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Phylogeography of *Toxoplasma gondii* Points to a South American Origin

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41 **Abstract**

42 *Toxoplasma gondii*, a protozoan found ubiquitously in mammals and birds, is the

43 etiologic agent of toxoplasmosis, a disease causing substantial Public Health burden

44 worldwide, including about 200,000 new cases of congenital toxoplasmosis each year.

45 Clinical severity has been shown to vary across geographical regions, with South

46 America exhibiting the highest burden. Unfortunately, the drivers of these

47 heterogeneities are still poorly understood, and the geographical origin and historical

48 spread of the pathogen worldwide are currently uncertain. A worldwide sample of 168 *T.*

49 *gondii* isolates gathered in 13 populations was sequenced for five fragments of genes

50 (140 single nucleotide polymorphisms from 3,153 bp per isolate). Phylogeny based on

51 Maximum likelihood methods with estimation of the time to the most recent common

52 ancestor (TMRCA) and geostatistical analyses were performed for inferring the putative

53 origin of *T. gondii.* We show that extant strains of the pathogen likely evolved from a

54 South American ancestor, around 1.5 million years ago, and reconstruct the subsequent

55 spread of the pathogen worldwide. This emergence is much more recent than the

56 appearance of ancestral *T. gondii*, believed to have taken place about 11 My ago, and

57 follows the arrival of felids in this part of the world. We posit that an ancestral lineage of

58 *T. gondii* likely arrived in South America with felids and that the evolution of oral

59 infectivity through carnivorism and the radiation of felids in this region enabled a new

60 strain to outcompete the ancestral lineage and undergo a pandemic radiation.

61 **Keywords:** *Toxoplasma gondii*, phylogeography, Maximum likelihood phylogeny, time

62 to the most recent common ancestor (TMRCA), genetic diversity

63

1. Introduction

Toxoplasmosis imposes a substantial disease burden across the world. Serological studies demonstrate its presence in virtually every country, with seroprevalence exceeding 60% in some parts of South America, Africa, and South-East Asia (Pappas et al., 2009). While asymptomatic in most patients, toxoplasmosis is a major cause of uveitis in immunocompetent patients and a potentially life-threatening illness in immunocompromised patients and fetuses (Montoya and Liesenfeld, 2004). Congenital toxoplasmosis alone has a yearly global incidence of about 200,000 cases, causing a burden exceeding 1 million disability-adjusted life year (DALYs) (Torgerson and Mastroiacovo, 2013). The overall disease burden attributable to all forms of toxoplasmosis is certainly far greater, and highest in South America where ocular toxoplasmosis is unusually frequent and severe (Glasner et al., 1992; de-la-Torre et al., 2008; Gilbert et al., 2008; Torgerson and Mastroiacovo, 2013).

The extent to which host parasite genetics, host immune status, and exposure rate contribute to the increased severity of toxoplasmosis in South America is unclear, but differences in the genetic makeup of *T. gondii* strains are likely to play a major role (Khan et al., 2006; Gilbert et al., 2008). In North America, Europe, Africa, and Asia, the population structure of *T. gondii* is dominated by a few prevalent clonal strains, whereas much greater genetic diversity is seen in tropical South America where the populations lack sign of recent genetic bottleneck and clonal structure seen in the other parts of the world (Shwab et al., 2014; Lorenzi et al., 2016).

86 Unfortunately, the drivers of the pathogen's genetic diversity are still poorly understood,

87 and the origin of extant lineages of *T. gondii* remains controversial. Recent work

88 suggested a potential South American origin, while another study advocated that co-

89 migration with felids led to the divergence of South American strains from pre-existing

90 North American ones (Lehmann et al., 2006; Khan et al., 2007). The estimation of the

91 time to the most recent common ancestor (TMRCA) of extant lineages is also disputed,

92 with estimates ranging from 150,000 to 10^7 years (Morrison, 2005; Khan et al., 2007).

93 In the present study, using a large collection of genetic sequences of *T. gondii* sampled

94 worldwide, we reconstructed the phylogeography of *T. gondii* as a basis to address the

95 controversial questions regarding the evolution of this parasite and its geographical

96 origin.

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98 **2. Materials and Methods**

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100 **2.1. Collection of *T. gondii* strains and selection of markers**

101 A total of 168 *T. gondii* strains from 13 populations collected worldwide in North

102 America, South America, the Caribbean, Europe, Asia, and Africa, were used in this

103 study (Supplementary information and S1 Table). Our collection was specifically

104 designed to ensure extensive geographic coverage of strains clustered in true

105 populations, and includes a large number of strains from Africa and China, which were

106 so far underrepresented or absent in the previous studies (Lehmann et al., 2006; Khan

107 et al., 2007). A preliminary genetic analysis with 15 microsatellite markers (Ajzenberg et

108 al., 2010) was performed to exclude clones of strains sampled in the same area. Each

109 isolate was sequenced in both directions for five markers (*GRA6, GRA7, SAG3, UPRT1*

110 and *UPRT7*) that had the highest polymorphic rates after a preliminary analysis of

111 genetic polymorphism of 30 fragments of genes retrieved from GenBank and ToxoDB

112 (Supplementary information and S2 Table).

113
114 **2.2. Phylogenetic analysis.**

115 *Hammondia hammondi* is the most closely parasite related to *T. gondii* and was used

116 as an outgroup in phylogenetic analyses. Sequences of the *H. hammondi* strain H.H.34

117 corresponding to *T. gondii* *GRA6*, *GRA7*, *SAG3*, *UPRT1* and *UPRT7* sequences were

118 retrieved from GenBank and ToxoDB, and aligned with MUSCLE (Edgar, 2004). We

119 used *ape* and *pegas* R packages to extract haplotypes and build phylogenetic trees with

120 three distance-based methods: NJ, BIONJ, and FastME which were used as starting

121 trees for the ML analyses. Maximum likelihood phylogenetic analyses were performed

122 with the R package *phangorn* using four partitions of the sequence data by crossing two

123 criteria: exons *vs.* introns on one side, and *GRA6*, *GRA7* and *SAG3 vs. UPRT1* and

124 *UPRT7* on the other (Supplementary information). A GTR + Γ + I model was used with

125 parameters that could vary among data partitions. The different model fits performed

126 with *phangorn* were compared with AIC. The three trees obtained with the distance-

127 based methods were all tested as initial trees.

128
129 **2.3. Geostatistical analyses.** We used the same geostatistics approach for inferring

130 the putative origin of *T. gondii* as previously used for uncovering the origins of *P.*

131 *falciparum* (Tanabe et al., 2010, 2013a, 2013b; Mita and Jombart, 2015). We implemented

132 this approach in the R package *geoGraph* (http://thibautjombart/geograph), in which we

133 provided extensive documentation replicating the analyses described below using

134 publicly available data (Cann et al., 2002). The method implemented in *geoGraph* relies

135 on the idea that migration events result in successive bottlenecks which reduce the

136 genetic diversity within populations as they are located further away from the origin

137 (Tanabe et al., 2010). Accordingly, we expect to observe a negative correlation between

138 within-population diversity and the distance from the origin. While in practice the true

139 origin is often unknown, one can infer the most plausible origin by assessing this

140 relationship for a number of candidate origins, and retaining the origin yielding the

141 strongest negative correlation. This method requires two types of distances, genetic and

142 spatial, to be computed. Here, the genetic diversity was mostly structured by varying

143 frequencies of a small number of haplotypes within populations (S3 Table and Fig 1).

144 Therefore, we used haplotype richness (i.e. number of distinct haplotypes) as a

145 measure of diversity within populations. Spatial distances through landmasses were

146 computed using *geoGraph*. The package models movements on the surface of the

147 Earth using a spherical, pseudo-regular grid with approximately 40,000 nodes. Each

148 node possesses an 'habitat' attribute, here used to distinguish landmasses from seas.

149 Shortest path between locations were computed using the dijkstra algorithm (Jungnickel,

150 2013) implemented in the R package RBGL (Edmonds et al., 2006; Carey et al., 2011). To

151   define candidate origins, 1,800 combinations of regularly spaced longitudes and

152   latitudes were used to cover the globe, which resulted in 433 non-redundant locations

153   on landmasses on the grid used by *geoGraph*. For each location, the shortest path

154   through each sampled population was identified, and the corresponding distance

155   computed in kilometers. These distances were then used to assess patterns of

156   decrease of genetic diversity from the putative origin using simple linear regression. The

157   most likely origin was inferred as the location which yielded the most negative

158   correlation between geographic distances and haplotype diversity within populations.

159

160   **2.4. Time to the most recent common ancestor (TMRCA).** In order to estimate the

161   time to the most recent common ancestor (TMRCA) of *T. gondii*, we used two different

162   approaches: a simple molecular dating method based on the divergence with *H.*

163   *hammondi* which is estimated to be around 11 My, and a coalescent approach using the

164   expectation of TMRCA which is equal to twice the effective population size (Ne). Both

165   approaches need an estimate of the mutation rate (μ), and the second one also needs

166   an estimate of the population parameter θ (= 2 μ Ne). We estimated μ for the non-

167   coding introns of *UPRT1* and *UPRT7*. We did two neutrality tests: D's Tajima and the

168   R2 test. We calculated a standard-error of this estimate using the variance of ratio of

169   two random variables, here the number of mutations per site and twice the time of

170   divergence. The former was estimated with a Tamura-Nei distance with its associated

171   variance, and the latter was 11 My with an arbitrary sd = 1 My. The population

172   parameter θ was estimated in two ways: with a Markov chain Monte Carlo (MCMC)

173   approach as implemented in the R package *coalescentMCMC*, and with the nucleotide

174   diversity (π) calculated with *pegas*. Both ways calculate the standard-error of the

175   estimate of θ. In the end, three estimates of TMRCA were obtained with their respective

176   95% confidence interval (CI).

177

178   **3. Results**

179   **3.1. Genetic diversity.**

180   Sequences of the five markers represented a total of 3,153 bp per isolate, including 140

181   variable sites. Without taking into account sites with gaps, 26, 30, 27, 32, and 25 SNPs

182   were identified in the *GRA6* (607 bp), *GRA7* (677 bp), *SAG3* (638 bp), *UPRT1* (574 bp),

183   and *UPRT7* (657 bp) genes, respectively (S4 Table and S1 Fig). Strains from the

184   Caribbean, Guiana shield, Northeast Brazil, and Southeast Brazil showed more

185   sequence polymorphism with 65, 90, 59, and 65 SNPs, respectively (S3 Table).

186   Polymorphism was lower in the African and European populations with a number of

187   SNPs ranging from one to 39. Polymorphism was intermediate in the Asian and North

188   American populations with 41, 60, 47, and 51 SNPs in Turkey, China, Minnesota, and

189   Pennsylvania, respectively.

190 Data concatenation revealed 60 haplotypes. The number of haplotypes ranged from

191 four in Europe to 32 in South America. Of the 32 genotypes in the 44 strains from South

192 America, 29 were endemic in South America whereas only three were common in other

193 populations (one in the Caribbean, one in Africa, and one both in Asia and Africa). In

194 contrast, of the four genotypes in the 34 strains from Europe, three were common in

195 other populations (one in Asia and Africa, one in North America, Asia and Africa, and

196 one in the Caribbean, North America, Asia and Africa) and the unique genotype differed

197 by only one SNP from the one common to North America, Asia, and Africa (S5 Table).

198 The higher values of haplotype diversity, estimated from concatenation of the five

199 markers by the number of haplotypes divided by the number of isolates, were observed

200 in South America and the Caribbean, whereas the lower values were observed in

201 Europe, Asia, and Africa (S3 Table). Haplotype diversity was intermediate in North

202 America. Overall the highest genetic diversity was found in South-America.

203

204 **3.2. Phylogeny of *T. gondii* strains**

205 Preliminary analyses of genetic diversity (Supplementary information, S6 Table and S2

206 and S3 Figs.) revealed different mutation patterns and rates of evolution between

207 coding and non-coding segments, and for the two *UPRT* genes compared to the others.

208 Accordingly, we defined four partitions of the sequence data crossing these two

209 categories, and reconstructed separate phylogenies by maximum likelihood (ML) to

210 investigate potential phylogenetic incongruence (Som, 2015). Statistical tests and

211 examination of model selection criterion (AIC) revealed the existence of distinct

212 topologies (Fig. 1), suggesting that these sequence partitions have undergone different

213 evolutionary histories and selective pressures. Interestingly, only South American

214 strains were consistently placed at a basal position (close to the root) in all topologies.

215 To investigate this pattern further and identify the common evolutionary history of these

216 genes, a consensus topology was inferred from the four ML-partitioned topologies (Fig.

217 2). This new tree supported the more ancestral status of South American isolates, with

218 35 out of 44 samples located at the root of the tree. However, as expected in the

219 presence of conflicting phylogenetic signal, this tree was only partially resolved, and

220 strains from other locations (China: 12 samples; Africa: 7 samples) also belonged to the

221 large basal multifurcation.

222

223 **3.3. On the geographic origin of *T. gondii***

224 As a complementary analysis, we used a geostatistical approach previously employed

225 for identifying the origin of *Plasmodium falciparum*, the main etiologic agent of malaria

226 (Tanabe et al., 2010, 2013b; Mita and Jombart, 2015). This method identifies likely

227 geographic origins as the locations from which patterns of decrease in genetic diversity,

228 expected to be observed due to repeated migration and founder effects, are most

229 consistent (Tanabe et al., 2010). Because of the low level of polymorphism observed in

230 the sequenced genes and the highly clonal nature of *T. gondii*, haplotype richness was

231 used as a measure of genetic diversity within populations (S3 Table). Testing a large

232 number of hypothetical origins across the world, this approach identified South America,

233 and more specifically Colombia as the most likely origin (r=-0.81, p=0.9x10^{-4}, Fig. 3).

234 While substantial uncertainty remains about the exact location, this analysis brings

235   strong support to a South American origin for *T. gondii* suggested by the phylogenetic

236   approach. Our results further suggest that *T. gondii* initially spread through the

237   Americas and then colonized Asia and Europe via the Bering Strait, before entering

238   Africa through two different migration routes (Fig. 3).

239

240   **3.4. Time to the most recent common ancestor (T$_{MRCA}$) of *T. gondii*.**

241   To understand the processes which may have led to a pandemic radiation of *T. gondii*

242   from South America, the emergence of this ancestral, highly successful lineage has to

243   be dated. To this end, we derived estimates of time to the most recent common

244   ancestor (MRCA) of the extant strains using standard molecular approaches. While

245   confidence intervals indicated substantial uncertainty, overall results suggest that the

246   MRCA of *T. gondii* appeared around 1.5 My ago (Table 1). This emergence is much

247   more recent that the existence of *T. gondii* itself, estimated to have diverged from its

248   closest ancestor *Hammondia hammondi* some 11 My ago (Morrison et al., 2004).

249

250   **4. Discussion**

251

252   A major event occurred in the evolutionary history of *T. gondii* which led to a selective

253   sweep about 1.5 My ago. We hypothesized that an ancestral form of *T.gondii* was

254   introduced in South America through the migration of Felidae after the emergence of the

255   Isthmus of Panama about 2 to 3 My ago, at the end of Pliocene (O'Brien et al., 2008). It is

256   believed that Felidae species quickly expanded after their arrival and diversified into the

257   "ocelot" lineage in South America. Interestingly the Muridae, potential intermediate

258   hosts for *T. gondii*, also showed extensive diversification in South America with the

259 appearance of several genera (Webb, 2006) around the same time. As previously

260 suggested (Webb, 2006), we posit that this expansion, diversification and mixing of host

261 populations certainly resulted in similar processes in their parasites and favoured the

262 accumulation of genetic diversity in *T. gondii*, which eventually led to a selective sweep

263 by a highly successful mutant lineage.

264

265 The selective pressures underlying this selective sweep can be debated. Previous work

266 attributed this radiation to the emergence of transmission through carnivorism (i.e., oral

267 infectivity of tissue cysts) between intermediate hosts in clonal strains 10,000 years ago

268 (Su et al., 2003). However, oral infectivity was shown to be also a trait of many South

269 American strains (Carme et al., 2002; Khan et al., 2007). Because South American strains

270 were the first to diverge from the MRCA, it is likely that transmission by carnivorism

271 evolved earlier than the apparition of clonal lineages. This trait conferred a better

272 transmission of the current form of *T. gondii* which likely outcompeted the ancestral form

273 arriving in South America with Felidae. The transmission of *T. gondii* between its

274 different hosts would allow some genotypes to migrate to North America, then to go

275 through the Bering Strait to colonize Asia, Europe and Africa. The current population

276 structure of *T. gondii* with a predominance of a few successful clonal strains in Africa,

277 Asia and Europe, is likely to be the consequence of the recent expansion of the

278 domestic cat, an Old World species until the sixteenth century, that tremendously

279 amplified a specific subset of pre-adapted genotypes (Müller and Howard, 2016).

280

281 In addition to being the likely origin of modern *T. gondii* strains, South America also

282 suffers from the highest burden of toxoplasmosis. Prevalence, incidence, and severity of

283 acquired and congenital ocular toxoplasmosis (OT) in some areas of Brazil, Colombia,

284 and Argentina are considerably higher than anywhere else, which makes OT a genuine

285 public health issue in South America (Glasner et al., 1992; de-la-Torre et al., 2008; Gilbert et

286 al., 2008; Rudzinski et al., 2016). Because South America is also the hotspot of *T. gondii*'s

287 genetic diversity, it has been hypothesized that severe forms of toxoplasmosis may be

288 the consequence of poor adaptation of the human host to the unusual diversity of

289 strains in this part of the world, resulting in impaired immune response and, thus, a

290 more aggressive disease (Khan et al., 2006; Gilbert et al., 2008; Demar et al., 2012;

291 de-la-Torre et al., 2013; Rudzinski et al., 2016). The societal and economic costs of

292 care for symptomatic cases of congenital toxoplasmosis can be considerable but the

293 cost-effectiveness of national routine prenatal screening and treatment program are still

294 debated (Wallon et al., 1999; Jones et al., 2014). There is a need for randomized placebo-

295 controlled trials to help determine the effectiveness of these interventions.

296

297 **5. Conclusion**

298 Our reconstruction of *T. gondii*'s phylogeography provides a new framework for

299 understanding patterns of genetic diversity in sampled populations of the parasite, and

300 for predicting diversity in unsampled locations. Because genetic diversity seems to

301 impact directly the severity of the disease, our results can be used as a basis for

302 explaining geographic heterogeneities in disease burden, and identifying priority targets

303 for potential future interventions.

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Table 1. Estimates of the time to the most recent common ancestor (TMRCA) of
Toxoplasma gondii **with three different methods on the introns of** *UPRT* **genes.**

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Method	TMRCA (Ma)	[95% CI]
Molecular dating	1.59	[0.00–3.46]
Coalescent	1.26	[0.94–1.57]
Nuc. div. (π)	1.20	[0.00–2.44]

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484   Nuc. div.: nucleotide diversity.
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