PERSISTENT EHRlichia chaffeensis INFECTION IN WHITE-TAILED DEER

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ABSTRACT: Four white-tailed deer (Odocoileus virginianus) were inoculated intravenously with a deer-origin isolate (15B-WTD-GA) of Ehrlichia chaffeensis. The course of infection was monitored using indirect fluorescent antibody (IFA), polymerase chain reaction (PCR), and culture over a 9 m period. All deer became rickettsemic within 24 days post inoculation (DPI), and all developed antibody titers >1:64 to E. chaffeensis by 17 DPI. Titers in all deer fell below 1:64 during 87 to 143 DPI. One deer exhibited a second period of seropositivity (peak titer of 1:256) from 207 to 271 DPI but was culture and PCR negative during this period. Rickettsemia was confirmed by reisolation of E. chaffeensis as late as 73 to 108 DPI in three deer. Positive PCR results were obtained from femur bone marrow of one deer and from rumenal lymph node of another deer at 278 DPI. None of the deer developed clinical signs, hematologic abnormalities, or gross or microscopic lesions attributable to E. chaffeensis. Two uninoculated control deer were negative on all tests through 90 DPI at which time they were removed from the study. Herein we confirm that white-tailed deer become persistently infected with E. chaffeensis, have initial rickettsemias of several weeks duration and may experience recrudescence of rickettsemia, which reaffirm the importance of deer in the epidemiology of E. chaffeensis.

Key words: Ehrlichia chaffeensis, epidemiology experimental study, Odocoileus virginianus, white-tailed deer.

INTRODUCTION

Human monocytotropic ehrlichiosis (HME), a recently recognized tickborne zoonosis caused by Ehrlichia chaffeensis, has been reported primarily in the southeastern, south-central, and mid-Atlantic regions of the United States (McDade, 1990; Walker and Dumler, 1996). Current epidemiologic evidence indicates that the white-tailed deer (Odocoileus virginianus) is a major vertebrate reservoir for E. chaffeensis. High prevalences of E. chaffeensis-reactive antibodies have been detected in deer from many locations in the southeastern and south-central United States (Dawson et al., 1994a; Lockhart et al., 1995, 1996; Little et al., 1997, 1998), and deer have been experimentally infected with a human isolate (Arkansas strain) of E. chaffeensis (Dawson et al., 1994b; Ew-
correlation between the distribution of 
HME cases and the geographic distri-
bution of this tick (Eng et al., 1990; 
Dawson et al., 1994a). Later, temporal and site-spe-
cific spatial relationships were confirmed 
between the presence of E. chaffeensis 
antibodies and lone-star tick infestations 
among deer populations (Lockhart et al., 
1995, 1996). Local lone star tick abun-
dance also has been related to the preva-
lence of human cases (Standaert et al., 
1995). Proof of vector status was provided 
by experimental transstadial transmission 
of E. chaffeensis from deer to deer by lone 
star ticks (Ewing et al., 1995).

Relatively little is known about the 
course, duration, or health consequences 
of E. chaffeensis infection in deer. A 1-mo-
long study of two deer inoculated intra-
venously demonstrated seroconversion, 
confirmed transient rickettsemia, and dis-
closed E. chaffeensis antigen within pres-
capular, retropharyngeal, and mesenteric 
lymph nodes. Infected deer did not de-
velop detectable evidence of clinical illness 
of specific pathologic changes (Dawson et 
al., 1994). Another short-term study of two 
needle-exposed deer produced similar re-
results (Ewing et al., 1995). Two deer that 
were infected with E. chaffeensis through 
the bite of infected lone star ticks also se-
roconverted, had evidence (PCR assays) of 
intermittent rickettsemia, and did not de-
velop clinical illness or pathologic changes 
specifically attributable to E. chaffeensis 
(Ewing et al., 1995). Among naturally in-
fected deer, E. chaffeensis DNA has been 
detected in blood, lymph node, and spleen 
(Lockhart et al., 1997a, b; Little et al., 
1997), and E. chaffeensis has been isolated 
from blood (Lockhart et al., 1997a) and 
lymph node (Little et al., 1998).

Persistent infection is characteristic of 
many species of Ehrlichia, and infection of 
at least several weeks duration has been 
described in laboratory mice and in hu-
mans infected with E. chaffeensis (Dumler 
et al., 1993; Telford and Dawson, 1996). 
However, other than the circumstantial 
evidence from naturally infected deer, there 
is no information on the ability of E. chaf-
feensis to establish a persistent infection in 
white-tailed deer. The purpose of this 
study was to evaluate the course of E. 
chaffeensis infection in white-tailed deer 
over a 9-mo period.

MATERIALS AND METHODS

Experimental design and sample collection

Six approximately 12-wk old, hand-reared 
white-tailed deer were acquired from the 
North Carolina Wildlife Resources Commission 
and moved to tick-free facilities (Department 
of Animal Resources, College of Veterinary 
Medicine, The University of Georgia, Athens, 
Georgia, USA). When the deer were acquired, 
indirect fluorescent antibody (IFA) testing of 
serum (Dawson et al., 1994a) and nested PCR 
testing of blood (Lockhart et al., 1997) from all 
produced negative results for evidence of 
E. chaffeensis. Four deer were ran-
domly selected to serve as principals, and two 
deer served as uninfected controls. Groups 
consisting of two principals and one control 
were co-housed in adjacent stalls. Deer were 
tranquilized by intramuscular injection of a 
mixture of 1.7 mg/kg of xylazine (Mobay Cor-
poration, Shawnee, Kansas, USA) and 0.1 mg/ 
kg ketamine (Fort Dodge Laboratories Inc., 
Fort Dodge, Iowa, USA) for experimental in-
oculations and blood sample collections and 
then reversed with 1.3 mg/kg of yohimbine 
(Lloyd Laboratory, Shenandoah, Iowa, USA) 
administered intravenously. Two principals 
(high-dose group) were inoculated intravenous-
ly with $3.7 \times 10^6$ E. chaffeensis-infected DH82 
cells, and two principals (low dose group) were 
similarly inoculated with $2.5 \times 10^4$ infected 
cells. Two control deer were injected with 
$5.2 \times 10^6$ uninfected DH82 cells. The E. chaffeens-
is strain (15-WTD-B) used in this study was 
originally isolated in DH82 cells inoculated 
with blood from a wild naturally infected white-
tailed deer from Clarke County, Georgia (Lock-
hart et al., 1997b).

For inoculation and blood sample collection, 
the lateroventral portion of the neck was 
shaved with electric clippers and the jugular 
groove was wiped with 95% ethanol. Blood 
samples were collected at Day 0 and at 10, 17, 
24, 32, 45, 59, 73, 87, 108, 123, 143, 164, 187, 
207, 227, 243, 248, 259, 271, and 278 days 
past-inoculation (DPI) from the principals. 
Control deer were sampled in the same way 
through DPI 90 (DPI 87 omitted) at which 
time they were humanely killed. Anticoagulat-
ed blood samples were collected in heparin for 
culture and in EDTA for PCR, light micros-
copy, and hematology. Serum was collected for serologic testing. Deer were monitored at one-to-four-day intervals for clinical signs. At necropsy, spleen and prescapular, rumenal, parotid, and iliac lymph nodes were collected aseptically and cultured as described by Lockhart et al. (1997b). Duplicates of these tissues plus bone (femur) marrow, heart, lung, liver, kidney, pancreas, skeletal muscle, brain, and bronchial and mesenteric lymph nodes were collected into 10% neutral buffered formalin for histopathologic examination. Tissues were processed for histopathologic study using standard procedures and stained using hematoxylin and eosin and Giemnnez procedures. Portions of spleen, bone marrow, and prescapular, rumenal, parotid, and iliac lymph nodes were collected in separate plastic containers and processed for PCR assays as described by Lockhart et al. (1997b).

Serologic tests

Serum samples were tested for _E. chaffeensis_ reactive antibodies using the IFA assay as described by Dawson et al. (1994a). Samples were screened at a dilution of 1:64 in 0.01 M phosphate buffered saline (PBS) on spot slides of _E. chaffeensis_-infected DH82 cells. Samples giving positive results at 1:64 were further tested to determine titer endpoints using serial twofold dilutions. Samples nonreactive at 1:64 were considered negative (Lockhart et al., 1997a, b).

**Isolation of organisms**

In vitro isolation from blood followed the procedures of Dawson et al. (1994b) and Lockhart et al. (1997a) with slight modifications. Briefly, 10 ml of heparinized blood was transferred to sterile plastic tubes containing 25 ml of lysing buffer (150 mM NH₄Cl, 0.7 mM TMAC, 2.5 units Taq DNA polymerase (Promega, Madison, Wisconsin, USA), and a few drops of EDTA whole blood. The mixture was incubated at room temperature for 5 min, centrifuged at 7,000 × g for 5 min, and the supernatant fluid discarded. An additional 1.5 ml of lysing solution was added to the pellet and the process repeated. Pelleted cells were washed once in 0.5 ml distilled water and centrifuged as above. The pellet was resuspended in 1 ml of fresh medium, sonicated in a water-cooled bell sonicator pulsed 90% of each sec for 15 sec at output control level 6 using a Branson Sonifier cell disruptor Model 450 (Branson, Danbury, Connecticut, USA), and the resulting sonicate returned to the culture flask.

**Molecular techniques**

A portion of cells harvested from EDTA blood was processed for use in a nested PCR assay as described by Dawson et al. (1994b) with modifications. Briefly, lysing solution was mixed at a 1:100 ratio with EDTA whole blood. The mixture was incubated at room temperature for 5 min, centrifuged at 7,000 × g for 5 min, and the supernatant fluid discarded. An additional 1.5 ml of lysing solution was added to the pellet and the process repeated. Pelleted cells were washed once in 0.5 ml distilled water and centrifuged as above. The pellet was resuspended in 0.5 ml PBS, and DNA was extracted using Instagene Purification Matrix (BIO-RAD, Hercules, California, USA) as per manufacturer’s directions. In the initial amplification, 10 µl of each sample was placed in a 100 µl reaction containing 10 mM of Tris-Cl, 50 mM KCl, 1.5 mM MgCl₂, 0.2 mM each dNTP, 5 µM Tetramethylammonium chloride (TMAC), 2.5 units Taq DNA polymerase (Promega, Madison, Wisconsin, USA), and 0.8 µM each of primer ECB (5′-CGTATTA-CCGCGGTGGCCTGGCA-3′) and ECC (5′-AGAACGAAACGCTGGCCGC-AAGGC-3′), which amplify a DNA fragment common among all known species of _Ehrlichia_ and a few other bacterial species (Dawson et al., 1994b). The temperature profile for the initial amplification was 40 cycles of 1 min at 94 C, 2 min at 45 C, and 30 sec at 72 C. For the nested PCR amplification, 1 µl of the product from the first amplification was run in a 100 µl reaction as above using the primers HE1 (5′-CAATTGGGTATAACCTTTTGTTTATAAT-3′) and HE3 (5′-TATAGTACCGTCATTATCT-TCCCTAT-3′), which amplify DNA only from _E. chaffeensis_ (Dawson et al., 1994b). The temperature
profile for the nested reaction was the same as the first reaction except that the annealing temperature was 55°C and the extension time was 15 sec. Amplification products were electrophoresed in 1.5% agarose and were detected by staining with ethidium bromide and ultraviolet transillumination. Negative (water) and positive (E. chaffeensis-infected DH82 cells) controls were run with each series of PCR amplifications. In addition to standard precautionary procedures for PCR assays such as use of disposable gloves, bench top paper, plugged pipette tips, and biocontainment hoods with ultraviolet decontamination capabilities, each step in the procedure (DNA extraction, primary PCR reaction, secondary PCR reaction, and gel electrophoresis) was conducted in a separate laboratory.

**Exposure of ticks**

To evaluate whether deer remained infective to lone star ticks for an extended period post-inoculation, lone star tick nymphs were fed on two of the deer several months post-inoculation. The two deer suspected most likely to be rickettsemic were selected based on the frequency and duration of the earlier PCR assay and culture results. At DPI 243, 25 × 25 cm areas on the lateral thorax of deer 18 and 19 were shaved and the perimeters of 15 × 15 cm cloth patches with a center access slit with a velcro closure were glued to the skin using Livestock Identification Tag Cement (W.J. Ruscoe Company, Akron, Ohio, USA). Approximately 500 uninfected laboratory-reared A. americanum nymphs were introduced into each cloth container. On DPI 248, the cloth containers were removed and the engorged ticks (>95% of those placed on deer) were placed in a humidity chamber maintained at room temperature. Subsamples of engorged nymphs and molted adult ticks from deer 18 and 19 were processed and assayed using PCR as described by Lochart et al. (1997a). These PCR assays were conducted on both individual ticks and pools of ticks. Engorged nymphs were processed for PCR assay 2 days after they were removed from the deer. Molted adults were processed for PCR assay between 33 and 60 days after removal from the deer (3 pools at 42 days, 5 pools at 49 days, and 15 individuals at 63 days).

**RESULTS**

**Serology, culture, and PCR**

All four inoculated deer developed E. chaffeensis antibody titers >1:64 by 17 DPI (Table 1). Maximal titers were higher in the high-dose deer (1:128 and 1:1024) than in the low-dose deer (1:64). The durations of the initial antibody responses in high- and low-dose deer were similar, in each case persisting to 87 to 123 DPI. Following a seronegative period of at least 44 days, one-high dose deer developed a second period of seroreactivity that lasted 64 days and had a peak titer of 1:256. Control deer were seronegative (<1:64) at each of nine sampling dates from 0 to 90 DPI when sampling was discontinued.

*Ehrlichia chaffeensis* was reisolated on multiple occasions from the blood of three of the four inoculated deer (Table 1). Isolations were intermittently successful up to 73 DPI in the two high-dose deer and were consistently successful from one low-dose deer from 17 through 108 DPI, including five consecutive sampling dates from 45 to 108 DPI. Sixteen (3 to 6 per deer) of 78 (20%) cultures of blood were lost because of contamination. Most cultures from tissues obtained at necropsy were lost to contamination within 32 days of incubation and therefore produced equivocal results. Reculture attempts using cells that had been suspended in cell culture medium and frozen in liquid nitrogen were all negative; however, the parotid lymph nodes of deer 15, 18, and 19 and iliac and rumenal lymph node from deer 15 were again contaminated upon reculture.

PCR assays infrequently detected *E. chaffeensis* DNA in the blood of three of four inoculated deer (Table 1). Two deer (one high- and one low-dose) were positive by PCR assay on two or more sampling dates from 10 to 32 DPI. Both low-dose deer had single positive PCR assays on blood well after inoculation (164 and 271 DPI).

PCR assays of brain, heart, lung, liver, spleen, bone marrow, and prescapular, parotid, mesenteric, iliac, bronchial, and rumenal lymph nodes obtained at 278 DPI detected *E. chaffeensis* DNA in the bone marrow of one high-dose deer and in the rumenal lymph node of one low-dose deer.
All blood samples (n = 9 each) and tissues (same as above) collected at 90 DPI from the two control deer were negative on all PCR assays.

**Clinical evaluations, blood films, and histopathology**

Clinical hematology conducted on principal and control deer through 45 DPI did not reveal any abnormalities attributable to *E. chaffeensis* infection (data not shown). Parameters monitored included white blood cell, erythrocyte, and platelet counts, differential white cell counts, hematocrit, mean corpuscular hemoglobin, and fibrinogen levels. Light microscopy of Giesma stained thin blood films through 45 DPI did not detect *E. chaffeensis* morulae in any deer; however, at each sampling period, all inoculated and control deer were infected with intraerythocytic organisms morphologically compatible with *Theileria cervi*. Deer 14 had circulating microfilariae morphologically compatible with those of the abdominal nematode *Setaria yehi*, and live and dead degenerating adult *S. yehi* were found in the abdominal cavity of this deer at necropsy.

Histopathologic examination of tissues collected at necropsy did not disclose any lesions specifically attributable to *E. chaffeensis*. Mild depletion of germinal centers was observed in the spleen in deer 14 and 15 and in mesenteric, prescapular, and/or iliac lymph nodes of deer 14, 15, 18, and 19. Scattered mild mineralization of renal collecting tubules was present in deer 14, 15, and 17, and mild chronic focal interstitial nephritis was noted in deer 15, 18, and 19. Mild diffuse hemosiderosis was

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**Table 1.** Indirect fluorescent antibody (IFA) titers, polymerase chain reaction (PCR) results, and culture results for white-tailed deer experimentally infected with *Ehrlichia chaffeensis*.

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*a Two control deer (nos. 16 and 17) were negative on all tests through DPI 90 at which time they were removed from the study. ND = not done; Con = contaminated (inconclusive results); NA = not applicable; - = negative result; + = positive result.

*Culture results for blood except for last row. Entries for DPI 278Nx provide results of PCR assays and isolation attempts on tissues (see next) collected at necropsy on DPI 278; positive PCR assays were obtained only from bone marrow of deer 18 and rumenal lymph node of deer 15.*
found in the spleen of deer 17 and 19 and in the lung of deer 17. Deer 19 had multifocal granulomatous pneumonia of unknown origin.

**Assays of ticks**

PCR assays of 106 unfed *A. americanum* nymphs (pools of 5–20 individuals), to test for pre-existing infection in the laboratory colony, were negative. PCR assays of 50 freshly engorged nymphs (25 each from deer 18 and 19 in pools of 5) were negative. PCR assays of 110 molted adult ticks from deer 18 and deer 19 (8 pools of 5 ticks and 15 individual ticks) also were negative.

**DISCUSSION**

Because prior experimental *E. chaffeensis* infections in white-tailed deer were short-term and were conducted with a human isolate (Arkansas strain) (Dawson et al., 1994; Ewing et al., 1995), a comparison of the early course of infection with our 15B-WTD-GA isolate is of interest. Through 32 DPI response to infection with the 15B-WTD-GA strain of *E. chaffeensis* was similar to that of needle-exposed deer infected with the Arkansas strain (Dawson et al., 1994b; Ewing et al., 1995). In each study, seroconversion occurred at 10 to 17 DPI, rickettsemia usually was confirmed from 7 to 17 DPI but always by 24 DPI, and clinical illness was not observed. Deer infected with *E. chaffeensis* (Arkansas strain) via the bite of *A. americanum* ticks also became rickettsemic within 18 DPI and remained clinically normal but seroconverted later (at 25 to 28 DPI) than needle-exposed deer (Ewing et al., 1995). This difference may be related to route, dose, or both. Thus, all experimental infections in white-tailed deer have produced generally consistent results during the first month following exposure regardless of the strain of *E. chaffeensis* or the route of exposure utilized. Likewise, in the only other comparison of experimental exposure routes, Telford and Dawson (1996) found that the kinetics of antibody responses did not differ among needle-exposed mice inoculated with *E. chaffeensis* by intracardiac, intraperitoneal, or subcutaneous routes.

The initial serologic responses of deer in this study were transient and remained above the seropositive threshold of 1:64 only through 87 to 123 DPI. In the only other experimental infection study of deer longer than one month, Ewing et al. (1995) also noted transient, but shorter duration (33–36 day), antibody responses in deer infected with *E. chaffeensis* via bite of lone star ticks. The higher peak antibody titers in our high-dose deer suggests that the initial antibody responses may have been dose dependent; apparent dose dependent antibody responses to *E. chaffeensis* have been noted previously in needle-exposed C3H/HeJ mice (Lockhart and Davidson, 1999). A second distinct period of seroreactivity from 207 to 271 DPI in deer 18 suggests recrudescence of infection, although this was not verified by either isolation or PCR assays. Deer 14 also returned to a seropositive status (1:64) at the last sampling date, but interpretation of a single, low titer is problematic. Experimentally infected C3H/HeJ mice also had transient antibody responses with peak titers at 19 DPI, which then declined significantly by 103 DPI (Telford and Dawson, 1996); however, one mouse remained seropositive for well over a year.

The inability to detect *E. chaffeensis* in lone star ticks fed on two of the deer 8 months post-exposure agrees with PCR and cell culture assays, which failed to confirm that the deer were rickettsemic during the 5-day period of tick feeding. However, these findings must be interpreted cautiously because (1) the number of deer evaluated was small; (2) one deer not selected for tick feeding had a positive PCR assay from blood at termination of the study; (3) based on PCR assays, two of four deer may have had organisms sequestered in tissues at the end of the study; (4) the sensitivity of PCR and cell culture to detect rickettsemia in deer and
the sensitivity of PCR to detect *E. chaffeensis* in ticks are unknown; and (5) the course of infection initiated by a single intravenous needle-inoculation may differ markedly from that of natural tick-induced infection. Furthermore, wild deer populations at locations where *A. americanum* is prevalent are almost certainly exposed to *E. chaffeensis*-infected ticks to at least some degree from March through October in most of the *E. chaffeensis* enzootic region of the United States. Thus, although the present study provides the first information on long-term *E. chaffeensis* infection in deer, from an epidemiologic standpoint, it likely is incomplete because it does not account for continuous exposure of wild deer to infected lone star ticks. Future experimental studies of the *E. chaffeensis* host/vector relationship between deer and ticks should be designed to include multiple or periodic tick-initiated exposures of deer to *E. chaffeensis* accompanied by multiple acquisition feeding attempts with uninfected ticks, which would more closely simulate natural circumstances. Future studies should also consider the possibilities of variation in individual animal response to exposure, intermittent or recrudescent rickettsemias, and sequestration of organisms, all of which are suggested from the present study. Finally, sensitivities of various diagnostic assays must be considered during interpretation of data during future studies.

Based on culture and PCR assays, two of four deer were frequently rickettsemic through 73 and 164 DPI; a third deer also was culture positive as late as 73 DPI. Rickettsemias of these durations are well beyond 40 DPI that previously was the longest documented rickettsemia in whitetailed deer (Ewing et al., 1995). The detection of *E. chaffeensis* DNA in lymph node and bone marrow of two deer at 278 DPI is evidence that deer may become persistently infected. Evidence of infection of reticuloendothelial tissues is consistent with an earlier experimental infection of deer where immunohistochemical staining detected *E. chaffeensis* within lymph node macrophages (Dawson et al., 1994b). It also is consistent with field studies in which up to 41% of the deer had *E. chaffeensis* DNA in lymph node or spleen (Lockhart et al., 1997a, b) and in which *E. chaffeensis* was isolated from the lymph node of a naturally infected deer (Little et al., 1998). Detection of *E. chaffeensis* DNA in blood of deer 15 at 271 DPI, 139 days after the last prior positive blood sample, is additional evidence that persistently infected deer may develop recrudescent rickettsemias and tends to corroborate the serologic evidence of recrudescence observed for deer 18. Collectively, these results suggest that deer may serve as a source of *E. chaffeensis* for ticks for months following an initial infection. This conclusion is consistent with data from field studies where 10 to 40% of the animals in seropositive deer populations are rickettsemic (Lockhart et al., 1997a, b; Little et al., 1997).

Chronic infection with persistent or recrudescent rickettsemias is characteristic of vertebrate reservoirs of other species of *Ehrlichia* and is an important epidemiologic feature favoring transmission to tick vectors (Rikihisa, 1991). Lockhart et al. (1997a, b) proposed that *E. chaffeensis* is maintained in nature primarily by a tick vector-vertebrate reservoir system consisting of lone star ticks and white-tailed deer. The asserted role of deer was based on serologic, molecular, and culture confirmation that *E. chaffeensis* infection was prevalent among wild deer populations parasitized by lone star ticks (Dawson et al., 1994a; Lockhart et al., 1995, 1996, a, b; Little et al., 1997) and was supported by experimental infections that showed deer were suitable hosts capable of infecting lone star ticks (Dawson et al., 1994b; Ewing et al., 1995). The new findings that deer become persistently infected, that initial rickettsemias can last for months, and that persistently infected deer may develop recrudescent rickettsemias months later support the concept that deer are im-
portant vertebrate reservoirs of *E. chaffeensis*.

**ACKNOWLEDGMENTS**

This work was supported by Grant No. 1 R15 AI37911-01 from the National Institute of Allergy and Infectious Diseases, National Institutes of Health. Sponsorship of the fish and wildlife agencies of Alabama, Arkansas, Florida, Georgia, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia also is acknowledged. We thank personnel with the North Carolina Wildlife Resources Commission for providing experimental deer and C. D. Baumann, M. R. Hensley, D. M. Kavanaugh, A. D. Meadows, C. T. Sewell, J. C. Wlodkowski, and E. Young for assistance with animal handling during this project.

**LITERATURE CITED**


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Received for publication 15 July 2000.