

The social parasite *Phengaris (Maculinea) nausithous* affects genetic diversity within *Myrmica rubra* host ant colonies

G. Solazzo, R. F. A. Moritz, J. Settele

Abstract Evolutionary theory predicts that high genetic variation maintains plasticity in a species' response to parasite pressure. However, higher genetic diversity might also cause easier infiltration by social parasites, because odour diversity is high and nest-mate recognition poor. Here we test if the obligate myrmecophile Lycaenid butterfly *Phengaris nausithous*, a parasite of colonies of the highly polygynous ant *Myrmica rubra* causes local adaptation by enhancing genetic variance in parasitized versus non parasitized ant populations. *M. rubra* colonies from six infested and three uninfested sites were assayed at five microsatellite loci to quantify genetic variation. Our results reveal isolation by distance and a significantly enhanced intracolony variance due to the parasite pressure.

Keywords Social parasites · *Myrmica* · Co-evolution · Monogyny · Polygyny · Host resistance

Introduction

Caterpillars of large blue butterflies *Phengaris (Maculinea)* Doherty 1891, are obligate myrmecophiles and need to be adopted into *Myrmica* Latreille 1804 colonies to complete their developmental cycle (Thomas and Settele 2004). After the hatching the caterpillar feeds on the foodplant, where the egg had been laid and starts its development up to the 4th larval instar. The 4th larval stage leaves the foodplant and falls to the ground where *Myrmica* ant workers need to find the larvae and transport them to the nest where they are adopted into the colony to pupate and eventually leave the nest as an imago. These social parasites impose a cost on the colony because the larvae feed by trophallaxis by workers or feed on the brood of the ants, which can even result in co-evolutionary arms races as in *P. alcon* Denis and Schiffermüller 1775 (Als et al. 2001, 2002; Nash et al. 2008) or *P. nausithous* Bergsträsser 1779 (Solazzo et al. 2013), with their specific host ant species.

Parasitism in general has been predicted to enhance variance in host populations because high levels of genetic variation can allow for swift adaptive responses of a species to specific diseases, parasites and predator pressure (Hamilton 1987; Sherman et al. 1988). Such a mechanism also might have driven enhanced genetic variability in *Formica lemani* Bondroit 1917 populations that are parasitized by its myrmecophilous syrphid fly *Microdon mutabilis* Linnaeus 1758 (Gardner et al. 2007). *M. mutabilis* directly boosts the production of queens by preferably feeding on small *F. lemani* brood (Schönrogge et al. 2006; Hovestadt et al. 2012). This increase in gyne production might be a mechanism to enhance genetic variability and reduce the effect of

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the social parasites on host fitness and allow the persistence of the parasite by enforcing dispersal in its host (Schönrogge et al. 2006; Nash and Boomsma 2008). High genetic variance within a colony may however also benefit the parasite at the ecological level. Since the adoption of social parasites into colonies of social insects often requires chemical camouflage (Hölldobler and Wilson 1990; Moritz et al. 1991) or mimicry of nest-mate recognition signals (Akino et al. 1999; Lenoir et al. 2001; Schönrogge et al. 2004), a high intracolony genetic variance would increase the variance in recognition signals among workers hence facilitating adoption (Als 2001; Gardner et al. 2007).

Often local ecological factors affect the sociogenetic organization of ants (e.g. queen number, nest-mate relatedness and population structure) (DeHeer et al. 2001). It is therefore important to understand whether social parasite pressure can be a local trait inferring with natural selection and affecting the population genetics of its host population. Here we use the host parasite system of *P. nausithous* and *Myrmica rubra* Linnaeus 1758 as a model system to screen for potential effects on the population genetic structure of the ant host population, as *P. nausithous* is a highly specialized social parasite for *M. rubra* across Europe (Thomas et al. 1989; Elmes et al. 1998; Tartally and Varga 2005; Munguira and Martin 1999; Stankiewicz and Sielezniew 2002; Witek et al. 2008; Patricelli et al. 2010). At the same time the understanding of the host-parasite dynamics may also have implications for the conservation of the butterfly. *P. nausithous* which has been regarded as highly vulnerable across its European range (it has been reported as Near Threatened species in European Red Lists, Van Swaay et al. 2010; Van Swaay and Warren 1999). Its role as a conservation icon together with the other *Phengaris* butterflies (e.g. Pyle et al. 1981; Settele et al. 2005) make *P. nausithous* a good item for discussing host-parasite co-adaptation in particular and large blue butterfly conservation in general. By comparing the genetic variability of *M. rubra* populations with and without *P. nausithous* parasitism we expect population genetic reveals local adaptation, similar to that found for host behaviour (Solazzo et al. 2013).

Materials and methods

Study area

The sampling was conducted on grasslands in the Upper Rhine Valley (Rhineland-Palatinate, Germany) in August 2011. We selected six sites (A-F) where *P. nausithous* occurrence has been regularly observed since 1989 (Settele 1998, 2005 and unpubl.; Anton et al. 2007) and three sites (G-I) where *P. nausithous* has been absent ever since or become extinct (Fig. 1, Table 1). Table 1 reports further site

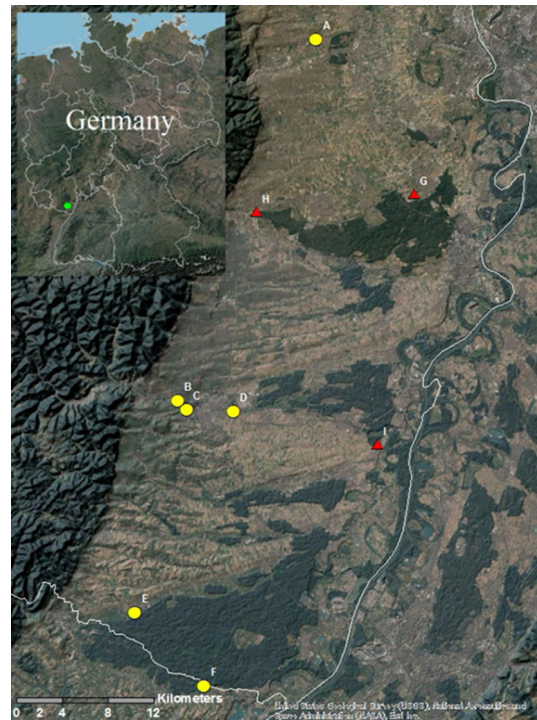


Fig. 1 Map of study area in the Upper Rhine Valley in the state of Rhineland-Palatinate (Germany). Yellow circles mark the six infested sites while red triangles indicate the three uninfested sites. Darkish areas = woods and forests; rest = grasslands or crops. White line = river Lauter (South; there also border between France and Germany) and river Rhine (East). Based on “NASA Landsat Program, United States Geological Survey (USGS), National Aeronautics and Space Administration (NASA), Esri Inc.”. (Color figure online)

characteristics and data on the long term occurrence of *P. nausithous* and estimates of the abundance of flowering shoots of the food plant *Sanguisorba officinalis* (Settele unpubl. and UFZ data-base). Data on host ants are only available for the year of the present study 2011.

Ant sampling

We collected the ant colonies from the wild, the ant species were identified directly in the field using a magnification glass and the morphometric key of Czechowski et al. (2002). As different to *P. nausithous* and *S. officinalis* we had not previous data on host ants, we sampled ant colonies within a period of 2 h on a large number of sites. Those sites in which it was not possible to obtain enough colonies were not included in the analyses. In total we sampled four colonies from each of the nine sites finally assayed. From each colony we stored 48 workers in 90 % ethanol at -25°C .

Microsatellite analyses

DNA was extracted from the thorax and legs of workers (12 per colony) using the Chelex method 100 (Walsh et al. 1991).

M. rubra workers were assayed at five microsatellite loci (Ms 2.12, Ms 36, Ms 3.62, Ms 26 from Azuma et al. 2005 and Msca 47 from Henrich et al. 2003). Primers were fluorescently labeled FAM, HEX or TET to be detected by a MegaBACE 1000 capillary sequencer (Table 2). Microsatellites were individually PCR-amplified in 10 µl of a solution containing 7.35 µl of distilled water, 1 µl of Buffer (PEQLAB), 0.2 µl dNTP, 0.4 µl of primer, 0.05 µl of tag polymerase (PEQLAB) and 1 µl of DNA. The DNA PCR-amplifications were performed according to the following protocol: initial denaturation at 95 °C for 3 min, subsequently cycles of denaturation at 95° for 30 s, annealing temperature (dependence of primers see Table 2) for 30 s, extension for 1 min at 72 °C and a final step was a prolonged extension for 5 min at 72 °C.

Afterwards 0.5 µl of every PCR-amplification product were mixed with 8.7 µl of distilled water and 0.3 µl of ET-ROX 400 size standard to be sequenced by MegaBACE 1000 capillary sequencer.

Data analysis

All genotypes were scored using the MegaBACE Fragment Profiler Version 1.2[®] (Amersham Biosciences 2003).

We first evaluated the genetic isolation of the ant populations which is an essential precondition for any local co-adaptation between *Phengaris* and their host (Nash et al. 2008) using standard F_{ST} estimates.

At the population level, estimates of allelic richness were used to assess any effect of *P. nausithous* on overall genetic diversity using Fstat Version 2.9.3.2 (Goudet 2002).

We also estimated the relatedness within ant colonies which may have great impact on parasitism. On the one

Table 2 List of microsatellite DNA loci, annealing temperature, cycles and label

Locus	Annealing temperature (°C)	Cycles	Label
Ms 2.12	46	40	FAM
Ms 36	52	40	FAM
Ms 3.62	46	40	HEX
MscA 47	58	40	HEX
Ms 26	58	40	TET

hand low relatedness increases odour diversity and facilitates the infiltration of social parasites (Als 2001; Gardner et al. 2007) on the other high genetic variance may lead to higher parasite resistance (Gardner et al. 2007).

Relatedness was estimated using Coancestry Version 1.0.0.1 (Wang 2011), to test for any difference between colonies of infested and uninfested populations. The queen genotype(s) of each colony were derived from the worker genotypes using Mendelian inference.

R (version 2.7.1: R Devel Core 2011) was used for statistical data analysis.

Results

Isolation by distance

All microsatellite DNA loci were polymorphic and informative for the population genetic analyses (Table 3). Since the different loci varied markedly for their specific effective number of alleles, we corrected the estimates of the population genetic parameter according to Petit et al. (2001).

Table 1 List of sampling locations, patch area, geographical coordinates, *P. nausithous* incidence, *S. officinalis* abundance and parasitism presence (assessments in study area since 1989; see Settele 1998)

Location (UFZ ID)	Area m ²	Latitude	Longitude	<i>S. officinalis</i> abundance ^a 2007–2011	<i>P. nausithous</i> incidence ^b 1989–2011 (no. of years assessed)	Parasitism presence (yes: present in 2011; no: permanently absent from 2008 or earlier until 2011)
A (72)	19,000	49°29'	8°14'	500–1,000	100 % (7)	Yes, since 2003 (first assessed)
B (58)	7,500	49°12'	8°05'	1–10	47 % (17)	Yes, since 1989
C (71)	8,300	49°12'	8°05'	1,000–5,000	87 % (16)	Yes, since 1989
D (102)	5,900	49°12'	8°09'	200–500	100 % (2)	Yes, since 2010 (first assessed)
E (17)	5,900	49°02'	8°02'	50–100	57 % (14)	Yes, since 1989
F (15)	23,000	48°59'	8°07'	50–100	54 % (11)	Yes, since 1989
G (100)	1,300	49°22'	8°22'	1–10	43 % (7)	No, since 2008 Location 14 in Anton et al. (2007) with investigation in 2003
H (part of 10)	5,000	49°21'	8°10'	1–10	0 (10)	No, since 1997 (first assessed); sub-patch with approx. 10 % of the total area of patch UFZ-ID 10
I (53)	41,000	49°10'	8°19'	20–50	22 % (9)	No, since 2001

^a n° flowering shoots (median of estimation ranges for entire area)

^b Parasite presence recorded/n° of years

Table 3 Number of alleles detected and effective number of alleles for the various loci in the screened population

Locus population	Ms 2.12	Ms 36	Ms 3.62	Mscs 47	Ms 26	Overall
A	2 (1.80)	2 (1.11)	3 ^a (2.01)	1	1	0.564
B	2 (1.99)	2 (1.18)	5 ^a (3.58)	1	2 (1.32)	0.984
C	2 (1.90)	2 (1.37)	5 (2.65)	1	1	0.999
D	2 (1.47)	3 (1.42)	2 (1.99)	1	2 ^a (1.21)	0.519
E	2 (1.75)	3 (2.31)	6 ^a (3.71)	3 ^a (1.09)	2 (1.23)	0.074
F	2 (1.79)	3 (1.21)	6 (3.08)	2 (1.03)	2 (1.03)	0.849
G	2 (1.90)	3 (1.12)	4 ^a (3.10)	2 (1.02)	2 (1.02)	0.111
H	2 (1.97)	3 ^a (1.84)	5 ^a (2.68)	1	2 (1.02)	0.302
I	2 (1.69)	2 (1.16)	4 (3.25)	1	2 (1.04)	0.088
Total n° alleles	2	3	6	3	2	

In no population did we observed a significant deviation from Hardy–Weinberg Equilibrium

^a Locus deviating from HWE

All populations did not significantly deviate from HWE (Table 3) but were genetically differentiated, as indicated by an overall $F_{ST} = 0.122 \pm 0.049$ (interval of confidence at 99 % 0.022–0.160 $p < 0.001$ jackknifing by Fstat). Although F_{ST} is statistically higher for the infested (0.128 ± 0.021) than the uninfested (0.093 ± 0.014) populations, an ANOVA shows that this difference is mainly due to geographical distance ($p = 0.003$) but not due to parasitism ($p = 0.297$).

Allelic richness

Allelic richness per locus and per population was estimated with Fstat’s rarefaction technique (Petit et al. 1998) with a minimum sample size of 36 workers. The allelic richness between the parasitized (2.407 ± 0.245) and non-parasitized populations (2.401 ± 0.293) was not significantly affected by parasitism (Mann–Whitney U test $p = 0.823$).

Relatedness

To screen for differences in the intracolony variance between colonies of infested and uninfested populations, we estimated the average intracolony relatedness within each population based on 12 workers using “Coancestry” triadic likelihood estimator (Table 4). It provides a robust estimation of pairwise relatedness, as it includes a third individual which better fits to our data set compared to the other estimators provided by “Coancestry” (TrioML Wang 2007). The relatedness estimates within ant colonies at infested ($r = 0.339 \pm 0.020$) and uninfested sites ($r = 0.481 \pm 0.044$) were significantly different (Kruskal–Wallis $p = 0.006$ $N = 2,324$ n° dyads of individuals Fig. 2). Since *M. rubra* queens mate with either one or two males (Seppä and Walin 1996), we determined the potential queen genotype of each colony by Mendelian inference. If

Table 4 Intracolony relatedness of the infested and the uninfested populations

	Colony			
	1	2	3	4
Infested pop				
A	0.353 ^a	0.551 ^a	0.407	0.426 ^a
B	0.423	0.253	0.372	0.293
C	0.342	0.284	0.293	0.439
D	0.293	0.555 ^a	0.328	0.274
E	0.333	0.194	0.326	0.338
F	0.365	0.140	0.265	0.289
Uninfested pop				
G	0.217	0.503 ^a	0.491 ^a	0.497
H	0.311	0.782 ^a	0.469	0.497
I	0.518 ^a	0.597 ^a	0.593 ^a	0.299 ^a

^a Monogynous colony as derived from Mendelian inference

we could explain the observed worker genotypes with the genotypes of a single queen and either one or two haploid males, we classified the colony as potentially monogynous. All other cases were considered to be polygynous colonies. Seven colonies out of 12 from the uninfested populations were inferred to be monogynous. In contrast, the frequency of potentially monogynous colonies (4 colonies out of 24) was significantly smaller in the infested population (Table 4) ($\chi^2 = 6.55$ $df = 1$ $p = 0.010$).

Discussion

The screened *M. rubra* populations in the Upper Rhine valley showed a significant isolation by distance which is an important precondition for any local co-evolution between host and parasite (Nash et al. 2008), in addition these

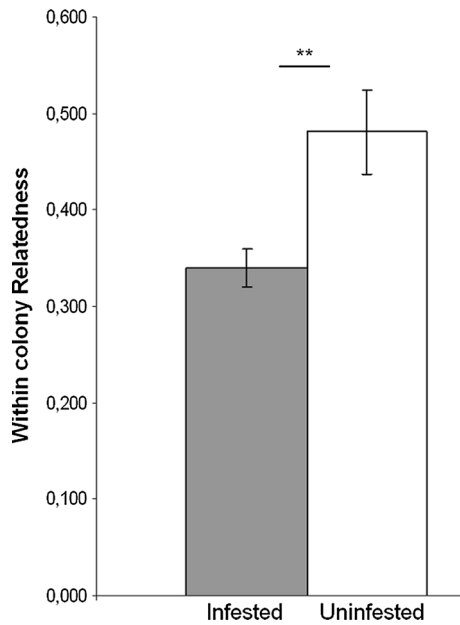


Fig. 2 Significant differences in colony relatedness (TrioML estimator) between infested and uninfested populations (Kruskal–Wallis $p = 0.006$ mean infested (\pm SE) = 0.339 (\pm 0.020) $N = 1,532$, uninfested = 0.481(\pm 0.044) $N = 792$)

findings support previous studies on the population structure of *M. rubra* (Seppä and Pamilo 1995; Nash et al. 2008).

None of the *M. rubra* populations did significantly deviate from Hardy–Weinberg Equilibrium, the mean of allelic richness varies across the populations but not with respect to the presence of *P. nausithous* and not enough to reveal a huge difference between ant populations' sizes.

The relatedness varied from 0.140 up to 0.782, confirming the extreme flexibility of the queen number in *M. rubra* (Seppä and Walin 1996), nonetheless we found a higher number of monogynous colonies and a higher relatedness within the uninfested populations than in the infested ones. This fits well with previous observations of Als (2001) and Gardner et al. (2007) who found similar patterns between the lower relatedness and the presence of other parasite (*P. alcon* and *M. mutabilis* respectively).

The higher intracolony genetic variance in the infested populations can be explained in two ways:

1. *P. nausithous* like *M. mutabilis* predate on small items of ant brood (Elfferich 1998) avoiding large queen larvae. *M. mutabilis* can prey as much as 53 % of eggs and first instar larvae of its host-ant colony. In consequence, then the supply food is allocated, by the nursing workers, towards the remaining large larvae which increase their probability to develop into queens (Schönrogge et al. 2006; Hovestadt et al. 2012). Since the young queens can be recruited in the mother colony (Elmes 1973) this mechanism has been suggested to facilitate polygyny and hence reduce the intracolony relatedness.

In *P. nausithous*, predation has also been reported to be preferentially on small ant brood (Elfferich 1998) even though it can also exploit the worker trophallaxis (Thomas and Settele 2004; Patricelli et al. 2010).

2. In ant societies the nest-mate recognition has been suggested to be based on detection of surface cuticular hydrocarbons (d'Etorre and Heinze 2001). The “Gestalt odour” hypothesis (Crozier and Dix 1979) predicts that nest-mates share a common colony specific label. This mechanism has been suggested to be the prevailing recognition mode for ant colonies (Vander Meer and Morel 1998; DeHeer et al. 2001) and hence genetically highly variable colonies will increase differences among genetically derived recognition labels reducing the efficiency of nest-mate recognition. A larger number of queens enhance genetic but also chemical diversity of cuticular hydrocarbons with a larger overlap of cues and a greater variance around the template that they have to tolerate to not reject nest-mates (Starks et al. 1998). Monogynous colonies tend to have a better defined “colony odour” due to the higher relatedness among colony members (Starks et al. 1998). This difference between monogynous and polygynous colonies and the threshold of acceptance towards intruders has been well reported for *M. rubra* (Fürst et al. 2012). The greater individual variance of the colony members around the mean colony odour may make the guarding workers more tolerant to deviations from the colony odour, but might also more easily allow for an infiltration of social parasites into the colony (Als 2001; Gardner et al. 2007).

It might therefore be possible that uninfested populations are resistant forms of host populations with better recognition mechanism. In that case polygyny is not the proximate result of predation, but monogyny is rather the result of selection against the parasite through enhanced nest-mate recognition. Irrespective of the actual mechanisms that drive the intracolony genetic variance, we here show again that lower intracolony relatedness is significantly associated with *P. nausithous* infestation and it might be worthwhile to test for differential adoption behaviour (Solazzo et al. 2013) in monogynous and polygynous colonies to pin down the actual mechanisms behind this phenomenon.

Although differences between pooled samples from infested and uninfested populations are statistically significant, *P. nausithous* occurs in *M. rubra* population A which is apparently not resistant despite three of four colonies being monogynous and it disappeared from uninfested population H where only a colony was monogynous. The food plant abundance might explain the difference between these patches, in site A the food plant is much more abundant than in population H. This likely helps *P. nausithous* to survive with such an antagonistic host population. On the other hand the food plants

abundance is similar for site H and the infested site B then the sociogenetics of *M. rubra* seem to be the reason of *P. nausithous* absence. Anyway our sample size is too small to understand how the habitat factors interfere with presence/absence of *P. nausithous* and the sociogenetic organization of *M. rubra*, therefore further works in this direction are need.

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Supplementary Material

Data section

Table S1. Genotypes of 12 workers each per colony at the tested loci (allele size in base pairs). Paternal and queen genotypes were inferred with Matesoft and confirmed by mendelian inference. Locus Msca 50 (Henrich et al. 2003), it was excluded from statistics because it gave only few products, but it is here reported to enhance the inference of queen and male genotypes. Colonies with more than two inferred males were considered to be polygynous because *M. rubra* queens only mate with up to two males. Inferred monogynous colonies are marked in red. The colour codes in the table reflect the inferred paternal genotypes and the corresponding worker patriline. For each locus male alleles were reported in the left side and queen alleles in the right side.

Population A

Colony	Loc Ms 2.12		Loc Ms36		Loc Ms 3.62		Loc Msca 47		Loc Ms 26		Loc Msca 50
Queen1	145	169	131	137	154	160	103	103	158	158	
Male 1	169		131		160		103		158		
Male 2	169		131		154		103		158		
1	169	169	131	131	154	154	103	103	158	158	
2	169	145	131	131	154	154	103	103	158	158	
3	169	169	131	131	154	160	103	103	158	158	
4	169	169	131	131	154	160	103	103	158	158	
5	169	169	131	131	154	160	103	103	158	158	
6	169	145	131	131	160	160	103	103	158	158	
7	169	145	131	137	160	160	103	103	158	158	
8	169	169	131	131	154	160	103	103	158	158	

9	169	145	131	131	154	160	103	103	158	158
10	169	145	131	131	154	154	103	103	158	158
11	169	145	131	131	154	154	103	103	158	158
12	169	145	131	137	154	160	103	103	158	158

Colony
2

Q	145	169	131	131	152	160	103	103	158	158
M	169		131		160		103		158	
1	169	169	131	131	160	160	103	103	158	158
2	169	169	131	131	160	160	103	103	158	158
3	169	145	131	131	160	160	103	103	158	158
4	169	169	131	131	160	160	103	103	158	158
5	169	145	131	131	160	160	103	103	158	158
6	169	169	131	131	160	160	103	103	158	158
7	169	169	131	131	160	160	103	103	158	158
8	169	145	131	131	152	160	103	103	158	158
9	169	169	131	131	152	160	103	103	158	158
10	169	169	131	131	160	160	103	103	158	158
11	169	145	131	131	152	160	103	103	158	158
12	169	145	131	131	160	160	103	103	158	158

Colony
3

Q	145	169	131	137	154	160	103	103	158	158
M	169		131		154		103		158	
M	169		131		160		103		158	
M	169		137		154		103		158	
1	169	145	137	137	154	160	103	103	158	158
2	169	145	131	131	154	154	103	103	158	158
3	169	169	131	131	154	160	103	103	158	158
4	169	145	131	131	154	160	103	103	158	158

5	169	169	137	131	160	160	103	103	158	158
6	169	145	131	131	154	154	103	103	158	158
7	169	169	131	131	160	160	103	103	158	158
8	169	145	131	131	154	154	103	103	158	158
9	169	145	131	131	154	154	103	103	158	158
10	169	145	131	131	154	154	103	103	158	158
11	169	145	131	131	154	160	103	103	158	158
12	169	145	131	131	154	160	103	103	158	158

Colony
4

Q	145	169	131	131	152	160	103	103	158	158
M	169		131		160		103		158	
M	145		131		154		103		158	
1	145	169	131	131	154	160			158	158
2	145	169	131	131	154	160	103	103	158	158
3	169	169			160	160	103	103	158	158
4	145	169	131	131	160	160	103	103	158	158
5	145	169	131	131	160	160	103	103	158	158
6	145	169	131	131	152	160	103	103	158	158
7	145	169	131	131	152	160	103	103	158	158
8	145	169	131	131	160	160	103	103	158	158
9	145	169	131	131	160	160	103	103	158	158
10	169	169	131	131	160	160	103	103	158	158
11	145	169	131	131	160	160	103	103	158	158
12	145	169	131	131	160	160	103	103	158	158

Population B

Colony

1

Q 145 169 131 131 152 158 103 103 158 158 187 190

M 145 131 158 103 158 190

M 145 131 160 103 158

M 169 137 158 103 158 187

1 145 169 131 131 160 152 103 103 158 158

2 145 169 131 131 152 158 103 103 158 158

3 145 169 131 131 152 158 103 103 158 158

4 145 169 137 131 152 158 103 103 158 158 187 187

5 145 169 131 131 158 158 103 103 158 158

6 145 169 131 131 158 158 103 103 158 158 190 190

7 145 169 131 131 152 158 103 103 158 158

8 145 169 131 131 158 158 103 103 158 158 190 187

9 145 169 137 131 152 158 103 103 187 187

10 169 169 137 131 152 158 103 103 158 158 187 187

11 145 169 131 131 152 158 103 103 158 158

12 145 169 131 131 158 158 103 103 158 158 190 190

Colony

2

Q 169 169 131 131 152 158 103 103 158 158 187 190

M 145 137 152 103 158 187

M 169 131 158 103 158

M 145 131 152 103 158

M 145 131 154 103 161 187

M 145 131 160 103 161 187

M 145 131 158 103 161 187

M 145 137 152 103 161

M 145 131 154 103 158 190

1 145 169 137 131 152 152 103 103 158 158

2	145	169	131	131	152	152	103	103	158	158		
3	169	169	131	131	158	158	103	103				
4	145	169			152	152	103	103	158	158		
5	145	169	131	131	152	152	103	103	158	158		
6	145	169	131	131	158	158	103	103	161	158	187	190
7	145	169	131	131	154	158	103	103	161	158	187	187
8	169	169	131	131	158	158	103	103	158	158		
9	145	169	131	131	160	158	103	103	161	158	187	187
10	145	169	137	131	152	152	103	103	161	158		
11	145	169	137	131	152	152	103	103	158	158	187	190
12	145	169	131	131	154	158	103	103	158	158	190	190

Colony
3

Q 169 169 131 131 152 160 103 103 158 158

M 145 131 152 103 158

M 145 137 158 103 158

M 145 131 158 103 161

M 145 131 160 103 158

1 145 169 160 160 103 103 158 158

2 145 169 131 131 158 160 103 103 158 158

3 145 169 131 131 152 160 103 103 158 158

4 145 169 131 131 152 160 103 103 158 158

5 145 169 158 160 103 103 161 158

6 145 169 137 131 158 152 103 103 158 158

7 145 169 131 131 158 160 103 103 161 158

8 145 169 131 131 152 152 103 103 158 158

9 145 169 131 131 160 160 103 103 158 158

10 145 169 131 131 160 160 103 103 158 158

11	145	169	131	131	152	160	103	103	158	158
12	145	169	131	131	152	160	103	103	158	158
Colony 4										
Q	169	169	131	131	154	160	103	103	158	161
M	145		131		160		103		161	
M	145		131		160		103		158	
M	145				174		103		158	
M	145		131		152		103		158	
M	145		131		158		103		158	
1	145	169			174	160	103	103	158	161
2	145	169			174	160	103	103	158	158
3	145	169			160	154	103	103	158	158
4	145	169	131	131	160	160	103	103	161	158
5	145	169	131	131			103	103	158	158
6	145	169	131	131	152	160	103	103	158	158
7	145	169	131	131	152	160	103	103	158	158
8	145	169	131	131	160	160	103	103	158	158
9	145	169	131	131	160	160	103	103	161	161
10	145	169	131	131	160	154	103	103	161	158
11	145	169	131	131	160	154	103	103	161	161
12	145	169	131	131	158	160	103	103	158	158

Population C

Colony 1										
Q	169	169	131	131	152	158	103	103	158	158
M	169		131		154		103		158	

M	145		131		158		103		158	
M	169		131		152		103		158	
M	169		137		152		103		158	
M	169		131		154		103		158	
M	145		131		152		103		158	
1	169	169	131	131	154	152	103	103	158	158
2	169	169	131	131	158	158	103	103	158	158
3	169	169	131	131	152	158	103	103	158	158
4	145	169	131	131	152	158	103	103	158	158
5	169	169	137	131	154	152	103	103	158	158
6	169	169	131	131	152	158	103	103	158	158
7	145	169	131	131	152	158	103	103	158	158
8	169	169	137	131	152	158	103	103	158	158
9	145	169	131	131	152	152	103	103	158	158
10	145	169	131	131	152	152	103	103	158	158
11	145	169	131	131	152	158	103	103	158	158
12	145	169			152	158	103	103	158	158

Colony

2

Q	145	169	131	137	0	152	103	103	158	158
M	169		131		152		103		158	
M	169		131		154		103		158	
M	145		131		158		103		158	
M	169		131		160		103		158	
1	169	145	137	131	154	152	103	103	158	158
2	169	169	131	131	154	152	103	103	158	158
3	169	145	137	131	152	152	103	103	158	158
4	169	145	131	131	154	152	103	103	158	158
5	169	145	131	131	160	0	103	103	158	158

6	169	169	131	131	158	152	103	103	158	158
7	169	145	131	131	152	152	103	103	158	158
8	169	145			152	152	103	103	158	158
9	169	145	131	131	152	0	103	103	158	158
10	169	145			152	0	103	103	158	158
11	169	145			152	0	103	103	158	158

Colony
3

Q	145	169	131	137	158	158	103	103	158	158	190	190
M	169		131		152		103		158		190	
M	169		131		154		103		158			
M	169		131		160		103		158		190	
1	169	145	131	131	154	158	103	103	158	158		
2	169	145	131	131	152	158	103	103	158	158		
3	169	145	131	137	152	158	103	103	158	158	190	190
4	169	145	131	131	160	158	103	103	158	158	190	190
5	169	145	131	137	152	158	103	103	158	158		
6	169	145	131	131	154	158	103	103	158	158		
7	169	145	131	131	152	158	103	103	158	158		
8	169	169	131	137	152	158	103	103	158	158	190	190
9	169	145	131	131	152	158	103	103	158	158		
10	169	169	131	137	152	158	103	103	158	158		
11	169	145	131	137	152	158	103	103	158	158		
12	169	145	131	137	152	158	103	103	158	158	190	190

Colony
4

Q	145	169	131	137	152	158	103	103	158	158	187	190
M	169		131		152		103		158		190	
M	169		131		158		103		158		190	
M	169		137		158		103		158		190	

1	169	145	131	131					158	158	190	190
2	169	145	131	131	152	158	103	103				
3	169	145	131	137	152	158	103	103				
4	169	145	131	131	158	158	103	103	158	158		
5	169	145	131	131	152	158	103	103	158	158		
6	169	169	131	131	158	158	103	103				
7	169	145	131	131	158	158	103	103			190	190
8	169	145	131	137	158	158	103	103	158	158		
9	169	145	131	137	158	158	103	103	158	158	190	190
10	169	145	131	131	158	158	103	103	158	158	190	187
11	169	145	131	131	152	152	103	103	158	158		
12	169	145	137	137	158	158	103	103	158	158	190	190

Population D

Colony												
1												
Q	145	169	131	137	152	158	103	103	158	158		
M	145		131		152		103		158			
M	169		131		152		103		158			
M	169		131		158		103		158			
1	145	169	131	131	152	158	103	103	158	158		
2	145	145	131	137	152	158	103	103	158	158		
3	169	169	131	137	152	152	103	103	158	158		
4	169	169	131	137	152	158	103	103	158	158		
5	169	169	131	137	152	158	103	103	158	158		
6	169	169	131	137	152	158	103	103	158	158		
7	145	169	131	131	152	158	103	103	158	158		
8	169	169	131	137	152	158	103	103	158	158		

9	145	169	131	131	152	152	103	103	158	158
10	145	169			152	152	103	103	158	158
11	169	169	131	131	158	158	103	103	158	158
12	145	169	131	131	152	152	103	103	158	158

Colony
2

Q	145	169	131	137	152	158	103	103	158	158
M	169		131		152		103		158	
1	169	145	131	131	152	152	103	103	158	158
2	169	145	131	131	152	158	103	103	158	158
3	169	145	131	137	152	158	103	103	158	158
4	169	145	131	131	152	158	103	103	158	158
5	169	145	131	131	152	152	103	103	158	158
6	169	145	131	131	152	158	103	103	158	158
7	169	145	131	131	152	152	103	103	158	158
8	169	145	131	131	152	158	103	103	158	158
9	169	145	131	131	152	158	103	103	158	158
10	169	145	131	131	152	158	103	103	158	158
11	145	145	131	137	152	152	103	103	158	158

Colony
3

Q	169	169	131	131	152	158	103	103	158	161	187	190
M	169		140		152		103		158		190	
M	169		131		152		103		161		187	
M	169		131		158		103		158		187	
M	169		137		158		103		158		187	
M	169		140		158		103		161		187	
1	169	169			152	152	103	103	158	158	187	190
2	169	169	140	131	158	158	103	103	161	161	187	190
3	169	169	140	131	152	158	103	103	158	158	190	190

4	169	169	131	131	152	158	103	103	158	158	187	187
5	169	169	131	131	158	158	103	103	158	158	187	190
6	169	169	137	131	158	158	103	103	158	158	187	190
7	169	169	131	131	158	158	103	103	158	158	187	190
8	169	169	131	131	152	158	103	103	161	161	187	187
9	169	169			158	158	103	103	158	158	187	190
10	169	169	131	131	158	158	103	103	158	158	187	187
11	169	169	131	131	158	158	103	103	158	158	187	190
12	169	169	131	131	158	158	103	103	161	158	187	190

Colony
4

Q 169 169 131 131 152 158 103 103 158 158 187 190

M	169		131		152		103		158		190	
M	169		131		152		103		161		187	
M	169		137		152		103		161		187	
M	169		140		158		103		158		187	
M	169		131		158		103		158		187	

1	169	169	131	131	152	152	103	103	158	158	190	187
2	169	169	140	131	158	158	103	103	158	158	187	187
3	169	169	131	131	152	158	103	103	158	158	190	187
4	169	169	137	131	152	158	103	103	161	158	187	190
5	169	169	140	131	152	158	103	103	158	158	187	190
6	169	169	131	131	152	158	103	103	158	158	190	187
7	169	169	131	131	158	158	103	103	158	158	187	190
8	169	169	131	131	152	152	103	103	161	158	187	190
9	169	169	131	131	152	158	103	103	158	158	190	190
10	169	169	140	131	152	158	103	103	158	158	187	190
11	169	169	131	131	152	158	103	103	158	158	187	187
12	169	169	131	131	152	158	103	103	161	158	187	190

Population E

Colony 1												
Q	145	169	131	137	158	160	103	103	158	158	190	190
M	145		137		160		103		161		187	
M	169		131		160		103		158	158	187	
M	169		131		160		103		161		187	
M	169		131		152		103		161		187	
M	145		137		158		103		158		187	
M	169				154		103		158		187	
1	145	169	137	131	160	160	103	103	161	158	187	190
2	145	169			154	158	103	103	158	158	187	190
3	145	169			158	160	103	103	158	158	187	190
4	169	169	137	131	160	160	103	103	158	158	187	190
5	145	169	131	131	152	160	103	103	161	158	187	190
6	145	169	137	131	158	158	103	103	158	158	187	190
7	145	169	131	131	160	160	103	103	161	158	187	190
8	145	169	137	137	160	160	103	103	161	158	187	190
9	145	169	137	131	160	160	103	103	158	158	187	190
10	169	169	137	131			103	103	161	158	187	190
11	169	169	131	131	152	160	103	103	161	158		
12	169	169	137	131	160	160	103	103	158	158	187	190
Colony 2												
Q	145	169	131	137	152	158	103	107	158	158	187	190
M	145		137		152		103		158		190	
M	169		140		154		103		158		190	
M	145		140		154		107		158		190	
M	145		131		154		103		158			

M	145		140		158		103		158		190	
M	169		131		158		103		158		190	
M	169		131		154		103		158		190	
1	145	169	137	140	154	158	103	103	158	158	190	187
2	145	169	137	140	154	158	107	107	158	158	190	190
3	169	169	131	131	152	154	103	103	158	158	190	187
4	145	169	131	131	158	158	103	103	158	158	190	190
5	145	169	137	137	152	158	103	103	158	158	190	190
6			137	137	152	158	103	103	158	158	190	187
7	145	169	137	140	158	158	103	103	158	158	190	187
8	145	169	137	140	154	158	103	103	158	158		
9	145	169	131	137			107	103	158	158	190	190
10	145	169	131	137	154	154	103	103	158	158		
11	169	169	137	140	154	158	103	103	158	158		
12	145	169	137	137	152	152	103	103	158	158		

Colony
3

Q	145	169	137	137	174	158	103	103	158	161	187	190
M	169		137		152		103		158		190	
M	145		131		152		103		158		190	
M	169		131		154		103		158		190	
M	169		131		158		103		158		190	
M	145				158		103		161		190	
M	145		137		158		103		158		190	
M	169		137		174		103		161		190	
1	169	169	137	137	152	158	103	103	158	158	190	187
2	169	169	137	137	174	174	103	103	161	161	190	187
3	145	169			152	158	103	103	158	158	190	190
4	145	169			154	158	103	103	158	158	190	190

5	145	169	131	137	158	158	103	103	158	158	190	190
6	145	169			158	158	103	103	161	161	190	187
7	169	169	131	137	154	158	103	103	158	158	190	187
8	145	169	137	137	158	158	103	103	158	158	190	190
9			131	137			103	103	158	158	190	190
10	145	169	131	137	152	158	103	103	158	158	190	187
11	145	169	137	137	154	158	103	103			190	187
12	145	169	137	137	152	158			158	158	190	190
Colony 4												
Q	145	169	131	137	0	158	103	103	158	158	187	190
M	169		131		152		103		158		190	
M	169		131		152		110		158		190	
M	169		137		158		103		158		190	
M	169		137		152		103		158		190	
1	169	169			158	158	103	103				
2	169	169	131	137					158	158		
3	169	169	131	137	152	158	103	103	158	158	190	187
4	169	145	131	131	158	158	103	103	158	158	190	187
5	169	169	131	131	152	0	103	103	158	158	190	187
6	169	169	137	137	158	158	103	103	158	158	190	187
7	169	169	131	131	152	0	103	103	158	158	190	187
8	169	169	131	137	158	158	103	103	158	158	190	190
9			131	131	152	0	103	103	158	158	190	190
10	169	145	131	137	152	158	110	103	158	158	190	190
11	169	145	137	137	152	0	103	103	158	158	190	187
12	169	169	137	137	158	158	103	103	158	158	190	190

Population F

Colony
1

Q	145	169	131	131	152	0	103	103	158	158	187	190
M	169		131		152		103		158		190	
M	169		140		152		103		158		190	
M	169		131		154		103		158		190	
M	169		137		158		103		161		190	
1	169	169	140	131	152	152	103	103	158	158	190	187
2	169	169	131	131	152	0	103	103	158	158		
3	145	169	131	131	152	0	103	103	158	158	190	187
4	169	169	131	131	152	0	103	103	158	158	190	187
5	169	169	131	131	152	0	103	103	158	158		
6	169	169	131	131	152	152	103	103	158	158		
7	169	169	131	131	152	152	103	103	158	158	190	187
8	169	169	137	131	158	0	103	103	161	158	190	190
9	169	169	131	131	154	0	103	103	158	158		
10	169	169	131	131	152	152			158	158	190	190
11	169	169	131	131	152	152	103	103	158	158		
12	169	169	131	131	154	0			158	158	190	187

Colony
2

Q	145	169	131	137	152	0	103	103	158	158	187	190
M	169		131		152		103		158		190	
M	169		131		154		103		158		190	
M	169		131		158		103		158		190	
M	169				158		107		103		190	
M	169		131		174		103		158			
1	169	145	131	131	152	0	103	103	158	158	190	190
2	169	169	131	137	152	0	103	103	158	158		
3	169	145	131	131	154	152	103	103	158	158	190	190

4	169	145	131	137	158	152	103	103	158	158	190	187
5	169	145	131	137	152	152	103	103	158	158	190	187
6	169	145			158	152	107	103	158	158	190	190
7	169	169			154	152					190	190
8	169	145	131	131	174	0	103	103	158	158		
9	169	145	131	137	152	152			158	158	190	187

Colony
3

Q	145	169	131	131	152	0	103	103	158	158	190	190
M	169		131		152		103		158			
M	169		131		154		103		158		190	
M	169		137		154		103		158		190	
M	169		131		158		103		158		190	
M	169		131		160		103		158			

1	169	145	131	131	152	0	103	103	158	158		
2					152	0	103	103	158	158		
3	169	145			154	152	103	103	158	158		
4	169	145					103	103	158	158		
5	169	145	131	131	160	0	103	103	158	158		
6	169	169	131	131	154	152	103	103	158	158		
7	169	145	131	131	152	152	103	103	158	158		
8	169	169	137	131	154	152	103	103	158	158	190	190
9	169	169	131	131	158	152	103	103	158	158	190	190
10	169	169	131	131	158	152	103	103	158	158		
11	169	145	131	131	152	152	103	103	158	158	190	190
12	169	145	131	131	154	152	103	103	158	158	190	190

Colony
4

Q	145	169	131	131	152	0	103	103	158	158	187	190
M	145				152		103		161		190	

M	145				152		103		158			
M	169				152		103		158			
M	145	131			154		103		158		190	
M	169	131			158		103		158		190	
1	145	145			152	0			161	158	190	187
2	145	169	131	131	154	152	103	103	158	158		
3	145	145	131	131	154	152	103	103	158	158		
4	145	169	131	131	158	158	103	103	158	158		
5	169	169			152	152	103	103	158	158		
6	145	145			152	152	103	103	158	158		
7	145	169	131	131	154	0	103	103	158	158	190	190
8	145	169					103	103	158	158	190	187
9	169	169	131	131	158	0	103	103	158	158	190	187
10	145	169	131	131	158	0	103	103	158	158	190	187
11	145	169	131	131	154	0			158	158	190	190
12	145	169	131	131	154	0	103	103	158	158	190	187

Population G

Colony												
1												
Q	145	169	131	131	154	152	103	103	158	158		
M	145		131		152		103		158			
M	169		131		152		103		158			
M	145		137		152		103		161			
M	169		140		152		103		158			
M	169		131		158		103		158			
M	169		131		160		103		158			
M	169		131		154		103					

1	169	169	131	131	152	152	103	103	158	158
2	145	145	131	131	152	152	103	103	158	158
3	169	169	137	131	160	154	103	103	158	158
4	169	169	131	131	154	154	103	103	158	158
5	169	169	131	131	160	154	103	103	158	158
6	169	169	131	131	154	154	103	103	158	158
7	145	169	131	131	160	152	103	103	158	158
8	145	145	131	131	152	152	103	103	158	158
9	169	169	131	131	154	154	103	103	158	158
10	169	169	131	131	158	154	103	103	158	158
11	169	169	140	131	152	154	103	103	158	158
12	145	169	137	131	152	154	103	103	161	158

Colony
2

Q	145	169	131	131	152	154	103	103	158	158
M	145		131		152		103		158	
M	169		137		160		103		158	
1	145	169	131	131	152	152	103	103	158	158
2	169	169	137	131	160	154	103	103	158	158
3	169	169	137	131	160	154	103	103	158	158
4	145	169	131	131	152	152	103	103	158	158
5	145	145	131	131	152	152	103	103	158	158
6	145	169	131	131	152	154	103	103	158	158
7	145	145	131	131	152	152	103	103	158	158
8	145	169	131	131	152	154	103	103	158	158
9	145	145	131	131	152	152	103	103	158	158
10	145	169			152	152	103	103	158	158
11	145	169	131	131			103	103	158	158
12	145	169			152	152	103	103	158	158

Colony
3

Q	145	169	131	131	154	160	103	103	158	158	187	190
M	169		131		154		103		158		187	
M	169		131		160		103		158		190	
1	169	169	131	131	154	160	103	103	158	158		
2	169	145	131	131	154	160	103	103				
3	169	145	131	131	154	160	103	103	158	158	187	190
4	169	145	131	131	154	154	103	103	158	158	187	187
5	169	169	131	131	154	160	103	103	158	158	190	190
6	169	169	131	131			103	103	158	158		
7	169	145	131	131			103	103	158	158	187	190
8	169	145	131	131	160	160	103	103	158	158	190	187
9	169	145	131	131	154	160	103	103	158	158	187	190
10	169	145			160	160	103	103	158	158	190	187
11	169	169	131	131	160	160	103	103	158	158	190	187
12	169	145	131	131	154	160	103	103	158	158	190	190

Colony
4

Q	145	169	131	131	154	160	103	103	158	158	187	190
M	145		131		154		103		158		190	
M	169		131		160		103		158		190	
M	169		131		158		110		158			
1	145	169			158	160	110	103				
2	145	169	131	131	154	160	103	103	158	158		
3	169	169	131	131	160	160	103	103	158	158		
4	169	169	131	131	154	160	103	103	158	158	190	187
5	145	169	131	131	160	160	103	103	158	158	190	187
6	145	169	131	131	154	160	103	103	158	158	190	187
7			131	131	154	160	103	103	158	158	190	187

8	145	169	131	131	154	160	103	103	158	158	190	190
9	145	169	131	131					158	158		
10	145	169	131	131	154	154	103	103	158	158		
11	145	169			160	160	103	103	158	158		
12	145	169	131	131	154	154	103	103				

Population H

Colony
1

Q 145 169 131 131 154 160 103 103 158 158

M 169 131 152 103 158

M 169 137 154 103 158

M 169 131 154 103 158

M 169 137 158 103 158

M 169 131 158 103 158

1 145 169 154 154 103 103 158 158

2 169 169 131 131 103 103 158 158

3 145 169 131 131 152 160 103 103 158 158

4 145 169 131 131 152 160 103 103 158 158

5 169 169 131 131 152 160 103 103 158 158

6 145 169 131 131 154 160 103 103 158 158

7 145 169 131 131 152 154 103 103 158 158

8 145 169 131 131 154 154 103 103 158 158

9 145 169 137 131 158 154 103 103 158 158

10 169 169 131 131 158 154 103 103 158 158

11 145 169 137 131 154 154 103 103 158 158

12 145 169 137 131 154 154 103 103 158 158

Colony

2

Q	145	169	131	131	152	158	103	103	158	158
M	169		131		152		103		158	
1	169	145	131	131	152	152	103	103	158	158
2	169	145	131	131	152	152	103	103	158	158
3	169	145	131	131	152	152	103	103	158	158
4	169	145	131	131	152	152	103	103	158	158
5	169	145	131	131	152	152	103	103	158	158
6	169	169	131	131	158	152	103	103	158	158
7	169	145	131	131	152	152	103	103	158	158
8	169	145	131	131	152	152	103	103	158	158
9	169	145	131	131	152	152	103	103	158	158
10	169	169	131	131	158	152	103	103	158	158
11	169	145	131	131	152	152	103	103	158	158
12	169	145	131	131	152	152			158	158

Colony
3

Q	145	169	131	140	152	152	103	103	158	161	187	190
M	169		131		152		103		158		187	
M	169		140		152		103		158		190	
M	169		131		158		103		158		187	
M	169		131		160		103		103		190	
1	169	145					103	103	161	158	187	190
2					152	152	103	103	161	158	187	190
3	169	169	131	131	152	152	103	103	158	158	187	190
4	169	169	131	140	158	152	103	103	158	158	187	190
5	169	145	131	140	152	152	103	103	158	158	187	190
6	169	145	131	140	152	152	103	103	158	158	187	187
7	169	145			152	152	103	103	158	158	187	187

8	169	145	131	140	158	152	103	103	158	158	187	187
9	169	145	131	140	152	152	103	103	158	158	187	187
10	169	145	131	131	152	152	103	103	158	158	187	187
11	169	145	131	140	160	152	103	103	158	158	190	190
12	169	145	140	140	152	152	103	103	158	158	190	190
Colony 4												
Q	145	169	131	137	158	158	103	103	158	158	187	190
M	169		137		152		103		158		187	
M	169		131		158		103		158			
M	169		137		160		103		158		187	
M	169		137		174		103		158		190	
1	169	145	131	137	152	158	103	103	158	158		
2	169	145	137	137	152	158	103	103	158	158		
3	169	145	131	137	152	158	103	103	158	158	187	187
4	169	145	137	137	160	158	103	103	158	158	190	190
5	169	145	137	137	174	158	103	103	158	158	190	190
6	169	169	131	131	158	158	103	103	158	158		
7	169	145	137	137	152	158	103	103	158	158	187	190
8	169	145	131	137	160	158	103	103	158	158		
9	169	145	137	137	160	158	103	103	158	158	187	190
10	169	169			160	158	103	103	158	158	187	187
11	169	145			152	158	103	103	158	158	187	190
12	169	145	131	137	174	158	103	103	158	158		

Population I

Colony
1

Q	145	169	131	131	158	160	103	103	158	161	187	190
M	169		131		158		103		158		190	
M	169		131		158		103		158		187	
1	169	169	131	131	158	158	103	103	158	158		
2	169	169	131	131	158	158	103	103	158	158	187	187
3	169	169	131	131	158	160	103	103	158	158	190	187
4	169	169	131	131	158	160	103	103	158	158	190	187
5	169	169	131	131	158	160	103	103	158	158	190	187
6	169	169	131	131	158	160	103	103	158	158	190	190
7	169	169	131	131	158	160	103	103	158	158	190	187
8	169	169	131	131	158	158	103	103	158	158	190	190
9	169	145	131	131	158	160	103	103	158	161	190	187
10	169	145	131	131	158	160	103	103	158	158	187	187
11	169	169	131	131	158	160	103	103	158	158		
12	169	145	131	131	158	160	103	103	158	158	190	187

Colony
2

Q	169	169	131	131	158	0	103	103	158	158	187	190
M	169		131		158		103		158		190	
M	169		131		152		103		158		190	
1	169	169	131	131	158	0	103	103	158	158	190	187
2	169	169	131	131	152	0	103	103	158	158	190	187
3	169	169	131	131	158	0	103	103	158	158	190	190
4	169	169	131	131	158	0	103	103	158	158	190	187
5	169	169	131	131	152	0	103	103	158	158	190	187
6	169	169	131	131	158	0	103	103	158	158	190	187
7	169	169	131	131	158	0	103	103	158	158	190	187
8	169	169	131	131	158	158	103	103	158	158	190	190
9	169	169	131	131	158	158	103	103	158	158	190	187

10	169	169	131	131	158	158	103	103	158	158	190	187
11	169	169	131	131	158	158	103	103	158	158	190	190
12	169	169	131	131	158	158	103	103	158	158	190	190

Colony
3

Q	145	145	131	131	152	160	103	103	158	158
M	145		131		152		103		158	
M	145		131		158		103		158	
1	145	169	131	131	158	152	103	103	158	158
2	145	169	131	131	158	160	103	103	158	158
3	145	145	131	131	152	152	103	103	158	158
4	145	145	131	131	152	152	103	103	158	158
5			131	131	152	160	103	103	158	158
6	145	169	131	131	152	160	103	103	158	158
7	145	145	131	131	152	152	103	103	158	158
8	145	145	131	131	152	152	103	103	158	158
9	145	145	131	131	152	152	103	103	158	158
10	145	145	131	131	152	152	103	103	158	158
11	145	169	131	131	152	152	103	103	158	158
12	145	169	131	131			103	103	158	158

Colony
4

Q	145	169	131	137	0	158	103	103	158	158
M	169		131		152		103		158	
M	169		137		152		103		161	
1	169	145	131	131	152	0	103	103	158	158
2	169	169	131	137	152	158	103	103	158	158
3	169	145	131	131	152	158	103	103	158	158
4	169	145	131	131	152	0	103	103	158	158
5	169	145	131	131	152	158	103	103	158	158

6	169	145	131	131	152	158	103	103	158	158
7	169	145	131	131	152	158	103	103	158	158
8	169	169	131	137	152	158	103	103	158	158
9	169	169	131	137	152	158	103	103	158	158
10	169	169	131	137	152	0	103	103	158	158
11	169	169	131	137	152	158	103	103	158	158
12	169	145	137	137	152	0	103	103	161	158