

Dominant Susceptibility Effect on the Murine Corneal Response to *Pseudomonas aeruginosa* (41592)

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Abstract. Natural host resistance to *Pseudomonas aeruginosa* corneal infection is regulated by two complementing dominant genes *PsCR1* and *PsCR2* (RS Berk, MA Leon, LD Hazlett. *Infect Immun* 26:1221-1223, 1979). In this study we have demonstrated a third dominant gene, which determines susceptibility to *P. aeruginosa*-induced eye damage. This gene was designated as *PsCS*. The F₁ progeny from matings between the resistant DBA/2J strain and the susceptible strain C57BL/6J and C3H/HeJ displayed the susceptibility phenotype. Backcross and F₂ studies using the C3H/HeJ and DBA/2J strains suggested the presence of two linked *PsCS* loci.

A number of studies recently have been performed in our laboratory to examine the response of the murine cornea to challenge with *Pseudomonas aeruginosa* (1-6). We have established that the Swiss-Webster, DBA/1J, and DBA/2J strains are naturally resistant to intracorneal infection and that the infection remains localized and spontaneously heals within 3 to 4 weeks (3, 4). On the other hand, the C57BL/6J, BALB/cJ, NZB, and C3H/HeJ strains are classed as susceptible, since the infection results in blindness 21 to 30 days after infection (2-4). An intermediate ocular response also has been observed in the A mouse congenic lines. Further studies suggested that at least two autosomal dominant nonlinked genes control natural resistance to intracorneal infection by *P. aeruginosa* and that they both reside outside the *H-2* complex (2, 3). We have provisionally designated the C57BL/6J resistance gene as *PsCR1* and the BALB/cJ resistance gene as *PsCR2* (3). However, current studies with C3H/HeJ mice suggest that the present view of the multigenic control of natural resistance to pseudomonas eye injury is more complex than expected. The purpose of this study is to establish the presence of two linked genes which are expressed as dominant susceptibility genes (*PsCS*).

Materials and Methods. *Bacterial cell cultures.* Stock cultures of *P. aeruginosa*, strain 19660 ATCC, stored at 25°C on tryptose agar slants (Difco, Detroit, Mich.) were used for

inoculation of 50 ml of broth medium containing 5% peptone (Difco) and 0.25% trypticase soy broth (Baltimore Biological Laboratories, Cockeysville, Md.). The culture was hemolytic, proteolytic, and produced lecithinase and exotoxin A. Cultures were grown on a rotary shaker at 37°C for 18 hr, centrifuged at 27,000g for 20 min (4°C), washed with saline, and resuspended in 0.9% sterile nonpyrogenic saline (Travenol Laboratories, Inc., Deerfield, Ill.) to a concentration of 2.5×10^{10} colony forming units (CFU)/ml using a standard curve relating viable counts to optical density of 440 nm.

Infection of animals. Inbred lines of all F₁, F₂, and backcross matings were bred in our own animal facilities or purchased from Jackson Laboratories (Bar Harbor, Maine). In all experimental studies involving either F₁ or F₂ animals, both male and female progeny were used in approximately equal numbers. Mice were infected at 5-6 weeks of age (18-22 g). Prior to infection, they were lightly anesthetized with ether and placed beneath a stereoscopic microscope. The corneal surface of the left eye was incised (three 1-mm-long incisions) with a sterile 26-gauge needle, taking care not to penetrate the anterior chamber or damage the sclera. A bacterial cell suspension (5 μ l) containing a final concentration of 1.25×10^8 CFU, was topically delivered onto the surface of incised corneas using a micropipette (Oxford Laboratories, Foster City, Calif.) with a sterile disposable tip. Control animals received a similar wounding and 5 μ l of sterile saline. All experimental data represent the re-

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sults of two or more independently performed experiments. In order to ensure objectivity, each animal evaluation was performed by one of the investigators without knowing the genetic background of the control and infected animals.

The ocular response was grossly examined at 24 hr after bacterial challenge and then at weekly intervals over a 3 to 6-week time period and compared with the contralateral eye as well as the saline control eyes. In addition, the eyes were monitored intermittently for the presence of bacteria by gently swabbing the cornea with a sterile cotton swab and inoculating tryptose agar plates. The plates were incubated at 37°C for 24–48 hr. All plates showing growth contained pure cultures of *P. aeruginosa*.

Results. Previous investigations have suggested that at least two dominant autosomal genes control natural resistance to intracorneal infection by *P. aeruginosa* (1–3). In order to determine the exact number of genes which confer resistance, F₁ studies were initiated to screen for an inbred mouse strain which lacked *PsCR1^R* and *PsCR2^R* genes. Once this *PsCR1^{r/r} PsCR2^{r/r}* strain was found, genetic analysis could be done using F₁, F₂, and backcross matings with the resistant DBA/1 or DBA/2 strains. These studies would determine the number of genes conferring resistance in DBA/1 and DBA/2. In our initial screening we found that progeny of C3H/HeJ mated with either BALB/c or C57BL/6J an-

imals were all susceptible to eye infection (Table I). From these data, we reasoned that the genotype of C3H/HeJ was *PsCR1^{r/r} PsCR2^{r/r}*. When (C3H/HeJ × DBA/2)F₁ were infected, an unexpected result was obtained. All these F₁ animals were susceptible to corneal infection and exhibited permanent eye damage. A dominant susceptibility effect, apparently contributed by the C3H parent, was the most likely explanation for this result. Furthermore, since C3H/HeJ appears to carry a dominant susceptibility effect, there is no longer sufficient data to support the proposed *PsCR1^{r/r} PsCR2^{r/r}* genotype of C3H/HeJ.

In order to demonstrate that the C3H susceptibility effect was under genetic control, (C3H × DBA/2)F₂ animals and progeny of (C3H × DBA/2)F₁ ♀ backcrossed with DBA/2 ♂ were examined for their susceptibility to *P. aeruginosa* infection. In the backcross progeny 33/94 (35.1%) recovered from the corneal infection, whereas 61/94 (64.9%) were permanently blinded (Table II). Since two nonlinked resistant genes, *PsCR1* and *PsCR2*, have previously been established (5), we proposed that a dominant susceptibility gene(s), provisionally designated as *PsCS* is involved. These backcross data were then statistically analyzed to determine if one or more dominant susceptibility genes were present. Both one gene ($X^2 = 8.32$, $P < 0.01$) and two nonlinked genes ($X^2 = 4.53$, $P < 0.05$) were rejected. The expected percentages of resistant backcross offspring are 50% and 25% for the one gene and the two genes hypotheses, respectively. Since the observed frequency was 35.1% resistant offspring, alternatives to simple Mendelian genetics were considered. One possibility is that two linked dominant susceptibility genes of C3H origin existed. Progeny carrying the recombinant genotypes would be phenotypically susceptible. Furthermore, all the resistant offspring would represent animals which lacked the C3H/HeJ dominant susceptibility alleles. Since the frequency of the resistant offspring (35.1%) represents half of the expected nonrecombinant DBA/2J parental genotype, the frequency of animals carrying the parental genotype would be 70.2%. Thus, the crossover frequency would equal the frequency of recombinant individuals, which is 29.8%. In order to properly assess the F₂ results using this theory, the number

TABLE I. RESPONSE OF F₁ HYBRIDS TO INTRACORNEAL CHALLENGE WITH *P. aeruginosa*^a

| Strains | Response | Resistant/ total |
|--------------------------------------|-------------|---------------------|
| Parental strains: | | |
| DBA/2 | Resistant | 75/75 |
| C57BL/6 | Susceptible | 0/24 |
| BALB/c | Susceptible | 0/115 |
| C3H/HeJ | Susceptible | 0/71 |
| F ₁ hybrids: ^b | | |
| (C57BL/6 × BALB/c)F ₁ | Resistant | 60/60 |
| (C3H × C57BL/6)F ₁ | Susceptible | 0/40 |
| (C3H × BALB/c)F ₁ | Susceptible | 0/23 |
| (C3H × DBA/2)F ₁ | Susceptible | 0/46 |

^a All mice received a topical application of 1.25×10^8 CFU *P. aeruginosa*.

^b ♀ × ♂.

TABLE II. SEGREGATION ANALYSIS OF THE C3H SUSCEPTIBILITY GENE

| Cross ^a | Response | | |
|--|------------------------|------------------|--------------------------|
| | | Experimental (%) | Theoretical ^b |
| 1. (C3H × DBA/2)F ₁ × DBA/2 | Resistant (33/94) | 35.1 | — |
| | Susceptible (61/94) | 64.9 | — |
| 2. (C3H × DBA/2)F ₁ × (C3H × DBA/2)F ₁ | Resistant (9/58) | 15.5 | 12.3 |
| | Susceptible (49/58) | 84.5 | 87.7 |

^a ♀ × ♂.^b Theoretical recombination values were calculated on the basis of the backcross data and thus are only presented for the F₂ cross.

of resistance genes in DBA/2 had to be determined. Previously, only a single gene controlling resistance was indicated by the segregation studies between DBA/2 and BALB/c (2). Since BALB/c carries the *PsCR2* gene, the segregating DBA/2 gene must be of another locus and is presumably *PsCR1*. If DBA/2 also carries the *PsCR2* gene (i.e., similar to BALB/c), then (DBA/2 × C57BL/6)F₁ animals should be resistant. Completed studies indicate that the progeny of DBA/2 × C57BL/6 matings were all susceptible (manuscript in preparation). It is apparent that the DBA/2 *PsCR2* allele is unlike that of BALB/c. The phenotypic expression of the DBA/2 *PsCR2* gene still remains to be elucidated. These experiments do suggest that DBA/2 has one gene conferring resistance and that this gene can be masked by susceptible gene(s) from C3H and quite probably from C57BL/6, too. In the F₂ offspring, the expected frequency of resistant animals can be calculated by squaring the frequency of resistant animals (35.1%) obtained in the backcross experiment. Using this information, one could predict that 12.3% of the F₂ animals should be resistant. F₂ progeny from the (C3H × DBA/2)F₁ × (C3H × DBA/2)F₁ matings were then examined for resistance to *P. aeruginosa* infection (Table II). Of 58 animals infected, 9 (15.5%) were resistant and 49 (84.5%) were susceptible. The supposition of two linked *PsCS* genes was accepted as indicated by the X^2 value of 0.291 ($0.7 > P > 0.5$). Other possibilities have been

considered using both allelic and epistatic interactions to explain both the backcross and F₂ data. So far, only the theory presented herein is consistent with previously published data and hypotheses.

Discussion. In general, the genetic control of natural resistance to bacterial infections has been described to be under dominant autosomal resistance gene(s). Infectivity of *Corynebacterium kutscheri* (7, 8), *Mycobacterium lepraemurium* (9–11), *M. tuberculosis* (12), *Listeria monocytogenes* (13–18), *Rickettsia tsutsugamushi* (19), *R. akari* (20), *Salmonella typhimurium* (21–27), and *P. aeruginosa* (1–3) has been demonstrated to be under this type of host regulation. This communication presents a unique finding where two linked dominant susceptibility genes also regulate the natural resistance to *P. aeruginosa* infection. Offspring of the susceptible strains C3H mated with the resistant DBA/2 strains incurred eye shrinkage (phthisis bulbi) as a result of infection. Data from (C3H × DBA/2)F₂ and (C3H × DBA/2)F₁ × DBA/2 backcross studies suggested the presence of two linked *PsCS* loci. If the *PsCS* loci were sex-linked, then only some of the F₂ males would have exhibited the resistance phenotype. However, this was not the case. Thus, the C3H *PsCS* genes are autosomal dominant alleles. The *PsCS* loci do not appear to be linked to the *PsCR1* locus. The relationship of these two linked *PsCS* genes with *PsCR2* cannot presently be assessed.

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