The Genome of a Pathogenic *Rhodococcus*: Cooptive Virulence Underpinned by Key Gene Acquisitions

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Abstract

We report the genome of the facultative intracellular parasite *Rhodococcus equi*, the only animal pathogen within the biotechnologically important actinobacterial genus *Rhodococcus*. The 5.0-Mb *R. equi* 103S genome is significantly smaller than those of environmental rhodococci. This is due to genome expansion in nonpathogenic species, via a linear gain of paralogous genes and an accelerated genetic flux, rather than reductive evolution in *R. equi*. The 103S genome lacks the extensive catabolic and secondary metabolic complement of environmental rhodococci, and it displays unique adaptations for host colonization and competition in the short-chain fatty acid–rich intestine and manure of herbivores—two main *R. equi* reservoirs. Except for a few horizontally acquired (HGT) pathogenicity loci, including a cytoadhesive pilus determinant (*rpl*) and the virulence plasmid *vap* pathogenicity island (PAI) required for intramacrophage survival, most of the potential virulence-associated genes identified in *R. equi* are conserved in environmental rhodococci or have homologs in nonpathogenic *Actinobacteria*. This suggests a mechanism of virulence evolution based on the cooption of existing core actinobacterial traits, triggered by key host niche–adaptive HGT events. We tested this hypothesis by investigating *R. equi* virulence plasmid-chromosome crosstalk, by global transcription profiling and expression network analysis. Two chromosomal genes conserved in environmental rhodococci, encoding putative chorismate mutase and anthranilate synthase enzymes involved in aromatic amino acid biosynthesis, were strongly coregulated with *vap* PAI virulence genes and required for optimal proliferation in macrophages. The regulatory integration of chromosomal metabolic genes under the control of the HGT–acquired plasmid PAI is thus an important element in the cooptive virulence of *R. equi*.


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Introduction

*Rhodococcus* bacteria belong to the mycolic acid-containing group of actinomycetes together with other major genera such as *Corynebacterium*, *Mycobacterium* and *Nocardia* [1]. The genus *Rhodococcus* comprises more than 40 species widely distributed in the environment, many with biotechnological applications as diverse as the biodegradation of hydrophobic compounds and xenobiotics, the production of acrylates and bioactive steroids, and fossil fuel desulfurization [2]. The rhodococci also include an animal pathogen, *Rhodococcus equi*, the genome of which we report here.

*R. equi*, a strictly aerobic cocobacillus, is a multihost pathogen that causes purulent infections in various animal species. In horses, it is the etiological agent of “rattles”, a lung disease with a high mortality in foals [3]. *R. equi* lives in soil, uses manure as growth substrate, and is transmitted by the inhalation of contaminated soil dust or the breath of infected animals. Pathogen ingestion may result in mesenteric lymphadenitis and typhlocolitis, and multiplication in the fecal content of the intestine contributes to dissemination in the environment. *R. equi* causes chronic pyogranulomatous adenitis in pigs and cattle and severe opportunistic infections in humans, often in HIV-infected and immunosuppressed patients. Human rhodococcal lung infection
**Author Summary**

*Rhodococcus* is a prototypic genus within the Actinobacteria, one of the largest microbial groups on Earth. Many of the ubiquitous rhodococcal species are biotechnologically useful due to their metabolic versatility and biodegradative properties. We have deciphered the genome of a facultatively parasitic *Rhodococcus*, the animal and human pathogen *R. equi*. Comparative genomic analyses of related species provide a unique opportunity to increase our understanding of niche-adaptive genome evolution and specialization. The environmental rhodococci have much larger genomes, richer in metabolic and degradative pathways, due to gene duplication and acquisition, not genome contraction in *R. equi*. This probably reflects that the host-associated *R. equi* habitat is more stable and favorable than the chemically diverse but nutrient-poor environmental niches of nonpathogenic rhodococci, necessitating metabolically more complex, expanded genomes. Our work also highlights that the recruitment or cooption of core microbial traits, following the horizontal acquisition of a few critical genes that provide access to the host niche, is an important mechanism in actinobacterial virulence evolution. Gene cooption is a key evolutionary mechanism allowing rapid adaptive change and novel trait acquisition. Recognizing the contribution of cooption to virulence provides a rational framework for understanding and interpreting the emergence and evolution of microbial pathogenicity.

Apart from the key role of the plasmid *vap* PAI, little is known about the pathogenic mechanisms of *R. equi*. We investigated the biology and virulence of this pathogenic actinomycete by sequencing an analyzing the genome of strain 103S, a prototypic clinical isolate. With its dual lifestyle as a soil saprotroph and intracellular parasite, *R. equi* offers an attractive model for evolutionary genomics studies of niche breadth in Actinobacteria. The comparative genomic analysis of *R. equi* and closely related environmental rhodococci reported here provides insight into the mechanisms of niche-adaptive genome plasticity and evolution in this bacterial group. The *R. equi* genome also provides fundamental clues to the shaping of virulence in Actinobacteria.

**Results/Discussion**

**General genome features**

The genome of *R. equi* 103S consists of a circular chromosome of 5,043,170 bp with 4,525 predicted genes (Figure S1) and a circular virulence plasmid of 80,610 bp containing 73 predicted genes [8]. Overall G+C content is 68.76%. Table 1 summarizes the main features of the *R. equi* genome.

**Comparative analysis.** Orthology analyses (Figure S1) and multiple alignments (Figure 1A) with representative published actinobacterial genomes showed the highest degree of homology and synteny conservation with *Rhodococcus jostii* RHA1 [10]. Next in overall genome similarity was *Nocardia farcinica*, followed by *Mycobacterium* spp., whereas *Streptomyces coelicolor* appeared much more distantly related, consistent with 16S rRNA-derived actinobacterial phylogenies. Some phylogenetic studies have been inconclusive, positioning *R. equi* either with the nocardiae or rhodococci [1,11]. Our genome-wide comparative and phylogenomic analyses indicate this species is a bona fide member of the genus *Rhodococcus* (Figure 1, Figure S2).

Interestingly, *R. equi* has a substantially smaller genome than the soil-restricted versatile biodegrader *R. jostii* RHA1 (9.7 Mb) [10] and two recently sequenced environmental rhodococci, *Rhodococcus erythropolis* PR4 (6.89 Mb) and *Rhodococcus opacus* B4 (8.17 Mb) (see http://www.nite.go.jp/index-e.html). The rhodococcal genomes also differ in structure: *R. equi* and *R. erythropolis* have covalently closed chromosomes, whereas those of *R. jostii* and *R. opacus* are linear (Table 1, Figure S2). Chromosome topology does not seem to correlate with phylogeny, as *R. equi* and *R. erythropolis* belong to different subclades, and the latter is the prototype of the

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**Table 1. General features of the genomes of *R. equi* 103S and the environmental species, *R. jostii* RHA1.**

<table>
<thead>
<tr>
<th>Replicon</th>
<th>Size (bp)</th>
<th>Topology</th>
<th>GC %</th>
<th>No. of CDS</th>
<th>Pseudo-genes</th>
<th>Coding %</th>
<th>Coding density (average CDS length in bp)</th>
<th>rRNA clusters</th>
<th>tRNAs</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>R. equi</em> 103S</td>
<td>Chromosome</td>
<td>5,043,170</td>
<td>Circular</td>
<td>68.82</td>
<td>4,525</td>
<td>14</td>
<td>90.3</td>
<td>0.89 (1009)</td>
<td>4</td>
</tr>
<tr>
<td>pVAPA1037</td>
<td>80,610</td>
<td>Circular</td>
<td>64.61</td>
<td>73</td>
<td>8*</td>
<td>72.7</td>
<td>0.81 (901)</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><em>R. jostii</em> RHA1</td>
<td>Chromosome</td>
<td>7,804,765</td>
<td>Linear</td>
<td>67.52</td>
<td>7,211</td>
<td>5</td>
<td>91.2</td>
<td>0.92 (987)</td>
<td>4</td>
</tr>
<tr>
<td>pHRL1</td>
<td>1,123,075</td>
<td>Linear</td>
<td>65.05</td>
<td>1,146</td>
<td>2</td>
<td>82.1</td>
<td>1.02 (805)</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>pHRL2</td>
<td>442,536</td>
<td>Linear</td>
<td>64.01</td>
<td>454</td>
<td>4</td>
<td>83.7</td>
<td>1.03 (816)</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>pHRL3</td>
<td>332,361</td>
<td>Linear</td>
<td>64.91</td>
<td>334</td>
<td>0</td>
<td>84.9</td>
<td>1.00 (845)</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

See http://www.nite.go.jp/index-e.html and Table S3 for data from two other sequenced genomes from environmental *Rhodococcus* spp., *R. erythropolis* PR4 and *R. opacus* B4 (released online by NITE, the Japanese National Institute for Technology and Evaluation).

*Of which seven in the HGT vap PAI.

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involved in central and intermediate metabolism ($n = 1,108$) and another quarter corresponds to surface/extracellular proteins ($n = 1,073$). “Regulators” is the next most populated functional category ($n = 464$, 10.3%). After adjusting for genome size, the number of membrane-associated proteins is average, but the regulome and secretome are clearly larger than in other Actinobacteria (Figure S4A, S4B, S4C), possibly reflecting specific needs associated with the habitat diversity of $R. \text{equi}$, from soil and feces to the macrophage vacuole. $R. \text{equi}$ has 25 two-component regulatory systems, more than twice as many as host-restricted Mtb [13], and more regulators as a function of genome size than $S. \text{coelicolor}$ [12] (Figure S4B). About 29% of the genome encodes products of unknown function. This percentage rises to 44.5% for secreted products (Figure S3B), 13% of which are unique to $R. \text{equi}$. Ortholog comparisons with representative closely related mycolata ($R. \text{jostii}$, $N. \text{farcinica}$ and Mtb) showed $R. \text{equi}$ to have the highest proportion of species-specific surface/extracellular proteins, consistent with its large secretome. By contrast, $R. \text{jostii}$ RHA1 has the largest proportion of unique metabolic genes (Figure S5), consistent with its catabolic versatility [10]. Indeed, $R. \text{jostii}$ RHA1 is unique among Actinobacteria in its unusual overrepresentation of metabolic genes (Figure S4D).

Expansive evolution of rhodococcal genomes

The 5.0 Mb $R. \text{equi}$ chromosome contains relatively few pseudogenes ($n = 14$, Table 1), most associated with horizontally acquired regions ($n = 10$, including two degenerate DNA mobility genes), consistent with a slow “core” gene decay rate. This suggests that the differences in chromosome size between rhodococci result mainly from genome expansion in environmental species rather than contraction in $R. \text{equi}$.

Gene duplication versus HGT. We analyzed the paralogous families and local DNA compositional biases to assess the impact of gene duplication (GD) and horizontal gene transfer (HGT) in rhodococcal genome evolution (Tables S1, S2). As expected, both contributed to the chromosome size increase, but with different patterns: linear for GD (i.e. similar percentage of duplicated genes, 32.1, 33.2 and 33.6%, in $R. \text{equi}$, $R. \text{erythropolis}$ and $R. \text{jostii}$, respectively), and exponential for HGT (9.5, 14.8 and 19.5%, respectively) (Figure 2). A possible explanation is that HGT involves the simultaneous acquisition of several genes (mean no. of genes per HGT “island” in rhodococci, 8.2 to 10.6). The probability of HGT in rhodococci also increases with chromosome size, as indicated by the mean frequencies of HGT events (1 every 87.0, 67.0 and 54.2 genes in $R. \text{equi}$, $R. \text{erythropolis}$ and $R. \text{jostii}$, respectively) (Table S1). Moreover, recently acquired HGT islands, mostly containing “non-adapted” DNA dispensable in the short term in the new host species, are likely to evolve more freely and to tolerate further HGT insertions. This may be the case for two large chromosomal HGT “archipelagos” of ≈90 and 190 Kb in 103S, which probably were generated by an accumulation of HGT events. The mosaic structure of these HGT regions and the diversity of source species, as indicated by reciprocal BLASTP best-hit analysis, suggest that they are a composite of several independent HGT events rather than the result of a single “en-block” acquisition (Figures S1 and S6). Rhodococcal genome expansion also involves a linear increase in the number of paralogous families (with larger numbers of paralogs per family) and non-duplicated genes (Table S2), and an increasing number of unique hypothetical proteins (e.g. 164 in $R. \text{equi}$, 408 in $R. \text{jostii}$). Thus, genome expansion in rhodococci involves greater functional redundancy, diversity and innovation.

About 20% of $R. \text{equi}$ HGT islands (Figure S1) are located close to tRNA genes, suggesting the involvement of phages or
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integrative plasmids in their acquisition. However, almost no DNA mobilization genes or remnants thereof were found associated with HGT regions, suggesting that the lateral gene acquisitions in the R. equi chromosome are evolutionarily ancient. Most HGT genes (52.5%) probably originated from other Actinobacteria, 3.5% of the best hits were from other bacteria, and 44% had no homologs in the databases. Only four integrase genes, one of them degenerate, and an IS1650-type transposase pseudogene were identified in the 103S chromosome. R. equi seems therefore to be genetically stable in terms of mobile DNA element-mediated rearrangements. DNA mobility genes —mostly associated with HGT regions and increasing in abundance with genome size—are more numerous in environmental rhodococci (Table S3). Thus, increasing genetic flux and plasticity are associated with increasing chromosome size in rhodococci.

Role of plasmids. Rhodococcal genome expansion can be largely attributed to extrachromosomal elements. R. equi has a single 80 Kbp circular plasmid whereas environmental rhodococci have three to five plasmids, including large linear replicons up to 1,123 Kbp in size, accounting for a substantial fraction of the genome (e.g. =20% in R. jostii RHA1) (Table 1, Table S3). Thus, as observed for chromosomal HGT DNA, the amount of plasmid increases exponentially with genome size. Indeed, one third of the plasmid DNA was HGT-acquired (32.4%), range 19.35–49.7 vs 14.5%, range 9.5–19.5 for the chromosomes), and plasmids may themselves be considered potentially mobilizable DNA. Rhodococcal plasmids also have a much higher density of DNA mobilization genes (Table S3), pseudogenes (Table 1), unique species-specific genes (mean 44.3±16.0% vs 3.6% to 3.6%), and niche-specific determinants (e.g. the intracellular survival tap PAI in R. equi [8] and 11 of the 26 peripheral aromatic clusters in R. jostii [10]) than the corresponding chromosomes. Rhodococcal plasmids are therefore clearly under less stringent selection and are key players in rhodococcal genome plasticity and niche adaptability.

Niche-adaptive features

Basic nutrition and metabolism. No genes with an obvious role in carbohydrate transport were identified in 103S, consistent with the reported inability of R. equi to utilize sugars [14], confirmed here by Phenotype MicroArray (PMA) screens [15] and growth experiments in chemically defined mineral medium (MM) (Figure S7A). By contrast, R. jostii, R. erythropolis, and R. opacus can grow on carbohydrates [16–18] and their genomes encode sugar transporters, including phosphoenolpyruvate-carbohydrate phosphotransferase system (PTS) permeases. Interestingly, the intracellular pathogens R. equi, Mtb and Tropheryma whipplei are the only mesophilic Actinobacteria lacking PTS sugar permeases (Table S4). However, Mtb grows on carbohydrates transported via non-PTS permeases. As the PTS is widespread in Actinobacteria, including nonpathogenic rhodococci and mycobacteria, the absence of PTS components in R. equi, Mtb and the genome-reduced obligate endocellular parasite T. whipplei probably results from gene loss.

The PMA and MM experiments showed that the only carbon sources used by R. equi 103S were organic acids (acetate, lactate, butyrate, succinate, malate, fumarate; but not pyruvate) and fatty acids (palmitate and the long-chain fatty acid-containing lipids Tween 20, 40 and 80) (Figure S7A). In addition to monocarboxylate and dicarboxylate transporters, the 103S genome encodes an extensive lipid metabolic network, with 36 lipases (16 of which secreted) and many fatty acid β-oxidation enzymes, with 40 acyl-CoA synthetases, 48 putative acyl-CoA dehydrogenases, and 23 enoyl-CoA hydratases/isomerases. Thus, R. equi seems to assimilate carbon principally through lipid metabolism. A mutant in the glyoxylate shunt enzyme isocitrate lyase (REQ38290) [19], required for anaplerosis during growth on fatty acids [20], has severely impaired intramacrophage replication and virulence [21], indicating that, as reported for Mtb [22], lipids are a major growth substrate for R. equi during infection in vivo.

The 103S genome encodes 21 putative amino acid/oligopeptide transporters, and PMA screens and MM growth assays confirmed that R. equi uses several amino acids (tryptophan, tyrosine, phenylalanine, cysteine, methionine) and dipeptides as sources of nitrogen. However, 103S also has pathways for the de novo synthesis of all essential amino acids, consistent with the ability of R. equi to grow in MM containing only an inorganic nitrogen source (Figure S7A). Thus, R. equi can flexibly adapt to fluctuating conditions of amino-acid availability and grow in amino acid-deficient environments, as typically encountered in the infected host by intracellular pathogens [23]. See Figure 3 for a schematic overview of R. equi 103S nutrition and metabolism.

Thiamine auxotrophy. R. equi strains cannot grow without thiamine and an analysis of the loci involved in its biosynthesis revealed that thisC is absent from 103S, probably due to an HGT event affecting the thicD gene (Figure S7B, S7C, S7D). The auxotrophic mutation is probably irrelevant for R. equi in the intestine and manure-rich soil owing to the availability of Rhodococcus equi Genotype and Cooptive Virulence

Figure 2. Role of gene duplication and horizontal gene transfer (HGT) in rhodococcal genome evolution. Scatter plots of (A) duplicated (paralogous) genes and (B) HGT genes versus the total number of genes in rhodococcal and actinobacterial genomes (curve fits of rhodococcal data in red, general trendline in black). HGT genes were excluded from the paralogy analyses. doi:10.1371/journal.pgen.1001145.g002
microbially synthesized thiamine. Host-derived thiamine is also probably available to R. equi during infection.

Specialized metabolism. We investigated the nutritional and metabolic aspects of rhodococcal niche adaptation by comparing the metabolic network of R. equi with that of R. jostii RHA1, the only other rhodococcal species for which a detailed manually annotated genome is available. RHA1 originated from lindane-contaminated soil and was identified by screening for biodegradative capabilities on multiple aromatic compounds, including polychlorinated biphenyls and steroids. Not surprisingly, its genome has an abundance of aromatic degradation pathways and oxygenases involved in aromatic ring cleavage [10].

R. equi is also soil-dwelling but is primarily isolated from clinical specimens and manure-rich environments, involving clearly different selection criteria and habitat conditions. We used reciprocal best-match BLASTP comparisons to identify the species-specific metabolic gene complements, in which the catabolic specialization is likely concentrated. The related pathogenic Actinobacteria, N. farcinica (which shares a dual soil saprophytic/parasitic lifestyle with R. equi) and Mtb (quasiobligate parasite) were also included in the analyses. R. jostii RHA1 contains a disproportionately larger number of unique metabolic genes than R. equi, N. farcinica and Mtb (n = 1,260 or 47.2% of total metabolic CDS vs only 326 to 375 or 22.9 to 29.2%, respectively) (Figure S8). The oversized metabolic network of RHA1 results from an expansion in the number and gene content of paralogous families (Table S5) and nonparalogous genes (643 CDS in RHA1 vs 209 to 288). Only three of the 29 aromatic gene clusters present in R. jostii [10] were identified in the 103S genome.
R. equi therefore has a much smaller metabolic network than, and essentially lacks the vast aromatic catabolome of, R. jostii RHA1.

R. equi resembles other environmental Actinobacteria in being able to produce oligopeptide secondary metabolites. The 103S genome encodes 11 large non-ribosomal peptide synthetases (NRPS), including three involved in siderophore formation (see below). The only polyketide synthase (REQ52090-50) is involved in the synthesis of mycolic acids. By contrast, RHA1 has 24 NRPS and seven polyketide synthases [10]. Thus, genome expansion in R. jostii has been accompanied by an extensive amplification of secondary metabolism.

**Other metabolic traits.** R. equi reduces nitrates to nitrites [14] through a NarGHI nitrate reductase (REQ04200-30). There is also a NirBD nitrite reductase (REQ82900-30), a NarK nitrate/nitrite transporter (REQ83940) and a putative nitric oxide (NO) reductase (REQ62800) (Figure 3). nirBD is conserved in environmental rhodococci whereas narGHIJ and REQ03290 are not, indicating that R. equi is potentially well equipped for anaerobic respiration via denitrification, a useful trait for survival in microaerobic environments, as typically found in necrotic pyogranulomatus tissue [24], the intestine or manure. A narG mutation has been shown to attenuate R. equi virulence in mice [25], consistent with the bacteria encountering hypoxic conditions during infection, although this may also reflect defective nitrate assimilation in vivo [26].

Intriguingly, R. equi possesses a D-xylulose 5-phosphate (X5P)/D-fructose 6-phosphate (F6P) phosphoketolase (Xfp, REQ21880), the key enzyme of the “Bifidobacterium” F6P shunt, which converts glucose into acetate and pyruvate and is the main hexose fermentation pathway in bifidobacteria [27]. Unexpected fermentative metabolism has been detected in some strictly aerobic bacteria, such as *Pseudomonas* and *Arthrobacter* [28], but no NAD⁺ (anaerobic)-dependent lactate dehydrogenase or other obvious pyruvate fermentation enzyme was identified in 103S. As R. equi does not use sugars, a catabolic role for the F6P shunt is possible only if fed via gluconogenesis/glycolysis. Alternatively, the F6P shunt may function in reverse (anabolic) mode in R. equi, in parallel to gluconogenesis, directing excess acetate and glyceraldehyde-3-phosphate (GAP), generated from lipid metabolism, into the pentose phosphate pathway (PPP) (Figure 3). R. equi 103S has a lutABC operon (REQ16290-320), recently implicated in lactate utilization via pyruvate in *Bacillus* [29].

**Alkaline optimal pH.** R. equi tolerates a wide pH range, but growth is optimal between pH 8.5 and 10 (Figure S9). This alkaline pH is similar to that of untreated manure, potentially providing a selective advantage for colonization of the farm habitat. The 103S genome encodes a urease (REQ45360-410), an arginine deiminase (REQ11880), an AmiE/F aliphatic amidase/formamidase (REQ26530, next to REQ26520 encoding a UreL-like urea/amidase transporter in an HGT island) and other amidases which, by releasing ammonia [30], may favor R. equi growth in acidic host habitats such as the macrophage vacuole (pH=5.5), the airways or the intestine (typical pH values in horse, 5.3–5.7 and 6.4–6.7, respectively [31,32]).

**Stress tolerance.** Like other soil bacteria [33], R. equi encodes a large number of σ factors (21 σ⁺) and stress proteins (e.g. eight universal stress family proteins [Usp], five cold shock proteins, three heat shock proteins and several Clp proteins). It also synthesizes the ppGpp alarmone involved in adaptation to amino acid starvation [34]. R. equi is transmitted by soil dust in hot, dry weather [3] and must therefore resist low water availability and dessication-associated oxidative damage. There are two ABC glycine betaine/choline transporters (REQ00540-70 and REQ14620-60), an aquaporin (REQ29580), and genes for the synthesis of an exopolysaccharide (see below) and the osmolytes ectoine (ectABC, REQ67850), hydroxyectoine (ectD, REQ07650) and trehalose (REQ27400-30), potentially important for osmoprotection and water stress tolerance. R. equi is well equipped to face oxidative stress, with four catalases, four superoxide dismutases, six alkyl hydroperoxide reductases and two thiol peroxidases. It also synthesizes the unique actinobacterial redox-storage thiol compound, mycodiol [35], the antioxidant thioredoxin (REQ47340-50), and the protein-repairing peptide-methionine sulfoxide reductases MsrA (REQ01570) and MsrB (REQ20650) [36]. Three homologs of the virulence-associated mycobacterial histone-like protein Lsr2 [37] (one plasmid tag PAL-encoded [8], REQ03140 and 05980 chromosomal), and a Dps family protein [38] (REQ4900, cotranscribed with REQ4890 encoding a CsdB-like putative stress protein [39]), may protect against oxidative DNA damage. NO reductase REQ03290 and a putative NO dioxygenase (REQ10890) may confer resistance to nitrosative stress (Figure 3).

**“Innate” drug resistance.** R. equi 103S showed a degree of resistance to many antibiotics in the PMA screens, including 13 aminoglycosides, nine sulphonamides, six tetracyclines, 10 quinolones, 18 β-lactams and chloramphenicol. Standard susceptibility tests confirmed the resistance of 103S to a number of clinically relevant antibiotics (Table S7). This correlates with the presence in 103S of an array of antibiotic resistance determinants, including five aminoglycoside phosphotransferases, 10 β-lactamases and four multidrug efflux systems. Except for β-lactamase REQ26610, none of the resistance genes are associated with HGT regions or DNA mobility genes, suggesting they are ancient traits selected to confer resistance to naturally occurring antimicrobials rather than recent acquisitions associated with the medical use of antibiotics. Soil organisms tend to carry multiple drug resistance determinants [40], and homologs of most R. equi resistance genes are present in the genomes of environmental rhodococci, at the same chromosomal location in some cases (Figure S10).

**Virulence**

Potential virulence-associated determinants were identified *in silico* based on (i) homology with known microbial virulence factors, (ii) literature mining for Mtb virulence mechanisms, (iii) automated genome-wide screening for virulence-associated motifs [41] and (iv) systematic inspection of HGT genes, the secretome, and of genes shared with pathogenic actinomycetes but absent from nonpathogenic species.

**Mycobacterial gene families.** The 103S genome harbors three complete mec (mammalian cell entry) clusters. Despite their name, the mechanisms by which these clusters contribute to mycobacterial pathogenesis remain unclear [42]. The mecA operon from R. jostii and its homolog mec2 in R. equi have recently been shown to mediate cholesterol uptake, consistent with emerging evidence that mec clusters constitute a new subfamily of ABC importers [43,44]. The recently reported lack of effect of an mec2 mutation on R. equi survival in cultured macrophages [43] does not exclude a role in cholesterol utilization *in vivo* or in IFNγ-activated macrophages, as shown for an Mtb mutant in the homologous mec operon [45]. The surface-exposed PE and PPE proteins account for ≈7% of the coding capacity of the Mtb genome due to massive gene duplication, and are thought to play an important role in mycobacterial pathogenesis [46]. The R. equi genome also harbors PE/PPE genes, although only a single copy of each (Figure S11A). They lie adjacent in an operon (REQ01750-80) with the PE/PPE genes, although only a single copy of each (Figure S11A).
Mtb ESX clusters, and to the single ESX cluster present in Corynebacterium diphtheriae. ESX loci encode two small proteins, ESAT-6 (REQ35460) and CFP-10 (REQ35440), and their type VII secretion apparatus, which also mediates the export of PE and PPE proteins. ESAT-6 and CFP-10 form heterodimeric complexes and are major T-cell antigens and key virulence factors in Mtb [48].

*R. equi* possesses six *mmpL* genes, encoding members of the “mycobacterial membrane protein large” family of transmembrane proteins, which are involved in complex lipid and surface-exposed polypeptide secretion, cell wall biogenesis and virulence [49]. There are also four Fbp/antigen 85 homologs (REQ01990, 02000, 08990, 20840), involved in Mtb virulence as fibronectin-binding proteins and through their mycolyltransferase activity, required for cord factor formation and integrity of the bacterial envelope [50].

**Cytoadhesive pili.** A nine-gene HGT island (REQ18350-430) encodes the biogenesis of Flp-subfamily type IVb pili, recently described in Gram-negative bacteria [51]. We confirmed the presence of pilus appendages in 103S (Figure 4). Gene deletion and complementation analysis demonstrated that the identified *R. equi* pilus (Rpl) mediated attachment to macrophages and epithelial cells (P. González et al., manuscript in preparation). The *rpl* island is absent from environmental rhodococci and is unrelated to the pilus determinants recently identified in Mtb and *C. diphtheriae* [52,53].

**Other putative virulence factors.** *R. equi* is thought to produce capsular material [7,54], and an HGT region encompassing REQ0580-780 contains genes potentially responsible for extracellular polysaccharide synthesis. Two other HGT islands encode sortases, transpeptidases that attach surface proteins covalently to the peptidoglycan and which are important for virulence in Gram-positive bacteria [55]. Both *st* islands encode the putative substrates for the sortases (secreted proteins of unknown function) (Figure S11B).

Several secreted products are putative membrane-damaging or lipid-degrading factors, including a transmembrane protein with a putative hemolysin domain (REQ12980), three cholesterol oxidases (REQ6750, REQ26500, and REQ43910/ChoE [56]), four “cutinases”/serine esterases (REQ00490, REQ02020, REQ0540, REQ46060) with potential phospholipase A activity [57], and 16 lipases. REQ34990 encodes a secreted lipoprotein homologous to MBP70 and MPB83, two major mycobacterial antigens strongly expressed in *Mycobacterium bovis* BCG [58]. The REQ34990 product has a FAS1/BigH3 domain involved in cell adhesion via integrins [59]. There are also homology of two mycobacterial cytoadhesins, the heparan sulfate-binding hemagglutinin HbhA (Rv0475) involved in Mtb dissemination (REQ38170), and the multifunctional histone-like/laminin- and glycosaminoglycan-binding protein Lhp/Hlp (REQ31340) [60] (Figure 3).

Iron is essential for microbial growth and the ability to acquire ferric iron from the host is directly related to virulence. Two NRPS, Rbt1/IupS (bimodular, REQ08140-60) and IupU (REQ23810), are involved in the formation of catecholic siderophores [61] or “rhequibactins”. A third NRPS homologous to *Mycobacterium smegmatis* Fxb (REQ07630) may be involved in the formation of an oligopeptidic ferriexochelin-like extracellular siderophore. This “rhequichelin” is probably transported by the *iupABC* (REQ24080-100)–encoded putative siderophore ABC permease [61], homologous to the *M. smegmatis* FxuABC ferriexochelin transporter [62] (Figure 3). The redundancy of iron acquisition systems may explain the lack of effect on virulence of individual *iupU*, *rbt1*/*iupS* and *iupABC* mutations [61].

**Virulence gene acquisition versus cooption.** Only a few species-specific putative virulence loci were found in the 103S
genome, all in HGT islands (e.g. the plasmid vap PAI or the chromosomal rpl locus). Most (~90%) of the potential virulence-related determinants identified in *R. equi* were present in the environmental *Rhodococcus* spp. and/or had homologs in nonpathogenic *Actinobacteria* (Table 2, Table S8). These included orthologs of many experimentally-determined Mtb virulence genes, most of which (~84%) are conserved among nonpathogenic mycobacteria or have close homologs in environmental actinomycetes (Table S9). The case of the *mce* ESX, and PE/PPE loci is illustrative. Initially thought to be *Mycobacterium*-specific virulence traits, members of these multigene families are present in *R. equi* and in nonpathogenic rhodococci (Table S8), consistent with growing evidence that they are actually widely distributed among high-G+C gram-positives, whether environmental or pathogenic [42,65,66]. Notwithstanding that some of the unknown function genes of the 103S genome may encode novel, previously uncharacterized pathogenic traits, these observations are consistent with a scenario in which *R. equi* virulence largely involves the “appropriation” or cooption of core actinobacterial functions, originally selected in a non-host environment. Gene cooption (also known as preadaptation or exaptation) is a key evolutionary process by which traits that have evolved for one purpose are employed in a new context and acquire new roles, thus allowing rapid adaptive changes [65–67]. Cooptive evolution operates through critical modifications in gene expression and function [65]. These changes are particularly feasible in the larger genomes of soil bacteria, with a characteristic profusion of regulators and functionally redundant paralogs [68,69]. Without the need for major changes, stress-enduring mechanisms and other housekeeping components, such as the cell envelope mycolic acids or the bacterial metabolic network, may directly contribute to virulence by affording nonspecific resistance or by enabling the organism to feed on host components. We suggest that a few decisive niche (host)-adaptive HGT events in a direct ancestor of *R. equi*, such as acquisition of the plasmid vap “intramacrophage survival” PAI [8] and the rpl “host colonization” HGT island (Figure 4), triggered the rapid conversion of a “preparastatic” commensal organism into a pathogen via the cooption of preexisting bacterial functions.

**Table 2. Bacterial groups in which homologs of potential *R. equi* virulence-associated genes were identified.**

<table>
<thead>
<tr>
<th>Categories</th>
<th>No. of genes</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Actinobacteria</em> (shared by pathogenic and non-pathogenic spp.)</td>
<td>228</td>
<td>84.75</td>
</tr>
<tr>
<td>No significant match (<em>R. equi</em>-specific)</td>
<td>25†</td>
<td>9.29</td>
</tr>
<tr>
<td><em>Rhodococcus</em> (non-pathogenic spp.)</td>
<td>10</td>
<td>3.71</td>
</tr>
<tr>
<td><em>Mtb</em> and/or pathogenic mycobacteria, <em>Nocardia farcinica</em></td>
<td>2</td>
<td>0.74</td>
</tr>
<tr>
<td><em>Chloroflexi</em></td>
<td>2</td>
<td>0.74</td>
</tr>
<tr>
<td><em>Cyanobacteria</em></td>
<td>1</td>
<td>0.37</td>
</tr>
<tr>
<td><em>Proteobacteria</em></td>
<td>1</td>
<td>0.37</td>
</tr>
<tr>
<td>Total</td>
<td>269†‡</td>
<td></td>
</tr>
</tbody>
</table>

Homology cutoff, ≥30% identity over 70% of sequence length. Mutually exclusive allocation to each category based on BLASTP best match. See Table S8 for complete list of genes.

†All in HGT islands, of which 76% in the virulence plasmid vap PAI.
‡72.0% present in *Mtb*.
*50.9% of the encoded products are surface proteins/extracellular proteins.

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Virulence plasmid–chromosome crosstalk

Based on the well-established principle that coexpression with pathogenicity determinants is a strong indicator of involvement in virulence [70,71], we sought to identify novel *R. equi* virulence-associated chromosomal factors through their coregulation with the plasmid virulence genes. The expression profiles of 103S and an isogenic plasmid-free derivative (103S<sup>C</sup>) were compared, using a custom-designed genomic microarray in *in vitro* conditions known to activate (37°C pH 6.5) or downregulate (30°C pH 8.0) the virulence genes of the plasmid vap PAI [72,73]. The plasmid had little effect on the chromosome in vap gene-downregulating conditions, but significantly altered expression was observed for numerous genes in vap gene-activating conditions (n = 88 with ≥2 fold change) (Table S10). Most of the differentially expressed genes (68%) were upregulated in the presence of the plasmid. These data suggest that the virulence plasmid activates the expression of a number of chromosomal genes, but whether this upregulation involves direct, specific (potentially virulence related) interactions or incidental pleiotropic effects is unclear.

**Network analysis.** To define the extent and nature of the virulence plasmid–chromosome crosstalk, we subjected the microarray expression data to network analysis. Unlike classical pairwise comparisons, the network approach captures higher-order functional linkages between genes, facilitating the graphic visualization of gene interconnections. It is thus more powerful for biological inference and gene prioritization for experimental validation. Noisy data also tend to be randomly distributed in the network structure [74]. We used BioLayout Express<sup>3D</sup>, an application that constructs three-dimensional networks from microarray data by measuring the Pearson correlation coefficients between the expression profiles of every gene in the dataset. This is followed by graph clustering using the Markov Clustering (MCL) algorithm to divide the network graph into discrete modules with similar expression profiles [75]. Microarray data of 103S bacteria exposed to various combinations of temperature (20°C, 30°C and 37°C) and pH (5.5, 6.5 and 8) were included in the computations to control for the excessive weight of the variable presence/absence of plasmid and strengthen the correlation analysis.

Figure 5A shows a network representation of the functional connections detected in the *R. equi* transcriptome with a Pearson correlation threshold r ≥0.85. The graph model grouped the virulence plasmid genes into two distinct coregulated modules or clusters: one comprised 36 of the 73 plasmid genes, almost all from the housekeeping backbone (replication and conjugal transfer functions) [8]; the other contained 15 of the 26 vap PAI genes together with a number of chromosomal genes (Table S11). The plasmid housekeeping backbone nodes clustered together outside the main regulation network, reflecting functional independence from the rest of the regulome, as would be expected from the autonomous nature of the extrachromosomal replicon (Figure 5A). This indicates that the graph structure is biologically significant and reflects actual functional relationships, validating the network model. By contrast, the vap PAI nodes were clearly embedded in the network and established multiple connections with chromosomal nodes (Figure 5A, Figure S12A), suggesting that the plasmid virulence genes have undergone a process of regulatory integration with the host *R. equi* genome. About half of the predicted products of the chromosomal vap PAI-coregulated cluster genes are metabolic enzymes, the others being transcriptional regulators and transporters (Table S11C). Raising the correlation threshold to a highly stringent r ≥0.95 disintegrated the network graph into a multitude of discrete, unconnected subgraphs (see Dataset S2). This did not substantially alter the structure of the two plasmid
gene-containing clusters, but isolated two chromosomal genes, REQ23860 and REQ23850, as the most significantly and strongly coregulated with the vap PAI genes (Figure 5B), suggesting a direct regulatory interaction [76].

The genes from the plasmid backbone cluster were expressed constitutively in the conditions tested, whereas those from the vap PAI-coregulated cluster responded strongly to temperature, with activation at 37°C. Chromosomal genes in this cluster, particularly REQ23860 and REQ23850, displayed the same pattern, with downregulation in 103SP2 at 37°C, suggesting that plasmid factors are required for their induction at high temperature (Figure S12B, Table S11B). The vap PAI encodes two transcription factors, VirR (orf4) and an orphan two-component regulator (orf8) [8], both of which have been shown to influence vap gene expression [77,78] and could be involved in the observed plasmid-mediated theroregulation of the vap PAI-coregulated cluster.

REQ23860 and REQ23850 are required for efficient intracellular proliferation in macrophages. REQ23860 and REQ23850 null mutants were constructed and tested in J774 macrophages to determine whether the observed coregulation with the plasmid vap PAI correlates with a role in virulence. The plasmidless derivative 103SP2, unable to proliferate intracellularly [5], was used as an avirulent control. The two mutants had a significantly attenuated capacity to grow in macrophages, restored to wild-type levels upon complementation with the deleted genes (Figure 6), indicating that REQ23860 and REQ23850 are required for optimal intramacrophage proliferation. The mutated genes encode an AroQ (type II) chorismate mutase (CM) and a bifunctional anthranilate synthase (AS) with fused TrpE and TrpG subunits, respectively, two key metabolic enzymes catalyzing the initial committed steps in aromatic amino-acid biosynthesis. CM generates prephenate, the first intermediate in the pathway leading to phenylalanine and tyrosine, whereas AS catalyzes the first reaction in tryptophan biosynthesis [79]. Downstream at the same locus, REQ23840 encodes a prephenate dehydrogenase (Figure 7), which catalyzes the oxidative decarboxylation of prephenate to the tyrosine precursor 4-hydroxyphenylpyruvate [79]. The intracellular growth defect caused by the mutations may therefore be related to a diminished capacity for de novo synthesis of aromatic amino acids. The R. equi genome encodes four other CM enzymes (including one in the vap PAI [8]) and an additional AS (bipartite, one subunit encoded in a trpECBA operon and the other by a solitary trpG gene elsewhere in the chromosome). Through their coregulation with the plasmid vap PAI, the redundant REQ23850-60-encoded chorismate-utilizing enzymes may be important for R. equi intracellular fitness and full proliferation capacity, by enhancing the de novo supply of aromatic amino acids, which generally appear to be present at limiting concentrations in

Figure 5. Network analysis of virulence plasmid–chromosome regulatory crosstalk. (A) Integration of the virulence plasmid vap PAI in the R. equi regulatory network. 3D graph of the R. equi 103S transcriptome (see text for experimental conditions) constructed with BioLayout Express3D, an application for the visualization and cluster analysis of coregulated gene networks [74,75]. Settings used: Pearson correlation threshold, 0.85; Markov clustering (MCL) algorithm inflation, 2.2.; smallest cluster allowed, 3; edges/node filter, 10; rest of settings, default. Network graph viewable in Dataset S1. Each gene is represented by a node (sphere) and the edges (lines) represent gene expression interrelationships above the selected correlation threshold; the closer the nodes sit in the network the stronger the correlation in their expression profile. Note that the plasmid vap PAI genes (red spheres) are embedded within, and establish multiple functional connections with, chromosomal nodes (see also Figure S12A) whereas those of the plasmid housekeeping backbone lie outside the main network, reflecting an independent regulatory pattern. (B) Isolated subgraph of the R. equi transcription network obtained with r = 0.95 Pearson correlation threshold, showing the coregulation of the chromosomal genes REQ23860 (putative AroQ chorismate mutase) and REQ23850 (putative TrpEG-like bifunctional anthranilate synthase) (see Figure 7) with the virulence plasmid vap PAI genes. Color codes for nodes as indicated in (A) (spheres, vap PAI-coregulated cluster; cubes, plasmid housekeeping backbone cluster). MCL inflation, 2.2, smallest cluster allowed, 3; rest of settings, default. See Dataset S3.
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intracellular proliferation defect, the two mutants were phenotypically
6
9.84
bacterial population. Bacterial counts per well at
6
proliferation, negative values reflect decrease in the intracellular
to the initial bacterial counts at
6
D
Figure 6. Intracellular growth kinetics of ∆REQ23860 and
6
∆REQ23850 mutants in J774 macrophages. Data were normalized
to the initial bacterial counts at t = 0 using an intracellular growth
coefficient (IGC); see Materials and Methods. Positive IGC indicates
proliferation, negative values reflect decrease in the intracellular
bacterial population. Bacterial counts per well at t = 0: 1035 (wild type),
9.84±0.55×10^6; 1035 ∆, 4.67±0.62×10^6; ∆REQ23860 (putative CM),
11.26±2.78×10^6; complemented ∆REQ23860, 4.24±0.10×10^6;
∆REQ23850 (putative AS), 9.67±0.12×10^6; complemented ∆REQ23850,
8.29±0.22×10^6. Means of at least three independent duplicate
experiments ±SE. Asterisks denote significant differences from wild
type with P<0.001 (two-tailed Student’s t test). Except for the
intracellular proliferation defect, the two mutants were phenotypically
indistinguishable from the wild-type parental strain 1035, including
growth kinetics in broth medium.
doi:10.1371/journal.pgen.1001145.g006

the in vivo replication niche of intramacrophage vacuole-residing
microbial pathogens [23,80,81].

Conclusions
Somewhat counterintuitively for an organism with a dual
lifestyle as a soil saprotroph and intracellular parasite, the R. equi
genome is significantly smaller than those of environmentalhodococci. This may reflect that the main R. equi habitats—
herbivore intestine, manure and animal tissues—provide a richer
and more stable environment than the chemically diverse and
probably nutrient-scarce environments of the nonpathogenic
species. In nutrient-poor conditions, the simultaneous use of all
available compounds as sources of carbon and energy may offer a
competitive advantage, driving the selection of expanded genomes
with greater metabolic versatility [10,68]. Indeed, the much larger
genome of the polychlorinated biphenyl-biodegrading R. jostii
RHA1 encodes a disproportionately large metabolic network [10],
with a wider diversity of paralogous families, unique metabolic
genes and catabolic pathways. The relatively small number of
pseudogenes and virtual lack of DNA mobilization genes in R. equi
suggests that this species has not experienced a sudden
evolutionary bottleneck with a concomitant relaxation of selective
pressure and increase in mutation fixation [82]. The “coprophilic”
and parasitic lifestyle specialization of R. equi seems to result from a
“non-traumatic” adaptive process in an organism that, despite
having suffered some specific functional losses (e.g. sugar
utilization, thiamine synthesis), remains an “average” soil
actinomycete with a normal-sized genome under strong selection.
The greater genomic complexity of the environmental Rhodococcus
spp. may reflect a “multi-substrate” niche specialization necessarily
linked to the strict selection criteria—for unusual metabolic
versatility—under which these species are generally isolated, [10].
Our analyses show that genome expansion in the environmentalhodococci has involved a linear gain of paralogous genes and an
accelerated pattern of gene acquisition through HGT and
extrachromosomal replicons, which evolve more rapidly and
clearly play a critical role in rhodococcal niche specialization.
The lipophilic, asaccharolytic metabolic profile and capacity for
assimilating inorganic nitrogen may be key traits for proliferation
in herbivore intestine and feces, which are rich in volatile fatty
acids [3], and in the macrophage vacuole and chronic pyogranu-
lome, presumably poor in amino acids and rich in membrane-
derived lipids [20,23]. The potential for anaerobic respiration via
denitrification may be critical for survival in the anoxic intestine
or, as suggested for Mtb [83,84], in necrotic granulomatous tissue.
The inability to use sugars, unique among related actinomycetes,
may confer a competitive advantage in the intestine and feces,
dominated by carbohydrate-fermenting microbiota generating
large amounts of short-chain fatty acids, which R. equi use as
main carbon source. Alkalophility is probably an advantage in fresh
manure, a major R. equi reservoir. R. equi is also well equipped to
survive desiccation, important for dustborne dissemination in hot,
dry weather, when rhodococcal foal pneumonia is transmitted
[3,4].

R. equi infections are notoriously difficult to treat due to the
intracellular localization of the pathogen, compounded by a lack of
susceptibility to antibiotics (e.g. penicillins, cephalosporins, sulfa-
mides, quinolones, tetracyclines, clindamycin, and chloramphen-
icol) (Table S7 and refs. therein). With its panoply of drug
resistance determinants, the 103S genome illustrates how naturally
selected resistance traits, typically abundant in soil organisms, may
have an important impact on the clinical management of
microbial infections [40].

Finally, our analyses suggest that the appropriation of
preexisting core actinobacterial components and functions are key
events in the evolution of rhodococcal virulence. Although the
underlying notion may be intuitively apparent when considering,
for example, the contribution of housekeeping genes to bacterial
virulence [85], here we are identifying it specifically as “gene
cooption”, a key mechanism enabling rapid adaptive evolution and
the emergence of new traits [63–67]. Underpinned by a few
critical “host niche-accessing” HGT events, such as acquisition of
the “intracellular survival” plasmid vap PAI or the “cytoadhesion”
chromosomal spl locus, this evolutionary mechanism is likely to
have facilitated the rapid conversion of what was probably an

Figure 7. Structure of the chromosomal locus of the putative
chorismate mutase (CM) and anthranilate synthase (AS) genes
REQ23860 and REQ23850. The locus contains two additional genes,
REQ23840 and REQ23830, encoding a putative prephenate dehydro-
genase (PD) and a hypothetical protein (HP), respectively. The four
genres are conserved at the same chromosomal location in the
environmental Rhodococcus spp (CDS numbers indicated), including
R. opacus B4.
doi:10.1371/journal.pgen.1001145.g007
animal-associated commensal into the pathogenic \textit{R. equi}. Given the pervasive distribution of the “virulence-associated” gene pool among nonpathogenic species (Tables S8, S9), the notion of cooptive virulence is possibly applicable to all pathogenic actinomycetes and, indeed, universally to bacterial pathogens. The incorporation of adaptive changes in the regulation of the “appropriated” genes is a key mechanism in genetic cooption [65]. Our genome-wide microarray experiments and transcription network analyses indicate that the plasmid \textit{pag} PAI, essential for intracellular survival and pathogenicity, has recruited housekeeping genes from the rhodococcal core genome under its regulatory influence. Among these are two chromosomal genes encoding key metabolic enzymes involved in aromatic amino-acid biosynthesis, coexpressed with the virulence genes of the \textit{pag} PAI in response to an increase in temperature to 37°C (the body temperature of the warm-blooded host). These two metabolic genes are required by \textit{R. equi} for full proliferation capacity in macrophages, providing supporting experimental evidence for the cooptive nature of \textit{R. equi} virulence. A cooptive virulence model is consistent with the sporadic isolation of “nonpathogenic” (pre-parasitic) \textit{Actinobacteria}, including environmental rhodococci (e.g. \textit{R. erythropolis} [86]), as causal agents of opportunistic infections. An appreciation of the importance of gene cooption in the acquisition of pathogenicity provides a conceptual framework for better understanding and guiding research into bacterial virulence evolution.

Materials and Methods

Genome sequencing and analysis

We sequenced the original stock of the foal clinical isolate 103, designated clone 103S, to avoid mutations associated with prolonged subculturing \textit{in vitro}. Strain 103 belongs to one of the two major \textit{R. equi} genogroups (DNA macrorestriction analysis, unpublished data), is genetically manipulable, and is regularly used for virulence studies [25,56]. Random genomic libraries in pUC19 were pair-end sequenced using dye terminator chemistry on ABI3700 instruments, with subsequent manual gap closure of shotgun assemblies and sequence finishing, as previously described [8]. The 103S genome sequence was manually curated and annotated with the software and databases listed in Table S12. A conservative annotation approach was used to limit informational noise [8]. For phylogenomic analyses, putative core ortholog genes were identified by reciprocal FASTA using a minimum cutoff of 50% amino acid similarity over 80% or more of the sequence. A noise [8]. The 103S genome sequence was manually curated and annotated with the software and databases listed in Table S12. A conservative annotation approach was used to limit informational noise [8]. For phylogenomic analyses, putative core ortholog genes were identified by reciprocal FASTA using a minimum cutoff of 50% amino acid similarity over 80% or more of the sequence. A noise [8].

Phenotype analysis and microscopy

The nutritional and metabolic profile of \textit{R. equi} 103S and its susceptibility to various drugs were analysed in Phenotype MicroArray screens (Biolog Inc., http://www.biolog.com) [15]. Substrate utilization was validated in supplemented mineral medium (MM) containing salts, trace elements, and ammonium chloride as the sole nitrogen source [19] (see Figure S7). For electron microscopy, a bacterial cell suspension in 0.1 M Tris-HCl (pH 7.5) was negatively stained with 1% uranyl acetate and observed at 80.0 kV in a Phillips CM120 BioTwin instrument (University of Edinburgh). Fluorescence microscopy was carried out on paraformaldehyde-fixed bacteria with an \textit{R. equi} whole-cell rabbit polyclonal antiserum and Alexa Fluor 488-conjugated secondary antibodies (both diluted 1:1000 in 0.1% BSA).

Microarray expression profiling and network analysis

Total RNA was obtained from logarithmically growing \textit{R. equi} bacteria (OD\textsubscript{600} = 0.8) in Luria-Bertani (LB) medium, by homogenization in guanidinium thiocyanate-phenol-chloroform (Tri reagent, Sigma) with FastPrep-24 lysing matrix and a FastPrep apparatus (MP bio), followed by chloroform-isopropanol extraction, DNAase treatment (Turbo DNA-free, Ambion) and purification with RNeasy kit (Qiagen). RNA quantity and quality were determined with a Nanodrop (Thermo Scientific) and 2100 Bioanalyzer with RNA 6000 Nano assay (Agilent). RNA samples (500 ng) were amplified with the MessageAmp II-bacteria kit and 5-(3-amionallyl)-UTP (Ambion), labeled with Cy3 or Cy5 NHS-ester reactive dyes (GE Healthcare), and purified with RNasey MinElute (Qiagen). Whole-genome 8*15K custom microarrays with up to four different 60-mer oligonucleotides per CDS (13,823 probes for the chromosome, 201 for the virulence plasmid) (Agilent) were hybridized in SurecHyb DNA chambers (Agilent) with 300 ng of Cy3/Cy5-labeled aRNA, using Gene Expression Hybridisation and Wash Buffer kits (Agilent). Three experimental replicates per condition were analyzed, one with dye swap. The hybridization signals were captured and linear intensity-normalized, with Agilent’s DNA microarray scanner and Feature Extraction software. Data were subsequently LOESS-normalized by intensity and probe location and analyzed with Genespring GX 10 software (Agilent). Network analysis of microarray expression data was carried out with Biolayout Express 3D software [74], using log base 2 normalized ratios of Cy3/Cy5 signals and methods described in detail elsewhere [75]. Biolayout Express 3D is freely available at http://www.biolayout.org/.

Mutant construction and complementation

In-frame deletion mutants of REQ23860 and REQ23850 were constructed by homologous recombination [56], using the suicide vector pSelAct for positive selection of double recombinants on 5-fluorocytosine (5-FC) [43]. Briefly, oligonucleotide primer pairs CMDEL1/CMDEL2 and CMDEL3/CMDEL4 were used for PCR amplification of two DNA fragments of \approx 1.5 Kb corresponding to the seven 3'- and six 5'-terminal codons plus adjacent downstream and upstream regions of REQ23860. The CMDEL2 and CMDEL3 primers are complementary and were used to join the two ampiclons by overlap extension. The PCR product carrying the \textit{REQ23860} allele was inserted into pSelAct, using SpeI and XbaI restriction sites; the resulting plasmid was introduced into 103S by electroporation and transformants were selected on LB agar supplemented with 80 μg/ml apramycin. The same procedure was followed for \textit{REQ23860}, with primers ASDEL 1 to 4. Allelic exchange double recombinants were selected as previously described [43,56]. For complementation, the REQ23860-50 genes plus the entire upstream intergenic region were amplified by PCR with CACOMP1 and 2 primers and stably inserted into the \textit{R. equi} chromosome, using the integrative vector pSET152 [88]. PCR was carried out with high-fidelity PfuUltra II fusion HS DNA polymerase (Strategene). The primers used are shown in Table S14.

Macrophage infection assays

Low-passage (<20) J774.A1 macrophages (ATCC) were cultured in 24-well plates at 37°C, under 5% CO\textsubscript{2} atmosphere, in DMEM supplemented with 2mM L-glutamine (Gibco) and 10% fetal bovine serum (Lonza) until confluence (\approx 2*10\textsuperscript{5} cells/
well). J774A.1 monolayers were inoculated at 10:1 MOI with washed R. equi from an exponential culture at 37°C in brain-heart infusion (BHI, OD_{600nm}=1.0). Infected cell monolayers were immediately centrifuged for 3 min at 172×g and room temperature, incubated for 45 min at 37°C, washed three times with Dulbecco’s PBS to remove nonadherent bacteria, and incubated in DMEM supplemented with 5μg/ml vancomycin to prevent extracellular growth. After 1 h of incubation with vancomycin and at specified time points thereafter, cell monolayers were washed twice with PBS, detached with a rubber policeman and lysed by incubation for 3 min with 0.1% Triton X-100. Intracellular bacterial counts were determined by plating appropriate dilutions of cell lysates onto BHI. The presence of the virulence plasmid was checked by PCR on a random selection of colonies, using tra-4 and sapA-specific primers [9] to exclude the possibility of intracellular growth defects being due to plasmid loss. As the intracellular bacterial population at a given time point depends on initial numbers, bacterial intracellular kinetics data are expressed as a normalized “Intracellular Growth Coefficient” [89] according to the formula IG = (IB_{t=0} - IB_{t=α})/IB_{t=0}, where IB_{t=α} and IB_{t=0} are the intracellular bacterial numbers at a specific time point, t=α, and t=0, respectively.

Supporting Information

Dataset S1 Layout file of expression network analysis with r = 0.85. Viewable with Biolayout Express 3D (http://www.biolayout.org/).

Found at: doi:10.1371/journal.pgen.1001145.s001 (0.34 MB ZIP)

Dataset S2 Layout file of expression network analysis with r = 0.95. Viewable with Biolayout Express 3D (http://www.biolayout.org/).

Found at: doi:10.1371/journal.pgen.1001145.s002 (0.06 MB ZIP)

Dataset S3 Layout file of expression network analysis with r = 0.95 (nodes not belonging to plasmid gene-containing clusters have been removed). Viewable with Biolayout Express 3D (http://www.biolayout.org/).

Found at: doi:10.1371/journal.pgen.1001145.s003 (0.03 MB ZIP)

Figure S1 Circular diagram of the R. equi 103S genome (chromosome and virulence plasmid). Outer two rings, coding sequences in the forward and reverse strand colored according to functional class (see Figure S3). Left, R. equi 103S chromosome with ortholog comparison and horizontally acquired (HGT) islands. Ortholog plots from 13 actinobacterial genomes are shown concentrically (outside to inside, from more to less related: R. jostii RHA1, Nocardia farcinica IFM10152, Mycobacterium smegmatis MC2 155, Streptomyces coelicolor A3(2), Mycobacterium tuberculosis H37Rv, Arthrobacter sp. FB24, Corynebacterium glutamicum ATCC 13032, Thermohydula fusca YX, Frankia sp. Ce13, Corynebacterium diphtheriae NCTC 13129, Propionibacterium acnes KPA171202, Bifidobacterium longum NCC2705 and Tropheryma whipplei TW08 27; see Table S13 for accession nos.). HGTV DNA identified by Alien Hunter [92] is shown in red (HGT “archipelagos” 1 and 2 boxed; see Figure S6). The HGTV islands tend to coincide with void areas in the ortholog plots, indicating they are species-specific DNA regions; note that they are regularly distributed across the genome. Inner plots: G+C % (gray) and G+C skew (violet/yellow, origin of replication is clearly detectable). Right, circular diagram of the pVAPA1037 virulence plasmid (not represented to scale); the sap PAI (HGTV-acquired) is indicated by a thick black line. A detailed annotation and analysis of pVAPA1037 has been published elsewhere [8].

Found at: doi:10.1371/journal.pgen.1001145.s004 (0.93 MB PDF)

Figure S2 Pairwise ACT alignments of rhodococcal chromosomes (R. equi 103S, R. jostii RHA1, R. opacus B4 and R. erythropolis PR4); see Figure 1A for interpretation. R. opacus has a large (72.5 Mb) linear chromosome like R. jostii (Table 1). The chromosome of R. erythropolis (6.32 Mb) is circular, as in R. equi.

The four rhodococcal species sequenced to date share a common core of 2,674 orthologs. Mean identity of shared core orthologs between R. equi and: R. opacus, 75.00%; R. erythropolis, 73.6. Between R. jostii RHA1 and: R. erythropolis PR4, 76.88%; R. opacus, 94.97%. The chromosomes of R. jostii and R. opacus are highly homologous and syntenic and share 72% of the coding sequences (CDS). Based on the number of shared orthologs, average percent identity among shared core genes, and overall genome homology, R. equi appears to be phylogenetically equidistant to R. erythropolis, R. jostii and R. opacus, while the last two species are clearly very closely related (see also Figure 1B), R. jostii RHA1 genome published in [10]. R. opacus B4 and R. erythropolis PR4 genomes published online by NITE, the Japanese National Institute for Technology and Evaluation (http://www.nite.go.jp/index-e.html; accession nos. in Table S13).

Found at: doi:10.1371/journal.pgen.1001145.s005 (3.23 MB PNG)

Figure S3 Functional classification of R. equi 103S genome. According to the Ecocyc classification scheme [93]. (A) Functional categories of R. equi 103S genes. “Surface/extracellular proteins” includes products with a signal sequence and/or transmembrane domain not allocated to another main functional category (e.g. central metabolism, degradation of small molecules, regulators, etc.). About 17% of R. equi CDSs correspond to “hypothetical proteins” or “conserved hypothetical” proteins. In addition to the 517 annotation entries as “putative membrane protein”, “integral membrane protein” or “secreted protein”, 28.5% of the R. equi genome products are of unknown function. (B) Functional categories of R. equi 103S secretome. The R. equi secretome comprises 736 CDSs, of which 44.5% encode proteins of unknown function, 20.3% correspond to transporters, 17.1% to lipoproteins, and 10.3% to extracellular enzymes possibly involved in nutrient breakdown and assimilation.

Found at: doi:10.1371/journal.pgen.1001145.s006 (0.17 MB PDF)

Figure S4 Scatter plots of selected functional categories vs genome size (≥4 Mb) of R. equi 103S and 10 other representative Actinobacteria. Data were inferred using the Comprehensive Microbial Resource (http://cmr.jcvi.org/) and the available genomes (Data Release 23.0). See Table S13 for accession nos. Membrane-associated and secreted proteins, as determined from TMHMM and SignalP outputs (see Materials and Methods). The number of regulator per genome has been calculated from keyword parsing of protein annotation. (A) Membrane-associated proteins. (B) Regulators. (C) Secreted proteins. (D) Metabolic proteins.

Found at: doi:10.1371/journal.pgen.1001145.s007 (0.11 MB PDF)

Figure S5 Species-specific gene complements of R. equi 103S, R. jostii RHA1, N. farcinica IFM10152, and M. tuberculosis H37Rv. The Venn diagram shows the number of chromosomal CDSs shared within a particular relationship (in brackets those unique to that relationship) as determined by ortholog comparisons (reciprocal FASTA best hits). Below the name of each species, the total number of genes in the genome is shown. The pie charts show the functional classification of the CDSs unique to each species and the shared common core.

Found at: doi:10.1371/journal.pgen.1001145.s008 (0.35 MB PDF)
Figure S6  Genetic structure of the two large chromosomal HGT regions in *R. equi* 103S. The position of these regions on the chromosome is indicated in Figure S1. Functional categories of the genes are indicated in color code as in Figure S3. Alien Hunter [92] HGT hits are indicated as black bars in the center. HGT region 1 (positions 1,684,996-1,775,619, REQ16110-770) encompasses 132 CDSs with a diversity of functional categories but mostly involved in metabolism. It also includes three of the 14 pseudogenes found on the *R. equi* 103S chromosome. The mosaic structure of these regions and the diversity of source species, as indicated by reciprocal BLASTP best-hit analysis, suggest they are a composite of several independent HGT events rather than the result of a single “en block” acquisition.

Found at: doi:10.1371/journal.pgen.1001145.s009 (1.14 MB PNG)

Figure S7  *R. equi* nutrition and metabolism. (A) Carbon source utilization. Growth assays of *R. equi* 103S in mineral medium (MM) [19] at 37°C. MM was supplemented (unless otherwise stated) with 20 mM of the indicated carbon sources and bacterial growth was monitored at OD600 every 30 min in a Fluostar Omega plate reader (BMG Labtech). Growth was detected only with lactate and acetate (mean of three experiments ±SD). Chemicals were purchased from Sigma. The nutritional and metabolic profile of *R. equi* (and its susceptibility to various chemicals and antibiotics) was initially investigated with Phenotypic MicroArray (PMA) screens [15]. In the PMA plates PM1 and PM2 (carbon sources), certain substrates (e.g. glucose, arabinose, ribose, xylose, D-glucosamine, dihydroxyacetone and lyssole) sometimes give false positive results due to abortive dye reduction (source: Michael Ziman, Biolog Inc). Experiments in MM confirmed that *R. equi* 103S does not utilize these substrates as sole carbon source. (B) ACT pairwise comparison of the thiamine biosynthesis gene clusters *thiCD* and *thiGSOE* in *R. equi* 103S and environmental rhodococci. In *R. equi*, the *thiC* gene has been replaced by an HGT region (black bar in the center) encoding proteins of unknown function. (C) Thiamine auxotrophy. Growth assay of *R. equi* 103S in 20 mM lactate MM medium. HMP, 4-amino-5-hydroxyethylpyrimidine phosphate (5% v/v of the crude preparation described in [94]). Negative control: no supplement. Most (> 90%) of the *R. equi* strains displayed thiamine auxotrophy. Experimental conditions as described in the legend to (A). (D) Diagram of the rhodococcal thiamine biosynthesis pathway. The *thiCD* genes are required for the production of 4-amino-5-hydroxyethyl-2-methylpyrimidine phosphophosphate; *thiG-SOM* are involved in the generation of 4-methyl-5-(β-hydroxyethyl) thiazole phosphate, the second substrate required for the *thiE*-mediated synthesis of thiamine phosphate. Thiamine phosphate is ultimately phosphorylated by the product of the *thl* gene, to generate the biologically active thiamine pyrophosphate. As shown in (C), HMP did not support *R. equi* 103S growth, indicating that the thiamine synthetic pathway of *R. equi* 103S is also functionally affected downstream from *thlC*.  

Found at: doi:10.1371/journal.pgen.1001145.s010 (0.61 MB PDF)

Figure S8  Species-specific metabolic gene complements of *R. equi* 103S, *R. jostii* RHA1, *N. farcinica* IFM10152, and *M. tuberculosis* H37Rv. Determined by ortholog comparison (reciprocal FASTA best hits). As the functional categories used for the annotation of the four genomes were not directly comparable, we first extracted the metabolism-related CDSs manually, on the basis of their predicted function. The Venn diagram shows the number of CDSs shared within a particular relationship (in brackets those unique to that relationship). Below the name of the species, the total number of metabolic genes present in the genome is shown. See Table S5 for paralogy analysis of the species-specific metabolic gene complements.

Found at: doi:10.1371/journal.pgen.1001145.s011 (0.36 MB PNG)

Figure S9  Optimal growth pH of *R. equi* 103S. Phenotype MicroArray [15] output of the relevant wells of plate PM10. Incubation was for 48 h at 37°C in an OmniLog instrument with readings taken every 15 minutes. Data were analyzed with OmniLog PM software. Consensus phenotypes for at least two replicates were determined based on the area difference under the kinetic curve of dye formation. Reported optimal pH values for other rhodococcal species: *R. suturensis* 7.0 [95], *R. koreensis* 7.0–7.8 [96], *R. kroppenstedtii* 8.0 [97], *R. faurii* 7.5–7.8 [98], *R. tytonensis* 7.0 [99], *R. percolatus* 7.0–7.5 [100], *R. pyridinivorans* 7.5–8.5 [101], *R. talsmanensis* 5.5–8.5 [102], *R. yunnanensis* 7.0–8.0 [103].

Found at: doi:10.1371/journal.pgen.1001145.s012 (0.23 MB PNG)

Figure S10  Examples of antibiotic resistance determinants located at the same chromosomal position in *R. equi* and two environmental *Rhodococcus* spp. Homologous resistance determinants indicated by yellow stripes in the ACT alignments.

Found at: doi:10.1371/journal.pgen.1001145.s013 (0.49 MB PNG)

Figure S11  Virulence-related loci of *R. equi* 103S. (A) PE/PPE locus and corresponding chromosomal regions in *R. jostii* RHA1, *R. erythropolis* PR4, *N. farcinica* IFM10152 and *M. tuberculosis* H37Rv. Arrows in ACT alignments indicate PE and PPE genes. The PE gene is of the “short” subclass (only a conserved N-terminal PE module of 99 to 102 residues); the PPE gene is of the “unique C-terminal domain” subclass [104]. The *R. equi* PE/PPE locus is inserted at the same chromosomal position in the nonpathogenic *Rhodococcus* spp. and in *N. farcinica*; no PE/PPE genes are present at the corresponding chromosomal region of *Meb*, other mycobacteria and corynebacteria, indicating this PE/PPE locus is specific to the *Nocardinae* within the *Corynebacterinae*. The PE/PPE genes are fused in *R. jostii* RHA1. (B) Sortase HGT islands *str1* and *str2* of *R. equi* 103S. ACT comparisons of *str1* (above) and *str2* (below) and corresponding regions of *R. jostii* RHA1 and *R. erythropolis* PR4. Alien Hunter [92] outputs indicated as black bars in the center. *str1* is unique to *R. equi* among the sequenced *Rhodococcus* spp., including *R. opacus* (B4) (not shown). The *str2* island is conserved in *R. erythropolis* but at a different chromosomal location and encoding only one of the two putative sortase substrates (*surface protein RER_38400*, which like its *R. equi* homolog REQ27480 contains an LPVTG sorting motif). Apart from a serine peptidase encoded by the *esx* locus (REQ35490), no proteins with the typical hallmarks of sortase substrates, i.e. a C-terminal membrane-spanning region preceded by a sortase recognition motif LPXTG, or a variant thereof [105], are encoded outside the two *str* islands.

Found at: doi:10.1371/journal.pgen.1001145.s014 (0.75 MB PDF)

Figure S12  Network analysis of *R. equi* microarray expression data. (A) Detail of the network graph of Figure 5A showing the web of functional linkages (edges) between the yap PAI-coregulated cluster (red nodes) and direct neighbor clusters (green nodes, plasmid backbone cluster; other clusters represented in different colors; individual directly connected nodes are in gray regardless of whether they belong to a larger cluster; chromosomal nodes are
represented as spheres, plasmid nodes as cubes). All other nodes have been removed. Predominant functional classes among neighbor clusters (n = 129 nodes): Central and energy metabolism (27.1%), Membrane-associated/surface proteins/transporters (23.3%), Hypothetical proteins (18.6%), Regulators (9.3%). Degradation of small molecules 7.75%. Metabolism-related products encoded by direct neighbor nodes include enzymes of the shikimate pathway/biosynthesis of aromatic amino acids (prephenate dehydratase gene: REQ0960, prephenate dehydratase gene: REQ0720); porphyrin metabolism (magnesium chelatase gene: REQ18110) and cobalamin biosynthesis (uroorphyrinogen-I-III C-methyltransferase gene: REQ2960), CoB homolog (REQ28830); synthesis of cysteine, activated sulfate (cydD, G, D, E/M, Q and N/C homologs); and mycophytol (mycophytol ligase MshC gene: REQ2990), urease (UreA, C, D, F, and G homologs), and nitrite reductase NirB1 (REQ2930). (B) Representative expression profiles of the plasmid gene-containing clusters identified with r = 0.85 Pearson correlation threshold (see Table S11). Maroon lines, vap PAI-coregulated cluster (red and yellow nodes in Figure 5A); green lines, plasmid backbone cluster (green nodes in Figure 5A). The individual profiles of three biological replicates per test condition are plotted. Note that the vap PAI-coexpressed cluster, which includes chromosomal genes, is activated by both plasmid and temperature (37°C) whereas the plasmid backbone cluster is expressed constitutively in the same conditions. Common reference: average signal of 103S at 37°C pH 6.5.

Found at: doi:10.1371/journal.pgen.1001145.s015

Table S1 Statistics of horizontal gene acquisition (HGT) in actinobacterial chromosomes. HGT DNA was identified with the Alien Hunter program (http://www.sanger.ac.uk/Software/anal-.../). Most independent acquisitions of horizontally transferred DNA segments identified with BLASTClust (see Table S12).
online by NITE, the Japanese National Institute for Technology and Evaluation (http://www.nite.go.jp/index-e.html).

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Table S14 Oligonucleotide primers used for mutant construction and complementation. SpeI, XbaI and EcoRV restriction sites used for the cloning of PCR products are underlined.

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References


