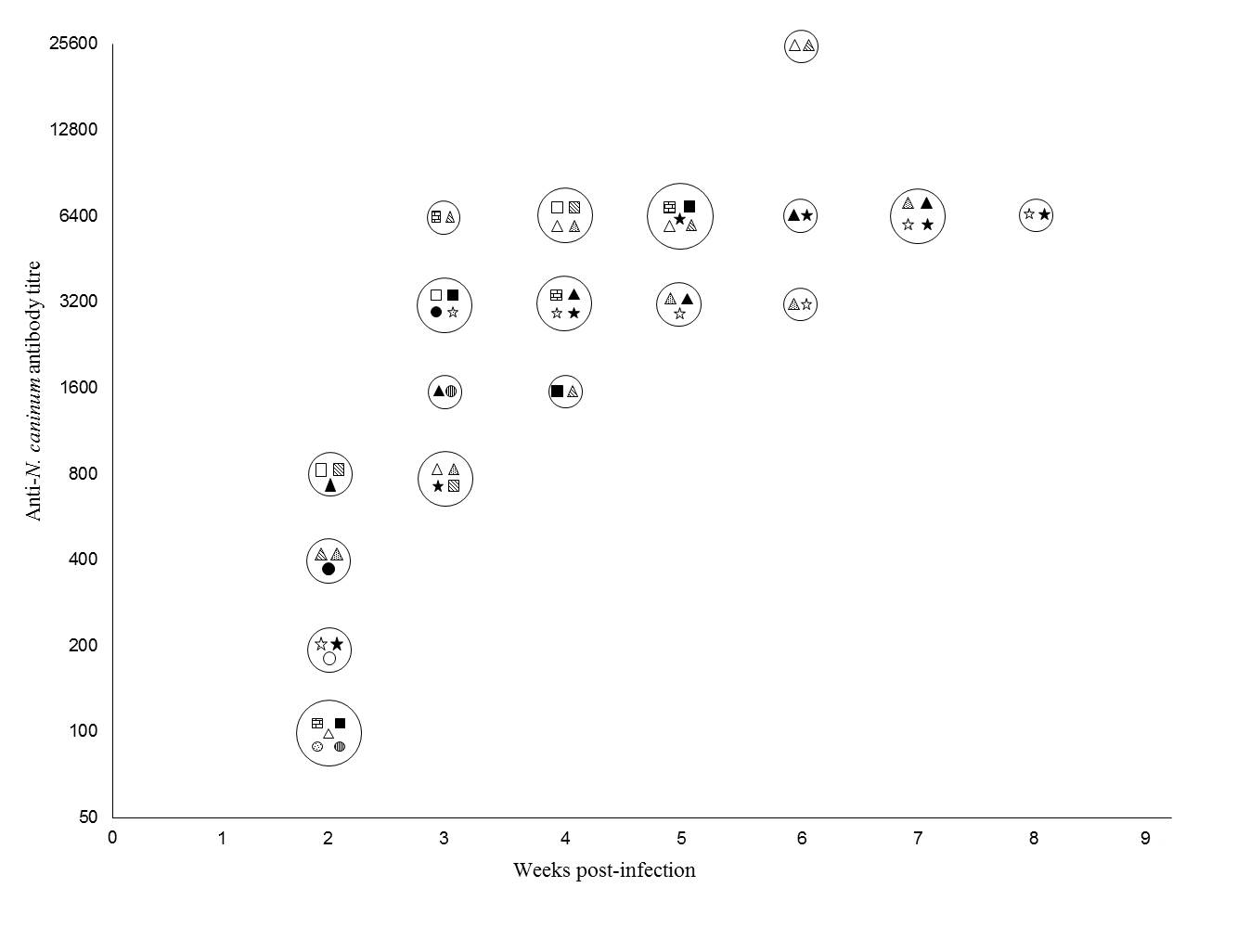
**Table S1.** Excretion of *Neospora caninum* oocysts by the dog

bioassayed during the experimental period.

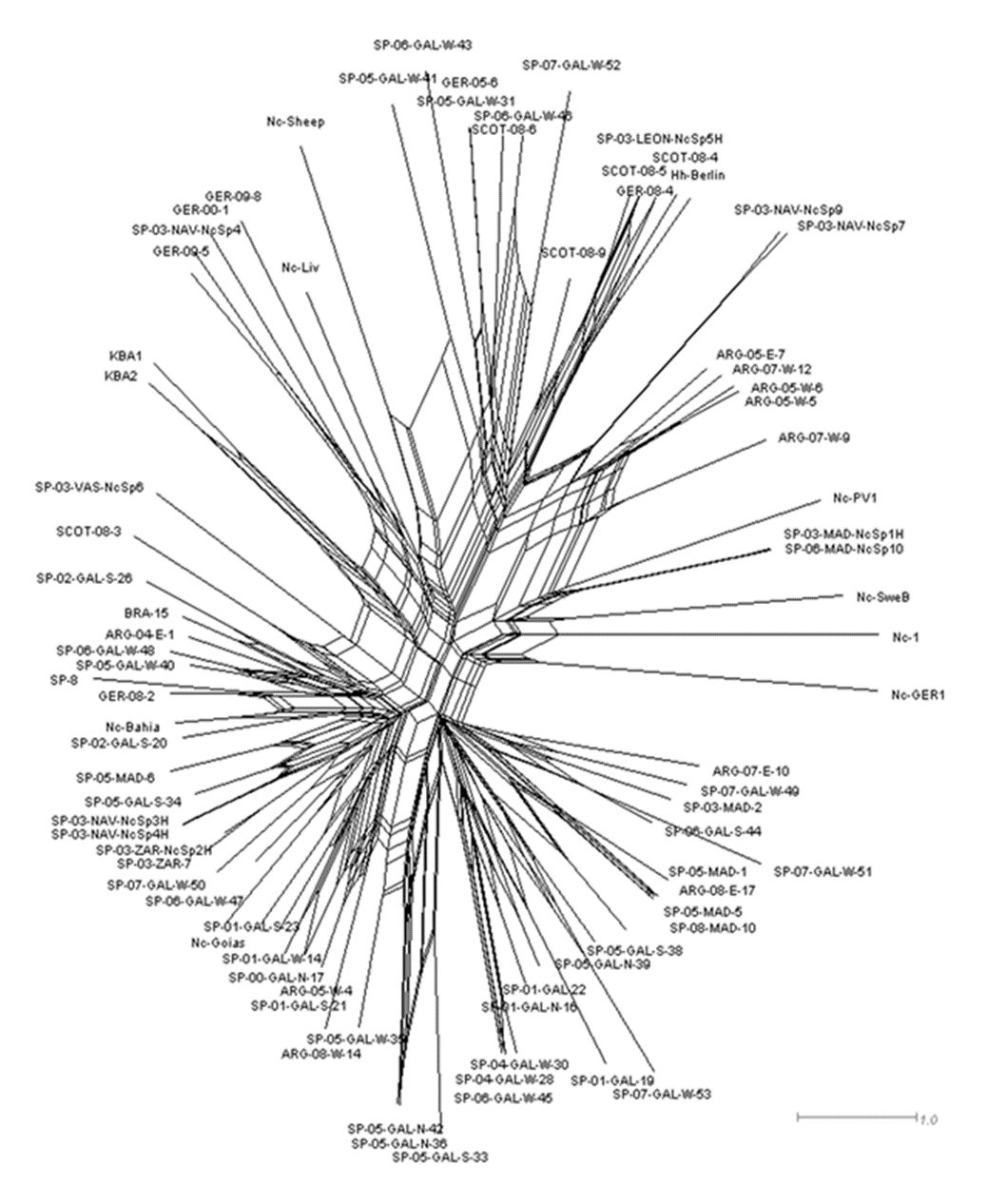
|  |  |  |  |
| --- | --- | --- | --- |
| **Days post inoculation** | **Amount of faeces/day (g)** | **N. of oocysts/g** | **Total of oocysts/ day** |
| 1 | 110 | 11 | 1210 |
| 2 | 102 | 15 | 1530 |
| 3 | 107 | 151 | 16157 |
| 4 | 122 | 34 | 4148 |
| 5 | 95 | 946 | 89870 |
| 6 | 99 | 25 | 2475 |
| 7 | 110 | 27 | 2970 |
| 8 | 156 | 53 | 8268 |
| 9 | 140 | 23 | 3220 |
| 10 | 100 | 122 | 12200 |
| 11 | 139 | 11 | 1529 |
| 12 | 90 | 2 | 180 |
| 13 | 139 | 5 | 695 |
| 14 | 138 | 2 | 276 |

**Fig. S1.** Titres of anti-*N. caninum* IgG antibodies in fourteen gerbils that were orally challenged with 200 oocysts of the isolate NC-SP1. Two gerbils were euthanised seven days PI (IFAT < 50). Each gerbil is represented by a symbol inside the circles.

**Table S2.**  *Neospora caninum* tissue distribution in gerbils that were orally challenged with 200 oocysts of the isolate NC-SP1, based on DNA detection\*.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Weeks post-inoculation** | | | | | | | |
| **Tissues collected** | **1st** | **2nd** | **3rd** | **4th** | **5th** | **6th** | **7th** | **8th** |
| Blood |  |  |  |  |  |  |  |  |
| Skeletal muscle |  |  |  |  |  |  |  |  |
| Tongue |  |  |  |  |  |  |  |  |
| Liver |  |  |  |  |  |  |  |  |
| Spleen |  |  |  |  |  |  |  |  |
| Diaphragm muscle | • |  |  |  |  |  |  |  |
| Reproductive system | • |  |  |  |  |  |  |  |
| Lung | • | • |  |  |  |  |  |  |
| Intestine |  | • |  |  |  |  |  |  |
| Heart |  | • |  |  |  |  |  |  |
| Kidney |  |  | • |  |  |  |  |  |
| Mesenteric lymph node | • | • | • | • |  |  |  |  |
| Eye |  | • |  |  |  | • |  |  |
| Spinal cord |  | • | • | • |  | • | • | • |
| Brain | • | • | • | • | • | • | • | • |

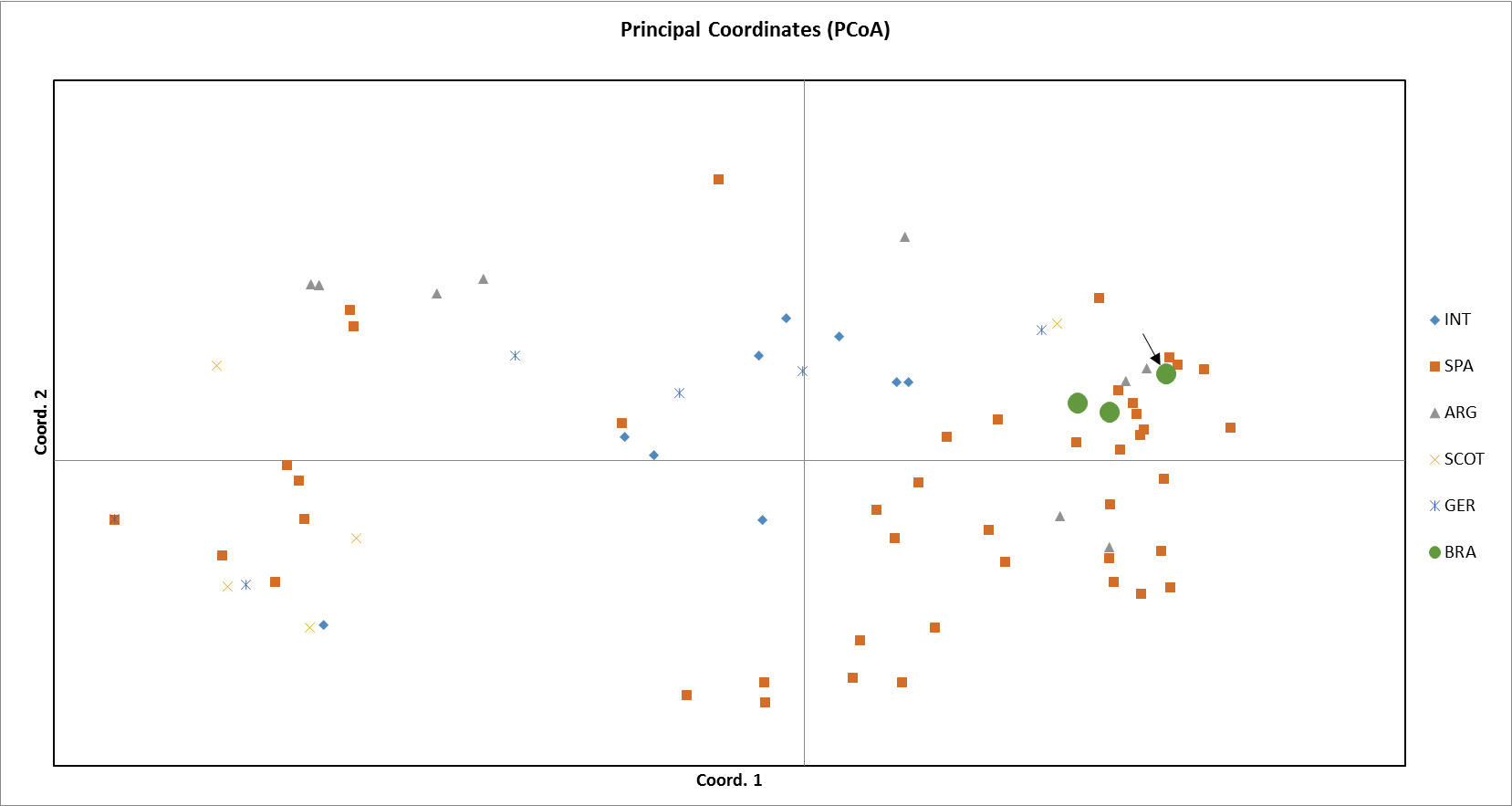
\* PCR assays using the primers Np6 plus and Np21 plus.



**Fig. S2.** Phylogenetic analysis showing genetic relationships of the *Neospora caninum* isolates and NC-SP1 isolate (BRA-15).

**Table S3.** Principal Coordinates Analysis (PCoA)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **PCoA via Covariance matrix with data standardization** | | | | | **No. of samples by population** | | | | | |
| **Data Sheet** | GD (2) | |  |  | **INT** | **SPA** | **ARG** | **SCOT** | **GER** | **BRA** |
| **Data Title** | ALLELE FREQ | |  |  |  |  |  |  |  |  |
| **No. Samples** | 82 | | **No. Pops.** | 6 | 10 | 49 | 10 | 5 | 6 | 2 |
| **Percentage of variation explained by the first 3 axes** | | | | |  |  |  |  |  |  |
| **Axis** | | **1** | **2** | **3** |  |  |  |  |  |  |
| **%** | | 15,28 | 8,38 | 7,01 |  |  |  |  |  |  |
| **Cum %** | | 15,28 | 23,66 | 30,68 |  |  |  |  |  |  |



INT: Reference strains; SPA: Spain; ARG: Argentina; SCOT: Scotland; GER: Germany; BRA: Brazil.

**Fig. S3.** Population structure based on principal coordinate analysis (PCA).