

Mycobacterium avium subsp. *paratuberculosis*, Genetic Susceptibility to Crohn's Disease, and Sardinians: the Way Ahead

Leonardo A. Sechi,^{1,2*} Maria Gazouli,³ John Ikonomopoulos,⁴ John C. Lukas,⁵ Antonio M. Scanu,⁶ Niyaz Ahmed,^{2,8} Giovanni Fadda,⁷ and Stefania Zanetti¹

Dipartimento di Scienze Biomediche, Sezione di Microbiologia Sperimentale e Clinica, Università degli Studi di Sassari, Viale S. Pietro 43/B, 07100 Sassari, Italy¹; ISOGEM Collaborative Network on Other Tubercle Bacilli (The International Society for Genomic and Evolutionary Microbiology), Sassari, Italy²; Department of Biology, School of Medicine, University of Athens, Athens, Greece³; Agricultural University of Athens, Department of Anatomy-Physiology, Faculty of Animal Science, Athens, Greece⁴; Department of Pharmacology, School of Medicine, Universidad del País Vasco, Leioa, Vizcaya, Spain⁵; Clinica Chirurgica, Università degli Studi di Sassari, Viale S. Pietro, 07100 Sassari, Italy⁶; Istituto di Microbiologia, Facoltà di Medicina e Chirurgia "Agostino Gemelli," Università Cattolica del Sacro Cuore, 00168 Rome, Italy⁷; and Pathogen Evolution Group, Centre for DNA Fingerprinting and Diagnostics, Hyderabad, India⁸

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The present study was performed to determine what proportion of people in Sardinia with or without Crohn's disease were infected with *Mycobacterium avium* subspecies *paratuberculosis* and had a preponderance of allelic variants of Nod2, an intracellular protein involved in Crohn's disease susceptibility. Genetic analysis of the alleles of the NOD2/CARD15 gene (*insC3020*, G908R, and R702W alleles), linked to susceptibility or genetic predisposition to Crohn's disease in humans, was carried out on specimens from 37 Crohn's disease patients and 34 patients without Crohn's disease. Our results show that more than 70 percent of people in Sardinia with Crohn's disease carry at least one of the susceptibility-associated NOD2/CARD15 alleles and were infected with *Mycobacterium avium* subspecies *paratuberculosis*.

Recent genetic and epidemiological studies provide suggestive evidence for the presence of genetic determinants of susceptibility to Crohn's disease (CD) and its clinical progression. In a recent report, Behr and colleagues documented the coexistence of *Mycobacterium avium* subsp. *paratuberculosis* infection and a permissive NOD2/CARD15 mutant in one individual with CD (1). CD is a disease of unknown etiology linked to immune dysregulation (10). An increasing amount of evidence supports the idea that CD is caused by *Mycobacterium avium* subsp. *paratuberculosis* (8, 11, 12). In 2001, three independent mutations within the NOD2/CARD15 gene were discovered to be strongly linked to CD in Europeans (3, 4, 9). According to the observation of Behr et al., the presence of a gene that is associated with an increased susceptibility to develop CD does not preclude the possibility that the disease may be infectious in etiology (1). It is possible that genetically identifiable subpopulations may have different tendencies to develop CD when exposed to the same infectious agent (3, 6). The following case study suggests an exploitation of these considerations in a group of Mediterranean patients with CD.

Endoscopic mucosal biopsy specimens were obtained from 37 patients with CD and 34 individuals without it who were attending the Clinic of Surgery, University of Sassari, for ileocolonoscopy. Biopsy specimens were taken both from the visibly inflamed regions in the patients with inflammatory bowel disease and from several regions throughout the intestines of

control subjects. Informed consent for sampling and publication of the results was obtained. Biopsy specimens were examined for the presence of *Mycobacterium avium* subsp. *paratuberculosis* and the carriage of NOD2/CARD15 mutations. All the individuals examined were living in Sardinia and were of Sardinian origin. Tissue samples were placed into liquid 7H9 medium, transported directly to the laboratory, and processed within 1 h. One biopsy specimen was used to make a smear and examined by Ziehl-Neelsen and rhodamine-auramine staining as previously described (12).

Samples for PCR analysis for bacterial presence were processed as previously described (7). Primers p89 and p92 described in our previous work (11, 12) were used to amplify a 284-bp fragment specific for *Mycobacterium avium* subsp. *paratuberculosis*. The reaction mixture (final volume of 50 μ l) comprised primers at a concentration of 0.5 μ M, Expand High Fidelity reaction buffer (1 \times), 200 μ M (each) dNTPs, and 3 U of Expand High-Fidelity *Taq* polymerase (Expand High-fidelity PCR system; Roche, Lewes, United Kingdom). Cycling conditions were 1 cycle of 94°C for 3 min and 36 cycles of 94°C for 40 s, 62°C for 40 s, and 72°C for 40 s, followed by a final step of 72°C for 5 min. Amplified fragments were visualized with ethidium bromide on 2.5% agarose-1000 gel (Life Technologies, Grand Island, NY) and purified with a QIAquick gel extraction kit (QIAGEN, Crawley, United Kingdom). Each amplicon was then sequenced in both directions by using p89 and p92 primers, and the sequences obtained had confirmed 100% homology to the IS900 locus (GenBank accession no. AF416985).

Mycobacterium avium subsp. *paratuberculosis* DNA was detected in 25 CD patients (67.6%) and in 7 controls (20.6%)

* Corresponding author. Mailing address: Dipartimento di Scienze Biomediche, Sezione di Microbiologia Sperimentale e Clinica, Università degli Studi di Sassari, Viale S. Pietro 43/B, 07100 Sassari, Italy. Phone: 39 079 228303. Fax: 39 079 212345. E-mail: sechila@uniss.it.

TABLE 1. Patient details^a

Patient	Sex	Disease or group	PCR result (presence of <i>M. avium</i> subsp. <i>paratuberculosis</i>)	Genetic analysis result for indicated allele			Patient	Sex	Disease or group	PCR result (presence of <i>M. avium</i> subsp. <i>paratuberculosis</i>)	Genetic analysis result for indicated allele		
				<i>insC3020</i>	R702W	G908R					<i>insC3020</i>	R702W	G908R
4	F	Crohn's disease	Pos	WT	WT	WT	5	M	Control	Pos	WT	HET	WT
6	F	Crohn's disease	Pos	HET	WT	WT	26	F	Control	Neg	WT	WT	WT
9	M	Crohn's disease	Pos	WT	WT	WT	54	M	Control	Pos	WT	WT	WT
10	M	Crohn's disease	Pos	WT	HET	WT	56	M	Control	Pos	WT	WT	WT
15	M	Crohn's disease	Pos	HET	WT	HET	57	M	Control	Neg	WT	WT	WT
16	M	Crohn's disease	Pos	WT	WT	WT	58	M	Control	Neg	HET	WT	WT
19	F	Crohn's disease	Pos	WT	HET	WT	59	M	Control	Neg	WT	WT	WT
24	F	Crohn's disease	Pos	WT	WT	WT	60	F	Control	Neg	WT	WT	WT
25	F	Crohn's disease	Pos	HOM	WT	HOM	64	F	Control	Neg	WT	WT	WT
28	F	Crohn's disease	Pos	WT	WT	WT	65	F	Control	Neg	WT	WT	WT
29	M	Crohn's disease	Neg	WT	WT	WT	68	F	Control	Neg	WT	WT	WT
55	F	Crohn's disease	Pos	WT	HET	HET	70	M	Control	Neg	WT	WT	WT
62	M	Crohn's disease	Neg	HET	WT	WT	71	M	Control	Neg	WT	WT	WT
63	M	Crohn's disease	Pos	WT	WT	WT	73	M	Control	Neg	WT	WT	HET
66	F	Crohn's disease	Pos	WT	WT	WT	75	M	Control	Neg	WT	WT	WT
67	M	Crohn's disease	Pos	WT	WT	HET	77	F	Control	Neg	WT	WT	WT
69	F	Crohn's disease	Neg	WT	WT	WT	84	M	Control	Neg	WT	WT	WT
72	M	Crohn's disease	Neg	WT	WT	WT	85	F	Control	Neg	WT	WT	WT
74	M	Crohn's disease	Pos	HET	HET	WT	87	F	Control	Neg	WT	WT	WT
78	F	Crohn's disease	Pos	WT	WT	WT	88	F	Control	Neg	HET	WT	WT
79	F	Crohn's disease	Neg	WT	WT	HET	89	F	Control	Neg	WT	WT	HET
81	M	Crohn's disease	Neg	WT	WT	WT	93	F	Control	Neg	WT	WT	WT
82	F	Crohn's disease	Pos	HET	WT	WT	103	F	Control	Neg	WT	WT	WT
83	M	Crohn's disease	Pos	WT	WT	WT	105	M	Control	Neg	WT	WT	WT
91	F	Crohn's disease	Neg	WT	WT	WT	108	M	Control	Neg	WT	WT	WT
107	M	Crohn's disease	Neg	WT	WT	WT	114	F	Control	Pos	WT	WT	WT
110	F	Crohn's disease	Neg	WT	WT	HET	116	M	Control	Pos	WT	WT	WT
111	F	Crohn's disease	Pos	WT	WT	WT	118	M	Control	Pos	WT	WT	WT
113	F	Crohn's disease	Pos	HET	WT	WT	128	F	Control	Neg	WT	WT	WT
117	F	Crohn's disease	Pos	WT	WT	WT	131	F	Control	Pos	HET	WT	WT
120	F	Crohn's disease	Neg	HET	WT	WT	137	M	Control	Neg	WT	WT	WT
125	M	Crohn's disease	Neg	WT	HET	WT	138	F	Control	Neg	WT	HET	WT
127	F	Crohn's disease	Neg	WT	WT	WT	139	F	Control	Neg	WT	WT	WT
130	F	Crohn's disease	Pos	HET	HET	WT	140	F	Control	Neg	WT	WT	WT
132	F	Crohn's disease	Pos	WT	HET	WT							
133	F	Crohn's disease	Pos	HET	WT	WT							
135	R	Crohn's disease	Pos	WT	HET	WT							

^a Abbreviations: M, male; F, female. Results of genetic analysis of the alleles of the NOD2/CARD15 gene are reported as wild type (WT), heterozygous for the mutation (HET), and homozygous for the mutation (HOM). Results of PCR for *M. avium* subsp. *paratuberculosis* DNA are shown as positive (Pos) or negative (Neg).

(Table 1). The results indicated that the presence of *Mycobacterium avium* subsp. *paratuberculosis* is significantly associated with CD ($P = 0.001$; odds ratio [OR], 4.94 [95% confidence interval {CI₉₅}, 1.85 to 13.29]).

Because of the recently published data showing genetic susceptibility to CD, we also performed genetic testing, aimed at susceptibility-linked alleles of the NOD2/CARD15 gene (*insC3020*, G908R, and R702W alleles), as previously described (2). Our results indicated that 19 (51.35%) of the CD patients were carriers of at least one of the susceptibility-associated NOD2/CARD15 alleles (10 carried the *insC3020* mutation, 8 the R702W mutation, and 6 the G908R mutation), whereas only 7 (20.6%) of the healthy controls carried at least one of the mutated NOD2/CARD15 alleles. A significant association between the carriage of at least one NOD2/CARD15 mutation and development of CD was observed ($P = 0.007$; OR = 4.07 [CI₉₅, 1.42 to 11.66]). The results confirm for the first time the associations of NOD2/CARD15 mutations and CD in the Sardinian population.

Among the CD patients who carried at least one of the susceptibility-associated NOD2/CARD15 alleles, 14 (73.7%) had evidence for the presence of *Mycobacterium avium* subsp. *paratuberculosis* DNA. This association was marginally significant ($P < 0.04$; OR = 1.7 [CI₉₅, 0.92 to 3.2]) in our study

group. Since several findings indicate that the presence of certain bacteria in the face of permissive NOD2/CARD15 mutations is necessary for development of CD (5, 7), it is possible that in individuals with NOD2/CARD15 mutations, the innate response to mycobacterial exposure would be inadequate, permitting establishment of a persistent mycobacterial infection. Chronic infection could then activate the inflammatory response which is characteristic of CD..

Collectively, our findings support and substantiate the suggestions of Behr et al. that these cases may illustrate a potential conceptual approach to CD etiology, mostly based on tandem searches for bacterial trigger and host susceptibility (1). However, further studies involving a larger number of cases and controls on a global scale are clearly needed to elucidate the mechanism behind the etiology of CD.

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