIDGVQVADGKR IPFKEETFTVEFLKNADEVIVSSTSAEVTPVVKLDGEQVGDGKV LPVLEEPMTKGDLLTMDEIIVSSVSSEVTPVIDVDGQQIGAGVP MPVKEIPFTTHEALKMDELFVTSTTSEITPVIELDGKLIRDGKV	263 262 262 262
LMDAT	264	GPITAQLHQYFVEEIITRACGELEFAK	289
Shaedat	263	GPVITRQLQEGFNKYIIESRSS	282
BSPHDAT	263	GEWTRKLQKAFEAKLPISINA	283
BSPDAT	263	GEWTRKLQKQFETKIIPKPLHI	283

FIG. 4. Linear alignment of deduced protein sequences of *D*-amino acid aminotransferases of *L. monocytogenes* (LMDAT), *S. haemolyticus* (SHAEDAT), *B. sphaericus* (BSPHDAT), and *Bacillus* sp. strain YM-1 (BSPDAT). Identical amino acids are boxed.



Time (min)

FIG. 5. Growth requirement for D-alanine of the *dal dat* double-mutant strain of *L. monocytogenes*. The *dal dat*  $(\bigcirc, \bullet)$  and wild-type  $(\square)$  strains of *L. monocytogenes* were grown in liquid culture (BHI medium) in the presence  $(\bullet)$  or absence  $(\bigcirc, \square)$  of exogenous D-alanine (100 µg/ml) at 37°C. An aliquot of the mutant culture was provided D-alanine at 90 min. The starting cultures were in log phase of growth. As D-alanine had no effect on the growth of wild-type *L. monocytogenes*, those data are not shown.

bacteria were associated with those mouse cells infected with the wild-type strain, few bacteria could be found in any cells following infection with the double mutant. Infection by double-mutant bacteria in culture medium containing D-alanine permitted bacterial growth indistinguishable from that seen after wild-type infection (Fig. 6C).

The number of intracellular bacteria (defined by gentamicin resistance) that could form colonies on medium containing D-alanine was determined at several times after infection (at a multiplicity of infection [MOI] of about 0.05 bacteria per mouse cell) (Fig. 7A). The data clearly show that the double mutant was unable to replicate in J774 cells and in fact slowly died during the course of the experiment. Figure 7A also shows that the replication-defective phenotype of the double mutant could be suppressed by the inclusion of D-alanine (at 100  $\mu$ g/ml) in the tissue culture medium at the time of infection and that the suppression was reversed 2 h after removal of the D-alanine. We also examined the phenotype of the mutant

bacteria in primary mouse bone marrow-derived macrophages and in the HeLa line of human epithelial cells and found that the double mutant was unable to replicate in either of those cell types as well (Fig. 7B and C).

Within a few hours after infection of cells by *L. monocytogenes* when the bacteria have escaped from the phagosome, host actin filaments form a dense cloud around intracytosolic bacteria and then rearrange to form a polarized tail which propels the bacteria through the cytoplasm (9, 47). The bacterium-associated actin can readily be visualized by fluorescencetagged phalloidin, while total bacteria can be detected with appropriately labelled anti-*Listeria* antibodies. To determine the intracytoplasmic status of the double-mutant bacteria following infection, we examined the distribution of cytoplasmic actin in the infected cells.

As shown in Fig. 8A and Table 1, at 2 h after infection (at an MOI of about 5 bacteria per cell), we found that 25.2% of wild-type bacteria associated with J774 macrophages were surrounded with a halo of stained actin and therefore were intracytosolic. By 5 h, 100% showed actin staining, some with long actin tails (Fig. 8B). However, the staining of actin in doublemutant-infected macrophages was much rarer (less than 2%). Nevertheless, if D-alanine was present during only the 30-min period of bacterial adsorption, at 2 h after infection 22% of the cell-associated mutant bacteria were surrounded with actin (Fig. 8C). At 5 h (D-alanine absent from 0.5 to 5 h), the number of intracytosolic bacteria was still only 26.7% (Fig. 8D). This indicated that few additional bacteria had entered the cytosol after removal of the D-alanine and that any bacteria already present in the cytosol had not replicated. If D-alanine was present during the entire infection (Fig. 8E), the results at 2 and 5 h were virtually indistinguishable from the wild-type infection.

Since J774 cells have been culture adapted and reflect few of the normal properties of tissue macrophages, we examined the entry of the mutant bacteria into the cytosol of primary bone marrow-derived macrophages which had been in culture for only 6 days. Because these cells show significant bacterial killing capacity, they were infected at a ratio of about 50 bacteria per cell. In this experiment, at 2 h after infection, 6.8% of the double-mutant bacteria were found to be associated with actin, and this number increased to the level seen after wild-type infection (20%) by inclusion of D-alanine during the first 30 min of the infection (18.2%) or during the entire 2-h infection (19.4%). Therefore, depending on the cell type examined, mu-



FIG. 6. Light micrographs showing the growth of wild-type (A) and *dal dat* double-mutant (B) strains of *L. monocytogenes* in J774 macrophages at 5 h after infection (at approximately 5 bacteria per mouse cell). (C) Infection by double-mutant bacteria in the continuous presence of D-alanine (80  $\mu$ g/ml).

Bacteria per coverslip, 10<sup>4</sup>

Bacteria per coverslip,  $10^5$ 

Bacteria per coverslip,  $10^3$ 

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mately  $7 \times 10^7$ . After sublethal infection of mice with wild-type L. monocytogenes, the bacteria survive and replicate in the spleens and livers of infected animals for up to 5 to 7 days, followed by the onset of a sterilizing immunity. The extent of the in vivo persistence of the mutant bacteria in the spleens of infected animals was therefore examined following infection with  $2 \times 10^7$ mutant bacteria and compared with the result of infection by  $4 \times 10^2$  wild-type organisms. The results in Fig. 9 show that whereas this low dose of wild-type L. monocytogenes resulted in a peak of replication at 2 to 3 days, increasing the number of bacteria in this organ by several logs, the mutant bacteria fell to almost undetectable levels within 2 days. The presence of D-alanine in the inoculum allowed a small number of organisms to survive somewhat longer.

Induction of an immune response with the dal dat double mutant. Infection of mice by L. monocytogenes produces a long-lived state of specific immunologic memory that enables the infected host to resist lethal challenge by the same organism for months after the primary infection. We determined whether infection of mice with sublethal doses of the dal dat bacteria could induce this important long-lasting state of protective immunity. Mice were injected intravenously with 2  $\times$ 10<sup>7</sup> double-mutant bacteria and challenged 3 to 4 weeks later with 10  $LD_{50}$  of wild-type L. monocytogenes. D-Alanine (20 mg) was provided in the initial inoculum of mutant organisms to be certain that the organisms were fully viable at the time of initial infection. The data in Fig. 10 shows that following a single infection with the mutant bacteria, the level of antilisterial protection was approximately 3 log10, similar to the protection generated by immunization with  $4 \times 10^2$  wild-type organisms. Infection with  $2 \times 10^7$  mutant bacteria without D-alanine provided little protection. The almost complete protection obtained with mutant bacteria occurred despite the fact that by 2 days postinfection more than 100-fold-fewer bacteria were detected in the spleens of mutant-infected mice than in animals infected with wild-type organisms (Fig. 9).

LLO peptide 91-99 is the major epitope of the LLO protein and one of the major epitopes to which mice respond when mounting a cell-mediated immune response against L. monocytogenes infection (4, 17, 31). To determine whether the protective immunity generated by infection with the attenuated dal dat bacteria was associated with the induction of cytolytic T cells, splenocytes from infected animals were assayed for the ability to lyse target cells loaded with this peptide. Figure 11B shows that animals that had been infected intraperitoneally with  $3 \times 10^7$  double-mutant bacteria and provided D-alanine subcutaneously (40 mg) before and after the infection showed strong CTL responses directed against the LLO peptide. Likewise, mice provided with D-alanine in their drinking water (0.2 or 2 mg/ml) before and after infection mounted a modest CTL



6

FIG. 7. Infection of mammalian cells with the *dal dat* double-mutant (O) and wild-type strains of L. monocytogenes (O). (A) J774 murine macrophage-like cells (MOI of about 0.05). Mutant infection in one culture (■) was in the continuous presence of D-alanine (100 µg/ml); cells in an aliquot of that culture (□) were resuspended in D-alanine-free medium at 4 h. (B) Primary murine bone marrowderived macrophages (MOI of about 5). (C) Human epithelial cells (HeLa) (MOI of about 5). Starting cultures of L. monocytogenes were in stationary phase of growth.

4

tant bacteria in the absence of D-alanine had either a low or a moderate efficiency of entering the host cytosol (or, alternatively, showed reduced binding of actin onto their surface). However, the brief presence of D-alanine during the initial phase of infection allowed a normal fraction of bacteria to enter the cytosol and bind actin.



FIG. 8. Association of actin with intracytosolic wild-type *L. monocytogenes* (A, 2 h; B, 5 h) or with the *dal dat* double mutant (C, 2 h with D-alanine [100  $\mu$ g/ml] present from 0 to 30 min; D, 5 h with D-alanine present from 0 to 30 min; E, 5 h with D-alanine present continuously) following infection of J774 cells. Photomicrographs in the top row show the binding of FITC-labeled antilisterial antibodies to total bacteria; those below show the binding of TRITC-labeled phalloidin to actin. Arrowheads indicate some actin-associated bacteria in the sparsely infected cells.

Log10 bacteria per spleen

response after single infection with  $3 \times 10^7$  mutant bacteria. In the absence of D-alanine, animals infected and boosted one time with  $3 \times 10^7$  double-mutant bacteria, or animals singly infected with  $3 \times 10^8$  bacteria (data not shown), also showed a modest CTL response to LLO peptide 91-99. Single infection with  $3 \times 10^7$  double-mutant bacteria in the absence of Dalanine produced no significant response (Fig. 11B).

# DISCUSSION

*L. monocytogenes* is a gram-positive facultative intracellular bacterium which has been used for decades as a model for the study of cell-mediated immunity (6, 26, 27). Long-term resistance to infection by this microorganism resides primarily in the MHC class I-restricted  $CD8^+$  T cells that are induced following primary infection (3, 17). These cells act by directly lysing antigen-expressing target cells, as well as through the action of the cytokines gamma interferon and tumor necrosis factor alpha (18). We and other investigators have been ex-

 
 TABLE 1. Intracytoplasmic status of bacteria following infection of J774 cells and bone marrow-derived macrophages

C 11	% Intracytosolic bacteria <sup>a</sup>				
Cells	2 h	5 h			
J774					
L. monocytogenes wild type	25.2 (35.6)	100 (100)			
dal dat mutant					
5 h D-ala <sup>b</sup>	22.7 (44.4)	95 (95)			
30 min D-ala <sup>c</sup>	22.0 (37.5)	26.7 (47.6)			
No D-ala	<2 (<5)	<2 (<5)			
Bone marrow macrophages					
L. monocytogenes <sup>+</sup> wild type	20.0 (68.0)	75.8 (77.8)			
dal dat mutant		· · · ·			
5 h D-ala	19.4 (65.4)	75.0 (80.0)			
30 min D-ala	18.2 (52.9)	24.8 (46.4)			
No D-ala	6.8 (36.4)	13.6 (40.6)			

<sup>*a*</sup> Percentage of total cell-associated bacteria that are intracytosolic, as defined by their staining for bacteria-associated actin. Numbers in parentheses represent percentages of infected macrophages containing intracytosolic, actin-associated bacteria.

<sup>b</sup> D-Alanine (100  $\mu$ g/ml) was present throughout the infection.

<sup>c</sup> D-Alanine (100 µg/ml) was present only during the first 30 min of infection.

ploring the use of recombinant forms of *L. monocytogenes* as a vehicle for the delivery of foreign antigens into the MHC class I pathway of antigen presentation (13, 15, 22, 32, 33, 40).

This strategy for vaccine development suffers, however, from the known pathogenicity of the organism, which is the cause of listeriosis, a food-borne disease characterized by meningitis, septicemia, abortion, and often a high rate of mortality. We therefore attempted to develop a suitably attenuated form of *L. monocytogenes* that could be used as a safe vaccine and adjuvant. Since virtually all bacterial species contain cell wall components that are unique to these organisms, we deduced that a strain of *L. monocytogenes* unable to synthesize one of these components, D-alanine (21, 43), would be crippled unless specifically supplied with this substrate.

D-Alanine appears to be synthesized by different pathways in different organisms. *E. coli* and *S. typhimurium* possess two weakly homologous alanine racemases, one constitutive and



Days after infection

FIG. 9. Recovery of bacteria from spleens of BALB/c mice following sublethal infection with wild-type *L. monocytogenes* ( $\bullet$ ), the *dal dat* mutant in the absence of D-alanine ( $\bigcirc$ ), and the *dal dat* mutant in the presence of 20 mg of D-alanine in the inoculation fluid ( $\square$ ). The points at day 0 show the total number of viable organisms injected, not bacteria per spleen.



FIG. 10. Protection of BALB/c mice against challenge with  $10 \times LD_{50}$  of wild-type *L. monocytogenes* by immunization with the *dal dat* double-mutant strain of *L. monocytogenes*. Column numbers represent groups of five mice immunized with the following organisms:  $1, 4 \times 10^2$  CFU of wild-type *L. monocytogenes*;  $2, 2 \times 10^7$  CFU of *dal dat* mutant (plus 20 mg of D-ala),  $3, 2 \times 10^5$  CFU of *dal dat* mutant (plus D-ala);  $4, 2 \times 10^4$  CFU of *dal dat* mutant (plus D-ala),  $5, 2 \times 10^7$  CFU of *dal dat* mutant (nD D-ala). Mice were challenged 21 to 28 days later. Log<sub>10</sub> protection was calculated as described in Materials and Methods. The largest error seen in all mouse groups was 0.17 log<sub>10</sub>.

one inducible, which can convert L-alanine to D-alanine. D-Alanine produced by the first enzyme is apparently used for peptidoglycan formation, while the latter enzyme may be utilized to provide substrate to a D-alanine dehydrogenase that converts the compound to pyruvate and ammonia (50, 52). In S. typhimurium, a mutation in either gene alone permits the synthesis of sufficient D-alanine for cell growth, while a double mutant displays the expected phenotype of an exogenous Dalanine requirement (50). In two Bacillus species, alanine racemases have also been identified (10, 46). Mutation of this gene in B. subtilis leads to a D-alanine requirement only when the bacteria are grown in rich broth or in synthetic media that contain L-alanine (10). A second enzyme, D-amino acid aminotransferase, that can convert D-glutamic acid and pyruvate to  $\alpha$ -ketoglutarate and D-alanine has also been identified in several gram-positive species and could be a source of D-alanine (12, 35, 45). Indeed, we have found that in L. monocytogenes, both a racemase gene and an aminotransferase gene are present, and both genes must be inactivated in order to produce a requirement for exogenous D-alanine.

The *dal dat* double mutant was found to be unable to replicate in bacteriological culture media devoid of added D-alanine. It was also unable to replicate following infection of several different lines of eukaryotic cells growing in standard tissue culture media. On infection of BALB/c mice with 10<sup>7</sup> of these bacteria, few organisms survived for longer than 1 to 2 days. Consequently, the *dal dat* strain was completely attenuated in BALB/c mice and showed an LD<sub>50</sub> in these animals of  $>8 \times 10^8$  (compared with 10<sup>4</sup> for the wild-type organism). These results support the view that if any D-alanine is present in eukaryotic cells and in mice, the levels are below the threshold required for growth of the D-alanine-requiring strain of *Listeria*.

Can this attenuated strain of *L. monocytogenes* induce an immune response in mice? When  $\sim 0.1 \text{ LD}_{50}$  of the double mutant was administered intravenously in the absence of D-alanine, little protection against a lethal challenge by the wild-type organism was obtained. Likewise, this dose of the double mutant (given intraperitoneally) produced no detectable *List*-



FIG. 11. Cytolytic activity of splenocytes isolated from mice 10 to 14 days after infection with wild-type *L. monocytogenes* ( $\bullet$ ,  $\bigcirc$ ) or naive controls ( $\blacksquare$ ,  $\square$ ) (A). Open and closed symbols represent independent experiments; b-alanine was not provided in either experiment. (B) *dal dat* double mutant: 3 × 10<sup>7</sup> bacteria (+), 3 × 10<sup>7</sup> bacteria with boost at 10 days ( $\blacktriangle$ ,  $\triangle$ ); 3 × 10<sup>7</sup> bacteria with animals provided D-alanine subcutaneously (40 mg at -6 h, time of infection, 6 h, and 12 h) ( $\bullet$ ,  $\bigcirc$ , 3 × 10<sup>7</sup> bacteria with D-alanine (2 mg/ml;  $\blacksquare$ ) or D-alanine (0.2 mg/ml;  $\square$ ) in drinking water from 24 h before infection to 36 h post-infection. Open and closed symbols represent independent experiments.

*eria*-specific CTL response. A booster infection of mice produced a modest increase in the *Listeria*-specific CTL response, as did single immunization with a higher dose of the mutant organisms. These weak responses were not surprising in view of the complete absence of any replication of these bacteria in eukaryotic cells. Indeed, the lack of D-alanine might in addition cause down-regulation of the synthesis of enzymes necessary for entry of the microorganism to the host cytosol, the minimum requirement for induction of a cell-mediated immune response. Our assays for intracytosolic bacteria (by the detection of binding of cytoplasmic actin) suggested that their entry to the cytosol was far less efficient than for wild-type *L. monocytogenes*.

However, the presence of D-alanine at the time of infection of cells in culture allowed the normal number of the doublemutant bacteria to enter the cytosol of infected cells. Additionally, we showed that eukaryotic cells were able to take up sufficient D-alanine from their growth medium to satisfy the growth requirement of the double-mutant bacteria. This uptake was reversible, so that when D-alanine was subsequently removed from the medium, the attenuation phenotype returned within several hours. It seemed possible that a similar paradigm could function in vivo to produce a novel means of in vivo suppression of the attenuating double mutation, resulting in both entry to the cytosol and transient survival and replication of the organism to generate a moderate to strong immune response. In vertebrates, D-amino acids, which originate almost exclusively from intestinal and food bacteria, are efficiently removed from the system by the action of D-amino acid oxidases (16, 20, 25, 29).

Indeed, intravenous inoculation of these organisms (at ~0.1  $LD_{50}$  in the presence of D-alanine) led to virtually full protection against a lethal challenge by wild-type organisms. Likewise, transient suppression of the defective phenotype of the double mutant by providing the host with D-alanine by subcutaneous injection or by inclusion in the drinking water at the time of intraperitoneal infection produced moderate or strong CTL responses against the major *L. monocytogenes* T-cell epitope, LLO peptide 91-99. Transient suppression of the attenuation thus appears to be an effective mechanism to produce a good immune response to these organisms.

The strong response seen in the protection experiment suggests that protective immunity is adequately stimulated within the first 1 or 2 days of infection, since after this time the bulk of the attenuated bacteria are gone. This result appears to differ from an early observation that showed that ampicillin administered 24 h after *L. monocytogenes* infection greatly reduced protection against subsequent challenge (30). A significant difference between these two experiments is the larger mass of antigen administered in 0.1  $LD_{50}$  of our attenuated strain.

Other modifications of L. monocytogenes have been suggested for use as vaccine vectors. Mutations in the *hly* gene produce a defective hemolysin and prevent the ingested organism from escaping into the host cytosol. Such mutants can be completely avirulent (28), but they fail to present antigens to  $CD8^+$  T cells (6) and therefore are a poor choice of vector for potential induction of CTL responses. It has been reported that heat-killed L. monocytogenes, which also should fail to enter the cytosol of infected cells, was able to induce protective CD8<sup>+</sup> T lymphocytes under appropriate circumstances. However, protection was short-lived (44). actA mutants are able to grow in the cytoplasm of infected cells but, because they fail to nucleate host actin, are unable to propagate the infection through cell-to-cell spread. These bacteria are capable of inducing effective CTL responses (15). However, such mutants are still virulent and persist for up to 7 days in the livers of infected mice. They also grow at normal rates in standard media; such growth represents a continuing source of bacteria that might through various genetic mechanisms become altered to regain greater virulence or even, unreverted, show virulence under unanticipated circumstances.

The hyperattenuated *dal dat* strain of *L. monocytogenes* described in this report, in which the pathways for synthesis of D-alanine have been abolished, appears to provide good immunogenicity while being unable to replicate in infected animals or in usual media and thus may represent a useful tool as a safe vaccine and adjuvant. The use of cell wall auxotrophy, as exploited here, has been explored previously as a mechanism for attenuation of virulence in *Shigella* (41).

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