Open Access

The Two-Component Regulatory System VicRK is Important to Virulence of *Streptococcus equi* Subspecies *equi*

Mengyao Liu, Michael J. McClure, Hui Zhu, Gang Xie and Benfang Lei*

Department of Veterinary Molecular Biology, Montana State University, Bozeman, Montana 59717, USA

Abstract: This study aims at evaluating the importance of the two-component regulatory system VicRK to virulence of the horse pathogen *Streptococcus equi* subspecies *equi* and the potential of a *vicK* mutant as a live vaccine candidate using mouse infection models. The *vicK* gene was deleted by gene replacement. The $\Delta vicK$ mutant is attenuated in virulence in both subcutaneous and intranasal infections in mice. $\Delta vicK$ grows less slowly than the parent strain but retains the ability of *S. equi* to resist to phagocytosis by polymorphoneuclear leukocytes, suggesting that the *vicK* deletion causes growth defect. $\Delta vicK$ infection protects mice against reinfection with a wild-type *S. equi* strain. Intranasal $\Delta vicK$ infection induces production of anti-SeM mucosal IgA and systemic IgG. These results indicate that VicRK is important to *S. equi* growth and virulence and suggest that $\Delta vicK$ has the potential to be developed as a live *S. equi* vaccine.

INTRODUCTION

Bacterial pathogens produce many two-component regulatory systems to regulate gene expression by specific environmental signals [1]. These systems consist of membrane protein sensors and cognate cytoplasmic response regulators. The regulator is phosphorylated by the sensor in response to a specific signal, activating or repressing the transcription of target genes. The two-component regulatory system VicRK or YycFG is specific for Gram-positive bacteria. The regulator component VicR is essential in Bacillus subtilis [2], Staphylococcus aureus [3], and Streptococcus pneumoniae [4-5] but appears not to be essential in Streptococcus pyogenes [6]. The deletion of the vick gene can be readily inactivated in S. pneumoniae [7], Streptococcus mutans [8], and S. pyogenes [6] but not in B. subtilis [2] and S. aureus [3]. Conditional and unconditional vicRK mutants display various phenotypes, including defects in morphology and cell wall synthesis, decreased competence, sensitivity to antibiotics and fatty acids, defects in biofilm formation, and attenuated virulence, growth defect, and sensitivity to osmotic pressure [3, 6, 8-11].

The vicRK system of Gram-positive bacterium Streptococcus equi subspecies equi (S. equi) has not been studied. This pathogen causes equine strangles, a highly contagious purulent lymphadenitis [12-13]. The infection initially causes nasal discharge and fever and, then, leads to abscess formation in local lymph nodes, causing respiratory difficulty. Although the infection at the lymph nodes cause massive infiltration of polymorphoneuclear leukocytes (PMNs) [14], S. equi resists phagocytosis by PMNs and rapidly multiplies, forming an abscess of large numbers of degenerating PMNs and long chains of S. equi [15]. The hyaluronic acid capsule and *S. equi* M-like protein (SeM) are both required for the resistance to phagocytosis by PMNs [16-17]. Most horses recovered from strangles have immunity against *S. equi* reinfection for up to 5 years [18]. It is believed that the immunity is mediated by mucosal antibodies specific to SeM and other protective antigens. An intranasal vaccine made of live attenuated strain has been used in USA, which lacks the hyaluronic acid capsule, and various adverse effects, including pharyngeal lymphadenopathy, limb edema, and bastard strangles abscesses, have been reported [15].

This study aims at evaluating the importance of VicRK to *S. equi* virulence and the potential of a *vicK* deletion mutant as a live vaccine using mouse infection models. We found that the *vicK* deletion attenuated *S. equi* virulence in mouse models of subcutaneous and intranasal infections and that infection with a *vicK* deletion mutant confers protection against subsequent infection with wild-type *S. equi* and induces production of mucosal and systemic immunoglobins to SeM in nasal infection.

MATERIALS AND METHODS

Bacterial Strains and Growth

S. equi strain SEM1 was isolated in 2003 from a horse with strangles in Montana, USA. SEM1 and its mutant were routinely grown in Todd-Hewitt broth supplemented with 0.2% yeast extract (THY) in 5% CO₂ at 37°C without and with 150 mg/liter spectinomycin, respectively.

Generation of a vicK Deletion Mutant

A *vicK* deletion mutant (Δ*vicK*) of *S. equi* SEM1 was generated by gene replacement (Fig. 1). The upstream and downstream flanking fragments of the deleted internal fragment (bases 451-1282) of *vicK* were PCR-amplified using paired primers 5'- GAAGCTTCTTATGACTAAGGACAT-CATTGGAAC-3'/5'-GAGATCTGGTGTAAGGTGAGTC ACTGTC-3' and 5'-AGGATCCCCTTTACCATTGTG TTA CCTTACG-3'/5'-AGTCGACCCTGTATCCGTCAGCATG

^{*}Address correspondence to this author at Department of Veterinary Molecular Biology, Montana State University, P.O. Box 173610, Bozeman, Montana 59717, USA; E-mail: blei@montana.edu

AC-3', respectively. The PCR products of the upstream and downstream fragments were sequentially cloned into pGRV [19] at the *Hind*III/*Bg*/II and *Bam*HI/*Sa*/I sites, respectively, to yield pGRV- $\Delta vicK$. pGRV- $\Delta vicK$ was introduced into *S. equi* strain SEM1 by electroporation using the conditions described previously for *S. pyogenes* [6], and the sample was plated on THY agar plate with 150 mg/liter spectinomycin. The obtained colonies, which could be derived from a single or double crossover recombination, were screened by PCR using primers 5'-GAGACTGCTC AAAAGCAGCTC-3' and 5'-GATTTGACTCAATCAAGTAGC-3' and DNA sequencing analyses to identify the desired deletion mutant.

S. equi Growth in Rabbit Blood

S. equi strains were harvested at the exponential growth phase, washed three times with pyrogen-free Dulbecco's phosphate-buffered saline (DPBS), and inoculated at 2×10^4 cfu/ml in heparinized rabbit blood. The samples were rotated end-to-end at 37°C for 4 h, and numbers of viable *S. equi* in the samples and actual inocula were determined by plating on THY agar. Growth factor is defined as the ratio of colony-forming units (cfu) of each sample after 4-h incubation to cfu in the inoculum.

Phagocytosis Assay

Phagocytosis assay was performed as described previously [6, 20]. Briefly, *S. equi* SEM1 wild-type and $\Delta vicK$ cells from exponential growth phase in THY were washed with phosphate-buffered saline (PBS) and labeled with 0.75 µg/mL FITC in PBS at 37°C for 20 min. The labeled bacteria were washed and suspended at 1 x 10° cfu/ml in PBS. Ten µl of the labeled bacteria were mixed with 100 µl of nonimmune heparinized rabbit or horse blood and incubated with gentle shaking at 37°C for 5 or 15 min. The samples were immediately processed using an Immunolyse Kit (Beckman Coulter) according to the manufacturer's protocol and analyzed by flow cytometry. The percentage of PMNs with fluorescent bacteria was used as a measure of phagocytosis efficiency.

Mouse Infections

S. equi strains were harvested at exponential phase, washed with DPBS, and inoculated subcutaneously or intranasally at inocula specified in figure legends into groups of 8 female outbred CD-1 Swiss mice. Survival rates were examined daily for 20 days after inoculation. At the end of the intranasal infection experiment, blood was collected from the surviving mice via cardiac puncture, and the nasal wash fluids were then obtained as follows. The trachea was perforated, a small tube was inserted into the opening, and the nasal cavity was slowly flushed with 1.0 ml DPBS through the tube. All animal procedures were approved by the Institutional Animal Care and Use Committee at Montana State University, Bozeman, USA.

Enzyme-linked Immunosorbant Assay (ELISA) and Western Blotting Analysis

Relative levels of anti-SeM IgG in sera of mice recovered from the intranasal *S. equi* infections were estimated by ELISA and Western blotting using a truncated recombinant SeM containing amino acids 38 to 260 (SeM³⁸⁻²⁶⁰) with described procedures [21]. Briefly for ELISA, microtiter plates were coated overnight with SeM³⁸⁻²⁶⁰ at a concentration of 0.25 µg/well. The plates were washed four times with PBS containing 0.1% (vol/vol) Tween 20 (PBS-T), blocked with 0.1% bovine albumin (BSA) in PBS-T for 2 h at room temperature, and washed as described above. The plate was incubated with 100 µl/well of mouse sera diluted at 1:100 to 1:51200 in 0.1% BSA in PBS-T and washed as described above. The wells were incubated with goat anti-mouse IgG (H + L)-peroxidase conjugate (1:4,000 dilution). The plates were washed as described above and washed four times with PBS to remove Tween 20. The plates were developed with 100 µl/well of ABTS solution for 30 min and the absorbance was measured at 405 nm. Titers were determined by the geometric method. The presence of SeM³⁸⁻²⁶⁰-specific IgA in the nasal wash samples were determined by A_{405} in the ELISA assay as described above using 100 µl of 2-folddiluted nasal wash samples and goat anti-mouse IgA HRP conjugate (Bethyl Laboratories, Inc.).

RESULTS

S. equi vicK Deletion Mutant

The S. equi vicRK genes were found by blasting the S. equi genome database (http://www.sanger.ac.uk/Projects/ S_equi) with the S. pyogenes vicRK sequence. Gene replacement strategy was used to generate vick-deletion mutant (Fig. 1A). The vector pGRV has two genes and and cmR for selections with spectinomycin and chloramphenicol, respectively. The two upstream and downstream flanking fragments of the internal vicK fragment from Tyr151 to Ser427 to be deleted were cloned at the upstream and downstream ends of the aad gene, respectively, resulting in suicide plasmid pGRV- $\Delta vicK$. Single crossover between one flanking fragment in pGRV- $\Delta vicK$ and the homologous region in the genome would lead to the insertion of the whole plasmid into S. equi genome, resulting in strains resistant to both spectinomycin and chloramphenicol. Double crossover at both of the flanking fragments would lead to the replacement of the vicK internal fragment with the aad gene, resulting in vicK deletion strains with resistance only to spectinomycin. The colonies on spectinomycin agar plates were tested for resistance to chloramphenicol. Three putative $\Delta vicK$ strains, which were spectinomycin-resistant and chloramphenicol-sensitive, were obtained. PCR analyses using the primers located beyond the deleted fragment resulted in the PCR product from these strains that were expectedly bigger than that from the wild-type strain because the replacing fragment was bigger than the displaced vick fragment (Fig. 1B). DNA sequencing confirmed the desired deletion. One deletion strain was randomly chosen for further characterization.

Growth of *∆vicK* in THY and Rabbit Blood

The growth curve of the $\Delta vicK$ mutant in THY displays a longer early growth phase and smaller slope in the exponential growth phase than that of the parent strain (Fig. 2A), indicating that the *vicK* deletion detrimentally affects *S. equi* growth. The effect of the deletion on *S. equi* growth in blood was also examined. The wild-type and $\Delta vicK S. equi$ strains



Fig. (1). Deletion of the *vicK* gene. A) schematic for *vicK* deletion by gene replacement. The two flanking fragments of the internal *vicK* fragment to be deleted were cloned into the up- and downstream ends of the *aad* gene in pGRV. The resulting plasmid pGRV- $\Delta vicK$ was introduced into *S. equi*, and double crossover in the homologous regions between the plasmid and *S. equi* genome resulted in $\Delta vicK$ mutants. B) PCR confirmation of the *vicK* deletion. The picture shows agarose gel analysis of PCR reactions using mutant (lane $\Delta vicK$) or wild-type (lane wt) genomic DNA as template and primers indicated by the arrows under the mutant genome.

were inoculated into 1 ml heparinized rabbit blood at an inoculum of approximately 20,000 cfu. The samples were incubated for 4 h, and the numbers of the bacteria in the samples and inocula at time zero were determined by plating. The growth factors, the ratio of cfu in the sample at 4 h over cfu at time zero, were 250 and 66 for the wild type and $\Delta vicK$ strains, respectively (Fig. **2B**). Thus, the $\Delta vicK$ mutant has significantly reduced ability to grow in rabbit blood (P < 0.0001).

No Effect of the *vicK* Deletion on Resistance of *S. equi* to Phagocytosis by PMNs

To determine whether the $\Delta vicK$ deletion affects the resistance of S. equi to phagocytosis by PMNs, the phagocytosis of wild-type and $\Delta vicK$ bacteria by PMNs in non-immune horse and rabbit blood was compared. FITC-labeled wildtype S. equi, $\Delta vicK$ mutant, and S. pyogenes spy1718::aad mutant were incubated with heparinized horse or rabbit blood for 5 and 15 min, and percentages of PMNs associated with fluorescent bacteria were quantified using flow cytometry analysis. The spy1718::aad mutant of S. pyogenes, which is no longer resistant to phagocytosis by PMNs, was used as a positive control in the assay. The percentages of PMNs with associated wild-type S. equi and spy1718::aad were low and high, respectively, indicating that the assay worked well to evaluate resistance of the bacteria to phagocytosis. There was no significant difference in the percentages of PMNs associated with wild-type and $\Delta vicK$ bacteria at both time points and in both horse and rabbit blood (Fig. 3), indicating that the $\Delta vicK$ mutant retains the ability of S. equi to resist to phagocytosis by PMNs.



Fig. (2). A) growth curves of wild-type and $\Delta vicK$ strains in THY. Cultures at the exponential phase were inoculated into fresh THY, and OD₆₀₀ was measured at the indicated times. **B**) growth of wild-type and $\Delta vicK$ strains in rabbit blood. Approximately 2 x 10⁴ cfu of each strain was inoculated into 1 ml blood in triplicate. Numbers of the bacteria in inocula and in the samples after end-to-end rotation at 37°C for 4 h were determined by plating. The growth factor (cfu at 4 h/ cfu at 0 h) ± SD is presented.



Fig. (3). Association of wild-type and $\Delta vicK$ bacteria with rabbit (A) and horse (B) PMNs. FITC-labeled bacteria (10⁷ cfu) were incubated with 100 µl heparinized blood at 37°C for 5 or 15 min. Red blood cells were lysed using an Immunolyse kit, and percentages of PMNs with associated (bound and phagocytosed) bacteria determined by flow cytometry are presented. A *S. pyogenes spy1718::aad* mutant was included as a positive control.

Attenuation of S. equi Virulence by vicK Deletion

Group of 8 mice were subcutaneously inoculated with 1.1 x 10^8 cfu wild-type or $\Delta vicK$ mutant strains. Seven of the 8 mice infected with the wild-type *S. equi* strain died, whereas 7 of the 8 mice inoculated with $\Delta vicK$ survived (Fig. **4A**). The infection was performed in a model of intranasal infec-

tion as well. All the 8 mice infected with $\Delta vicK$ survived, whereas 5 of the 8 mice infected with the wild-type *S. equi* strain died (Fig. **4B**). These results indicate that the *vicK* deletion significantly attenuated *S. equi* virulence in both mouse models of subcutaneous (P = 0.0066) and nasal (P = 0.0085) infections.



Fig. (4). Attenuation of *S. equi* virulence by *vicK* deletion and protection of mice against wild-type *S. equi* infection conferred by preceding $\Delta vicK$ infection. Groups of 8 CD-1 mice were inoculated subcutaneously (**A**) and intranasally (**B**) with 1.1 x 10⁸ cfu of each strain, and survival rates were determined daily. Panel A also includes the results of the subcutaneous infection with 1.5 x 10⁸ cfu of the wild-type strain on the 7 mice survived from the subcutaneous $\Delta vicK$ infection (the open circles).

Δ*vicK* Infection Confers Protection of Mice against Reinfection with Wild-Type *S. equi*

To test whether $\Delta vicK$ infection confers immunity against *S. equi* infection, the seven mice recovered from the subcutaneous $\Delta vicK$ infection was reinfected subcutaneously with 1.5 x 10⁸ cfu wild-type *S. equi* 30 days after the first infection and monitored for 18 days. Six of the 7 mice survived the reinfection (Fig. **4A**), suggesting that the $\Delta vicK$ infection induces immunity against *S. equi* infection.

Intranasal $\Delta vicK$ Infection Induces SeM-Specific Mucosal IgA and Systemic IgG

To examine the humoral immune responses in the intranasal $\Delta vicK$ infection, nasal wash and serum samples were collected from the 8 mice infected intranasally with $\Delta vicK$ and 3 surviving mice infected with the wild-type *S. equi* 30 days after infection. Half of the nasal wash samples from the mice infected with $\Delta vicK$ had similar levels of SeM³⁸⁻²⁶⁰-IgA reactivity with those from the mice infected with the wildtype strains. Similarly, these 4 mice with higher IgA levels also had higher levels of SeM-specific systemic IgG (Fig. **5B**). Western blotting analysis was used to confirm the presence of SeM-specific IgG. The wild-type sera and 5 of the 8 $\Delta vicK$ samples had strong immunoreactions with SeM³⁸⁻²⁶⁰ in Western blotting analysis (Fig. **5C**). Thus, the $\Delta vicK$ mutant has the ability to induce mucosal and systemic immune responses, though there was host variation in these responses caused by $\Delta vicK$ infection.



Fig. (5). Assessment of SeM-specific mucosal IgA and systemic IgG production in mice with the intranasal *S. equi* infection by ELISA and Western immunoblot. Nasal wash and serum samples were collected from the surviving mice in the nasal infections with wild-type and $\Delta vicK$ strains of Fig. 4B on day 30 after inoculation. **A**) immunoreactivity of SeM³⁸⁻²⁶⁰ with IgA in the nasal wash samples. **B**) the reciprocal of anti-SeM³⁸⁻²⁶⁰ IgG titers in the serum samples. **C**) immunoblots demonstrating anti-SeM³⁸⁻²⁶⁰ IgG in the serum samples, which were diluted by 1:1000 in the assay.

DISCUSSION

VicK is essential in *B. subtilis* [2] and *S. aureus* [3] but not in *S. pneumoniae* [7], *S. mutans* [8], and *S. pyogenes* [6]. We successfully deleted the *vicK* gene of *S. equi*. Thus, VicK is not essential in *S. equi*. However, the $\Delta vicK$ mutant is attenuated in virulence in both mouse models of subcutaneous and intranasal *S. equi* infections, indicating that VicRK is important to virulence. The results provide the further evidence for the importance of VicRK to virulence of Gram-positive pathogens.

S. equi $\Delta vicK$ mutant does not grow as well as the wildtype strain in both THY and blood, suggesting that the vicK deletion causes defect in growth, a plausible reason that likely contributes to the attenuation of S. equi virulence in the mouse infection models. This suggestion is further supported by the observations that both the wild-type and $\Delta vicK$ mutant strains are resistant to phagocytosis by PMNs, which suggest that VicRK is not required for the evasion of S. equi to the innate immunity. As introduced earlier, the various phenotypes have been described for the vicRK mutants of the various pathogens. Whether the phenotypes are specific to particular organisms is not known. The phenotypes of the S. equi $\Delta vicK$ mutant are similar to those of the S. pyogenes $\Delta vicK$ mutant [6], suggesting that the growth defect phenotype may be a common feature of the vicRK mutants of various Gram-positive pathogens.

The $\Delta vicK$ mutant appears to possess the properties of a potential live vaccine. First, it is attenuated in virulence in the mouse infection models. Secondly, $\Delta vicK$ inoculation protects mice against subsequent infection with wild-type *S. equi.* Thirdly, most of the mice with intranasal $\Delta vicK$ infection produce mucosal IgA and systemic IgG specific to protective antigen SeM. However, whether $\Delta vicK$ can be an

Streptococcus equi vicK Mutant

effective live vaccine and whether the $\Delta vicK$ mutant has any advantages over the current live *S. equi* vaccine require the test of the mutant in horses since *S. equi* does not naturally infect mice. We hope to perform this expensive test in future when funds are available.

ACKNOWLEDGEMENTS

This work was supported by grants from the NRI Competitive Grants Program of the U.S. Department of Agriculture (grant no. 2006-01690 and 2007-35204-18306) and P20 RR-020185 from the National Center for Research Resources, and the Montana State University Agricultural Experimental Station and USDA Formula Funds.

REFERENCES

- Hoch JA. Two-component and phosphorelay signal transduction. Curr Opin Microbiol 2000; 3(2): 165-70.
- [2] Fabret C, Hoch JA. A two-component signal transduction system essential for growth of *Bacillus subtilis*: Implications for antiinfective therapy. J Bacteriol 1998; 180(23): 6375-83.
- [3] Martin PK, Li T, Sun D, Biek DP, Schmid MB. Role in cell permeability of an essential two-component system in *Staphylococcus aureus*. J Bacteriol 1999; 181(12): 3666-73.
- [4] Lange R, Wagner C, de Saizieu A, et al. Domain organization and molecular characterization of 13 two-component systems identified by genome sequencing of *Streptococcus pneumoniae*. Gene 1999; 237(1): 223-34.
- [5] Throup JP, Koretke KK, Bryant AP, et al. A genomic analysis of two-component signal transduction in *Streptococcus pneumoniae*. Mol Microbiol 2000; 35(3): 566-76.
- [6] Liu M, Hanks TS, Zhang J, et al. Defects in ex vivo and in vivo growth and sensitivity to osmotic stress of group A Streptococcus caused by interruption of response regulator gene vicR. Microbiology 2006; 152(Pt 4): 967-78.
- [7] Kadioglu A, Echenique J, Manco S, Trombe MC, Andrew PW. The MicAB two-component signaling system is involved in virulence of *Streptococcus pneumoniae*. Infect Immun 2003; 71(11): 6676-9.

Received: May 22, 2008

Revised: June 06, 2008

Accepted: June 09, 2008

© Liu et al.; Licensee Bentham Open.

This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.5/), which permits unrestrictive use, distribution, and reproduction in any medium, provided the original work is properly cited.

- [8] Senadheera MD, Guggenheim B, Spatafora GA, et al. A VicRK signal transduction system in *Streptococcus mutans* affects gtfBCD, gbpB, and ftf expression, biofilm formation, and genetic competence development. J Bacteriol 2005; 187(12): 4064-76.
- [9] Ng WL, Kazmierczak KM, Winkler ME. Defective cell wall synthesis in *Streptococcus pneumoniae* R6 depleted for the essential PcsB putative murein hydrolase or the VicR (YycF) response regulator. Mol Microbiol 2004; 53(4): 1161-75.
- [10] Echenique JR, Trombe MC. Competence repression under oxygen limitation through the two-component MicAB signal-transducing system in *Streptococcus pneumoniae* and involvement of the PAS domain of MicB. J Bacteriol 2001; 183(15): 4599-608.
- [11] Mohedano ML, Overweg K, de la Fuente A, et al. Evidence that the essential response regulator YycF in *Streptococcus pneumoniae* modulates expression of fatty acid biosynthesis genes and alters membrane composition. J Bacteriol 2005; 187(7): 2357-67.
- [12] Timoney JF. Strangles. Vet Clin North Am Equine Pract 1993; 9(2): 365-74.
- [13] Harrington DJ, Sutcliffe IC, Chanter N. The molecular basis of *Streptococcus equi* infection and disease. Microbes Infect 2002; 4(4): 501-10.
- [14] Mukhar MM, Timoney JF. Chemotactic response of equine polymorphonucelar leucocytes to *Streptococcus equi*. Res Vet Sci 1988; 45(3-4): 225-9.
- [15] Timoney JF. The pathogenic equine streptococci. Vet Res 2004; 35(4): 397-409.
- [16] Timoney JF, Artiushin SC, Boschwitz JS. Comparison of the sequences and functions of *Streptococcus equi* M-like proteins SeM and SzPSe. Infect Immun 1997; 65(9): 3600-5.
- [17] Anzai T, Timoney JF, Kuwamoto Y, Fujita Y, Wada R, Inoue T. In vivo pathogenicity and resistance to phagocytosis of Streptococcus equi strains with different levels of capsule expression. Vet Microbiol 1999; 67 (4): 277-86.
- [18] Woolcock JB. Immunity to S. equi. Aust Vet J 1975; 51(12): 554-9.
- [19] Hanks TS, Liu M, McClure MJ, Lei B. ABC transporter FtsABCD of *Streptococcus pyogenes* mediates uptake of ferric ferrichrome. BMC Microbiol 2005; 5:62.
- [20] White-Owen C, Alexander JW, Sramkoski RM, Babcock GF. Rapid whole-blood microassay using flow cytometry for measuring neutrophil phagocytosis. J Clin Microbiol 1992; 30(8): 2071-6.
- [21] Lei B, Liu M, Chesney GL, Musser JM. Identification of new candidate vaccine antigens made by Streptococcus pyogenes: Purification and characterization of 16 putative extracellular lipoproteins. J Infect Dis 2004; 189(1): 79-89.