SUPPLEMENTARY INFORMATION

‘Individual- and population-level drivers of consistent foraging success across environments’

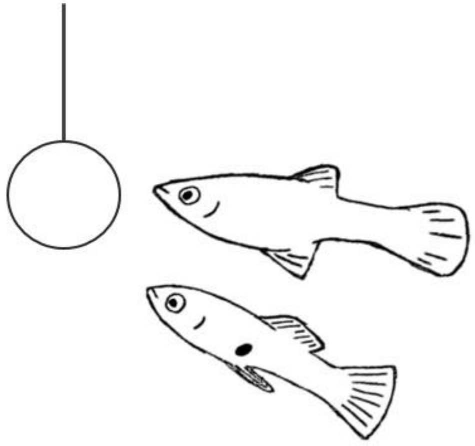
Snijders et al.

Supplementary Methods and Results

- **Video observation checklist and inter-observer agreement**
- **Additional information on model selection**
- **Additional information on subpopulation size corrections for Υ-measure**
- **Additional statistical analysis: Are males better in food resource detection?**
- **Supplementary literature**

Supplementary Tables

- **Table 1 | Individual repeatability estimates for foraging success**
- **Table 2 | Timeline of experiment**
- **Table 3 | Details subpopulation composition**
- **Table 4 | Starting model summary**
- **Tables 5 – 13 | Summary tables for final model statistics of fixed effects**



Supplementary Figures

- **Fig. 1 | The proportion of control and food resources reached by at least one fish of the subpopulation.**
- **Fig. 2 | The number of bites individuals gained in relation to the proportion of resources they reached.**
- **Fig. 3 | The number of bites individuals gained in the first pool compared to the second pool.**
- **Fig. 4 | The proportion of resources at which an individual arrived first in relation to its sex.**
- **Fig. 5 | The proportion of resources reached first by an individual, relative to the total resources reached by the same individual, for the second pool against the first pool.**
- **Fig. 6 | Likelihood that first arrivals are joined by subpopulation members in relation to their sex.**
- **Fig. 7 | Pool characteristics**

SUPPLEMENTARY METHODS AND RESULTS

Video observation checklist and inter-observer agreement

All the BORIS[1] video analysis files were compared with data from the field notes. When the number or ID of the fish in the analysis did not match the data in the field notes, the videos were checked by a third observer (L.S.), who was also present during the colour marking of the fish in the field. All fish in the video analysis could be reliably identified in this way. Agreement between the two video observers was tested by means of the second observer repeating 18 of the video analyses done by the first observer. These videos included three different subpopulations of fish (six videos per subpopulation). Arrival latencies scored by the observers were highly correlated (latency first fish: $R^2 = 0.995$) and there was complete agreement on the number of fish present per trial (Number of fish: $R^2 = 1$). 97% of the visiting fish were assigned the same ID by both observers. The misidentified 3% comprised of two times the same juvenile fish. However, because this misidentification also did not agree with the field notes, this mistake was picked-up by our standard validation procedure, leading to 100% agreement in individual fish identification.

Additional information on model selection

With the exception of the first model (model 1, Supplementary Table 4), undetected resources (8%) were excluded from all analyses. We used the package ‘*rptR*’[2] to calculate repeatability (N bootstraps = 1,000, N permutations = 1,000), yet due to the package restrictions, random effects (Subpopulation identity and Individual identity) could not be nested and dependent variables were treated following a Gaussian distribution. Nevertheless, conclusions from these models did not differ from models with nested random factors and a Binomial distribution (run in ‘*lme4*’). Moreover, Subpopulation identity did not significantly explain variation in resource visitation in both the control and food treatments (Repeatability (R) < 0.04). Control variables inherent to the research design were kept in the final model at all times, also when they were not significant. When an interaction between variables was significant, these variables were not further tested for main effects (due to lack of interpretability). Pool identity, when not part of a nested structure, was included as a fixed and not as a random effect (because it consisted of only four levels). Supplementary Table 4 presents all full models and Supplementary Tables 5 to 13 present the final model statistics. All GLMMs were running with ‘bobyqa’ as optimizer. Linear model fit was evaluated by visual inspection of the fitted versus residual plot and the frequency distribution of the residuals. Binomial model fit (proportional data) was evaluated by testing for over-dispersion with the ‘*sjstats*’ package[3]. For models that showed (minor) deviations from fit (e.g. over-dispersion ratio < 1.25, $P < 0.05$), potential outlier individuals (*Cook’s D* > 4/n) were removed, starting with the largest outlier (all potential outliers were below *Cook’s D* < 0.5). Outliers were determined using the ‘*influence.ME*’ package[4]. These models significantly improved after the removal of the same single individual. When such adjusted models did not result in qualitatively different conclusions for our variables (and their interactions) of interest, we deemed the original models acceptable. Conclusions for socially dependent variables (i.e. Social time, Υ-measure) were drawn based on permutation models (see Methods). Juveniles (six out of 68 individuals), which could not be sexed and therefore were excluded from models including Sex or Υ-measure, only represented 3% of all visits.

Additional information on subpopulation size corrections for Υ-measure

During our observations of social phenotypes, we had six subpopulations of eight individuals and two subpopulations of seven individuals (Supplementary Table 3). Because the Υ-measure is sensitive for differences in subpopulation size, we ran the analyses with Υ-measure values corrected for subpopulation size. We did not change the Υ-values for the subpopulations with eight individuals but adjusted the Υ-values for the individuals in the two subpopulations with seven individuals. From the definition of the Υ-measure it follows that the smallest possible values in a group of seven ("$G7$") and in a group of eight ("$G8$") differ by a factor of 6/7 = 0.857, more precisely $G8 = 0.857 * G7$, while the largest possible Υ-value (= 1) is the same for all group sizes. Therefore, the factor needed for the adjustment lies in the range 0.857 - 1. We determined that the mean Υ-values in randomized networks with seven and eight individuals in the absence of individual preferences differed by a factor of 0.862, and in our data that the mean Υ-values in the subpopulations with seven and eight individuals differed by a factor of 0.895. For our analyses, we used the factors 0.857 and 0.895. The P-values were almost the same. Therefore, we only reported the results for the factor 0.895.

Additional statistical analysis

Are males better in food resource detection?

Although males reached more food resources than females, the sexes did not differ in their likelihood to be the first fish to reach a food (or control) resource (Pairwise contrast[5] females to males in Food Treatment: *Z ratio* = -1.80, *P* = 0.27; Control Treatment: *Z ratio* = 0.89, *P* = 0.81; Supplementary Table 12; Supplementary Fig. 3). This suggests that females did not reach less food resources because they were poorer detectors or that males reached more resources because they were more strongly attracted to the food resource. Most resources reached by an individual were reached after another fish arrived first (62%), suggesting that individual food detection ability was not the primary mechanism of individuals to reach a food resource. It should, however, be noted that more than 56% of the arrival latencies between a first and second fish were within three seconds. We can therefore not conclusively designate all first arrivals as the initial detectors of a resource; i.e. first arrivals could have followed another fish and just have swum a bit faster. Juveniles (six out of 68 individuals, unsexed) only represented 3% of all first arrivals.

Supplementary literature

1. Friard, O. & Gamba, M. BORIS: a free, versatile open-source event-logging software for video/audio coding and live observations. *Methods Ecol. Evol.* **7,** 1325–1330 (2016).
2. Stoffel, M. A., Nakagawa, S. & Schielzeth, H. rptR: Repeatability estimation and variance decomposition by generalized linear mixed-effects models. *Methods Ecol. Evol.* **8,** 1639–1644 (2017).
3. Lüdecke, D. *sjstats: Statistical Functions for Regression Models*. R package version 0.13.0 (2017).
4. Nieuwenhuis, R., te Grotenhuis, H. & Pelzer, B. Influence.ME: Tools for detecting influential data in mixed effects models. *R J.* **4,** 38–47 (2012).
5. Lenth, R. V. Least-Squares Means: The R Package lsmeans. *J. Stat. Softw.* **69,** 1–33 (2016).

SUPPLEMENTARY TABLES

Table 1 | Individual repeatability estimates for foraging success (models 2 & 6 in Supplementary Table 4). Pool and Relocation were always included as fixed (control) factors and Subpopulation and Individual were always included as random factors. Repeatability of Individual is estimated, including specific individual (physical and behavioural) traits to evaluate if these traits substantially explain Individual variation in the foraging measure. When there is no longer substantial repeatability of the Individual (i.e. confidence intervals reach zero and *P* > 0.05 in bold), it suggests that the included individual traits might be at least partly responsible for the consistent individual foraging differences across environments.

Measure	**Explanatory factors added**	***Repeatability (R)***	***SE***	***CI***	***P***
Proportion of detected food resources reached	-	0.34	0.13	0.09 – 0.59	0.02
	Sex + Social time	0.00	0.11	**0.00 – 0.35**	**0.50**
	Sex	0.10	0.12	**0.00 – 0.42**	**0.28**
	Social time	0.26	0.14	**0.00 – 0.53**	**0.07**
	Body length	0.35	0.13	0.12 – 0.61	0.01
	Bite rate	0.34	0.13	0.09 – 0.63	0.02
Total number of bites relative to total number of detected food resources	-	0.36	0.13	0.12 – 0.62	0.01
	Sex + Social time	0.19	0.12	0.01 – 0.49	0.06
	Sex	0.28	0.12	0.09 – 0.57	0.02
	Social time	0.30	0.13	0.03 – 0.57	0.04
	Body length	0.23	0.13	**0.00 – 0.52**	**0.07**
	Bite rate	0.03	0.11	**0.00 – 0.36**	**0.42**

Table 2 | Timeline of experiment

Date March 2016:		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
Pool 1	Activity	Focal observations			Pilot*	Foraging Trials			Focal		Trials				Focal		Trials			
	Subpopulation	1A							2A				2C	*Fish missing*	3A				3C	
Pool 2	Activity	Focal observations			Pilot*	Foraging Trials			Focal		Trials				Focal		Trials			
	Subpopulation	1B							2B				2A		3B				3A	
Pool 3	Activity	Focal observations			Pilot*	Foraging Trials							Trials						Trials	
	Subpopulation	1C						*Fish missing*					2B						3B	
Pool 4	Activity								Focal		Trials				Focal		Trials			
	Subpopulation								2C						3C					

*data not included in analysis

Table 3 | Details subpopulation composition

Subpopulation	N Focal	N Trials	N Adults	N Females	N Males	Sex ratio
1A	8	8	8	5	3	1.67
1B	8	8	4	3	1	3.0
1C	8	6	5	2	3	0.67
2A	8	8	8	6	2	3.0
2B	7	7	7	5	2	2.5
2C	7	7	6	4	2	2.0
3A	8	8	8	6	2	3.0
3B	8	8	8	6	2	3.0
3C	8	8	8	6	2	3.0

Table 4a | Starting model summary.

#	Dependent	Independent variables	Random factors	Unit of analysis	Subset	# Observations	# Individuals	# Subpopulations	Weights	Distribution	R package
1	Yes/No detection	Treatment*Time + Drop + Relocation	Pool/ Zone + Subpopulation	Resource	.	1,135	.	9	.	Binomial / binary	glmer (lme4)
2a0	Proportion of detected resources reached	Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2b0	Proportion of detected resources reached	Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Control resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2a1	Proportion of detected resources reached	Sex + Social time + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources & adults	107	62	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2a2	Proportion of detected resources reached	Sex + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources & adults	107	62	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2a3	Proportion of detected resources reached	Social time + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2a4	Proportion of detected resources reached	Body length + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
2a5	Proportion of detected resources reached	Bite rate + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
3a	Reached resources / Total detected resources	Treatment*Sex + Treatment*Social time + Treatment*Bite rate (sex centred) + Treatment*Sex ratio+ Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Adults	214	62	9	Total detected resources	Binomial / prop	glmer (lme4)
3b	Reached resources / Total detected resources	Treatment*Sex + Treatment*Body length + Treatment*Bite rate (sex centred) + Treatment*Sex ratio+ Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Adults	214	62	9	Total detected resources	Binomial / prop	glmer (lme4)
4a	Total number of bites / Total detected resources	Prop. resources reached + Bite rate + Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Food resources	114	68	9	.	Gaussian	lmer (lme4)
4b	Total number of bites / Total detected resources	Sex + Social time + Sex ratio + Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Food resources & adults	107	62	9	.	Gaussian	lmer (lme4)
5	Total number of bites / Total time at resource (Bite rate)	Sex + Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Food resources & adults	107	62	9	.	Gaussian	lmer (lme4)

Table 4b | Starting model summary *continued*.

#	Dependent	Independent variables	Random factors	Unit of analysis	Subset	# Observations	# Individuals	# Subpopulations	Weights	Distribution	R package
6a	Total number of bites / Total detected resources	Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
6a1	Total number of bites / Total detected resources	Sex + Social time + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources & adults	107	62	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
6a2	Total number of bites / Total detected resources	Sex + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources & adults	107	62	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
6a3	Total number of bites / Total detected resources	Social time + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
6a4	Total number of bites / Total detected resources	Body length + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
6a5	Total number of bites / Total detected resources	Bite rate + Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
7a	Resources reached first / Resources reached	Pool + Relocation	Subpopulation + Individual	Individual/ Pool	Food resources	114	68	9 (6 rpt)	.	Gaussian	rptGaussian (rptR)
8	First arrival joined (yes/no)	Treatment*Males first*Time + Treatment*Social time first*Time + Relocation + Drop	Pool/ Zone + Subpopulation/ Individual	Resource	Adults (excl. simultaneous first arrivals)	907	62	9	.	Binomial / binary	glmer (lme4)
9	Number of individuals arriving at a resource during trial / Subpopulation size during foraging trial	Treatment*Males first*Time + Treatment*Social time first*Time + Relocation + Drop	Pool/ Zone + Subpopulation/ Individual	Resource	Adults (excl. simultaneous first arrivals)	907	62	9	Total adults in trials	Binomial / prop	glmer (lme4)
10	First arrivals at resources / Total detected resources	Treatment*Sex + Treatment*Social time + Treatment*Bite rate (sex centred) + Treatment*Sex ratio + Pool + Relocation	Subpopulation/ Individual	Individual/ Pool	Adults (excl. simultaneous first arrivals)	214	62	9	Total detected resources	Binomial / prop	glmer (lme4)

Summary tables for final model statistics of fixed effects

To test the significance of the fixed effects, we compared models with and without the fixed effect of interest using Log Likelihood Ratio (LLR) tests. The full model details are listed in Supplementary Table 4. Variables of interest and control variables inherent to the research design were kept in the final model at all times, also when they were not significant ($P > 0.05$). When an interaction between variables was significant or tended to be significant ($P < 0.1$), we did not test these variables further for main effects (due to lack of interpretability), resulting in corresponding empty table cells for *P values*. Conclusions for socially dependent fixed effects (i.e. Social time, Υ-measure) on total number of bites and proportion of resources reached were based on permutation models (see Methods). In other models, Social time was added as control variable and its (non-)significance was thus not evaluated with permutation tests, likewise resulting in corresponding empty table cells for *P values.*

Table 5 | Fixed effect final model statistics for initial resource detection (model 1). Significance values based on final model comparison including and excluding the variable. Zone (nested in Pool) (*N* = 36), Subpopulation (*N* = 9) and Pool (*N* = 4) were included as random factors.

Explanatory	***Estimate (SE)***	***z***	χ^2	***P***
Treatment (food)	0.83 (0.24)	3.41	10.99	< 0.001
Relocation (2nd pool)	-0.30 (0.37)	-0.80	1.63	0.20

Number of observations = 1,135

Table 6 | Fixed effect final model statistics for proportion of resources reached (model 3a). Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) ($N = 62$), and Subpopulation ($N = 9$) were included as random factors. We ran additional permutation models for food and control treatment separately, replacing Sex with Υ-measure**.**

Explanatory	***Estimate (SE)***	***z***	χ^2	***P***
Treatment (food)	0.34 (0.06)	5.38	.	.
Sex (male) [Υ-measure]	0.23 (0.11)	2.08	.	.
Social time	0.07 (0.06)	1.25	.	.
Bite rate (sex centred)	0.13 (0.05)	2.73	.	.
Sex ratio	-0.13 (0.07)	-1.99	.	.
Pool 2	0.22 (0.09)	2.55	17.11	< 0.001
Pool 3	-0.06 (0.15)	-0.43		
Pool 4	-0.09 (0.12)	0.73		
Relocation (2nd pool)	0.28 (0.09)	3.18	8.09	0.004
Treatment:Sex	0.34 (0.11)	3.00	9.02	0.003
[Treatment:Υ-measure]				0.017 / 0.032*
Treatment:Social time	0.12 (0.05)	2.22	.	0.001 / 0.07*
Treatment:Bite rate	-0.11 (0.05)	-2.08	4.31	0.04
Treatment:Sex ratio	0.22 (0.06)	3.50	12.18	< 0.001

Number of observations = 214

**P-value based on randomization tests for Food / Control treatment, respectively (see Methods and Results)*

Table 7 | Fixed effect final model statistics for proportion of resources reached (model 3b). Same model as previous but with social time replaced by body length (collinearity). Only statistics for body length are given. Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) (*N* = 62), and Subpopulation (*N* = 9) were included as random factors.

Explanatory	**Estimate (SE)**	**z**	**χ^2**	**P**
Body length	-0.04 (0.06)	-0.70	.	.
Treatment:Body length*	0.12 (0.06)	1.94	3.78	0.052

Number of observations = 214

**Significant after removal of a potential outlier*

Table 8 | Fixed effect final model statistics for total number of bites per detected food resource (model 4a). Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) (*N* = 68), and Subpopulation (*N* = 9) were included as random factors.

Explanatory	***Estimate (SE)***	***t***	**χ^2**	***P***
Proportion of resources reached	3.84 (0.30)	12.67	100.10	< 0.001
Bite rate	3.89 (0.30)	13.00	103.85	< 0.001
Pool 2	1.50 (0.82)	1.83	8.11	0.04
Pool 3	3.31 (1.28)	9.14		
Pool 4	0.32 (1.04)	0.31		
Relocation (2nd pool)	-2.29 (0.77)	-2.96	8.42	0.004

Number of observations = 114

Table 9 | Fixed effect final model statistics for total number of bites per detected food resource (model 4b). Same model as previous but with proportion of resources reached and bite rate replaced by sex, social time and sex ratio. Subsequently, sex was replaced by ϒ-measure and social time by body length (due to collinearity). Only statistics for sex, social time, sex ratio, ϒ -measure and body length are given. Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) (*N* = 62), and Subpopulation (*N* = 9) were included as random factors.

Explanatory	***Estimate (SE)***	***t***	χ^2	***P***
Sex (male)	-2.10 (1.31)	-1.60	2.53	0.11
[ϒ-measure]	0.62 (0.66)	0.96	.	0.83*
Social time	1.87 (0.67)	2.82	.	0.004*
[Body length]	1.80 (0.69)	2.60	5.24	**0.02**
Sex ratio	2.11 (0.96)	2.19	5.82	**0.02**

Number of observations = 107

** P-value based on randomization tests (see Methods and Results)*

Table 10 | Fixed effect final model statistics for bite rate (bites per second present at food resource (model 5). Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) (*N* = 62), and Subpopulation (*N* = 9) were included as random factors.

Explanatory	***Estimate (SE)***	***t***	χ^2	***P***
Sex (male)	-0.18 (0.06)	-3.19	10.13	0.001
Pool 2	-0.06 (0.06)	-1.01	5.18	0.16
Pool 3	0.03 (0.09)	0.31		
Pool 4	-0.14 (0.07)	-1.95		
Relocation (2nd pool)	-0.07 (0.05)	-1.27	1.78	0.18

Number of observations = 107

Table 11 | Fixed effect final model statistics for likelihood of first arrival being joined at the resource (model 8). Significance values based on final model comparison including and excluding the variable. Zone (nested in Pool) (*N* = 36), Individual (nested in Subpopulation) (*N* = 62), Subpopulation (*N* = 9) and Pool (*N* = 4) were included as random factors. Interactions with Social time were added as control.

Explanatory	***Estimate (SE)***	***z***	χ^2	***P***
Treatment (food)	-0.97 (0.16)	-5.92	36.76	< 0.001
Sex (male)	0.58 (0.22)	2.59	.	.
Social time	-0.04 (0.11)	-0.38	.	.
Time (trial number)	-0.29 (0.16)	-1.80	.	.
Relocation (2nd pool)	-0.06 (0.32)	-0.20	0.04	0.84
Sex:Time	0.60 (0.18)	3.28	10.99	< 0.001
Time:Social time	-0.25 (0.09)	-2.83	.	.

Number of observations = 907

Table 12 | Fixed effect final model statistics for proportion of subpopulation present at a resource (model 9). Significance values based on final model comparison including and excluding the variable. Zone (nested in Pool) (*N* = 36), Individual (nested in Subpopulation) (*N* = 62), Subpopulation (*N* = 9) and Pool (*N* = 4) were included as random factors. Interactions with Social time were added as control.

Explanatory	***Estimate (SE)***	***z***	χ^2	***P***
Treatment (food)	0.47 (0.05)	8.69	76.03	< 0.001
Sex (male)	-0.29 (0.09)	-3.22	.	.
Social time	-0.00 (0.05)	-0.00	.	.
Time (trial number)	0.21 (0.06)	3.74	.	.
Relocation (2nd pool)	-0.02 (0.12)	-0.13	0.02	0.90
Drop resource after 1st arrival (yes)	-0.31 (0.13)	-2.33	5.57	0.02
Sex:Time	-0.15 (0.06)	-2.36	5.59	0.02
Time:Social time	0.06 (0.03)	2.21	.	.

Number of observations = 907

Table 13 | Fixed effect final model statistics for proportion of times an individual was first arrival* (model 10). Significance values based on final model comparison including and excluding the variable. Individual (nested in Subpopulation) (*N* = 62) and Subpopulation (*N* = 9) were included as random factors.

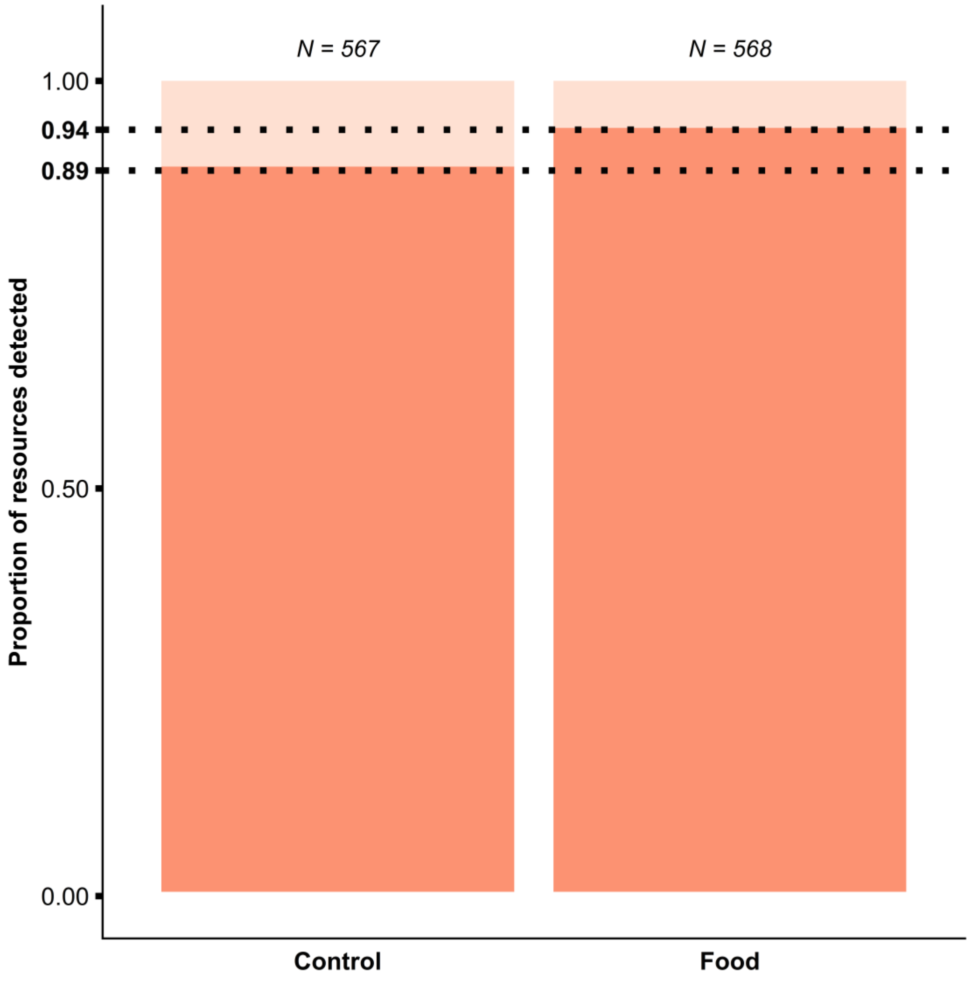
Explanatory	***Estimate (SE)***	***z***	χ^2	***P***
Treatment (food)	-0.13 (0.09)	-1.51	.	.
Sex (male)	-0.13 (0.15)	-0.89	.	.
Social time	0.07 (0.07)	1.08	.	.
Pool 2	0.17 (0.10)	1.61	5.22	0.16
Pool 3	0.34 (0.15)	2.22		
Pool 4	-0.08 (0.14)	-0.58		
Relocation (2nd pool)	-0.19 (0.10)	-1.93	3.67	0.055
Treatment:Sex	0.38 (0.16)	2.40	5.77	0.02**
Treatment:Social time	0.18 (0.07)	2.53	.	.

Number of observations = 214

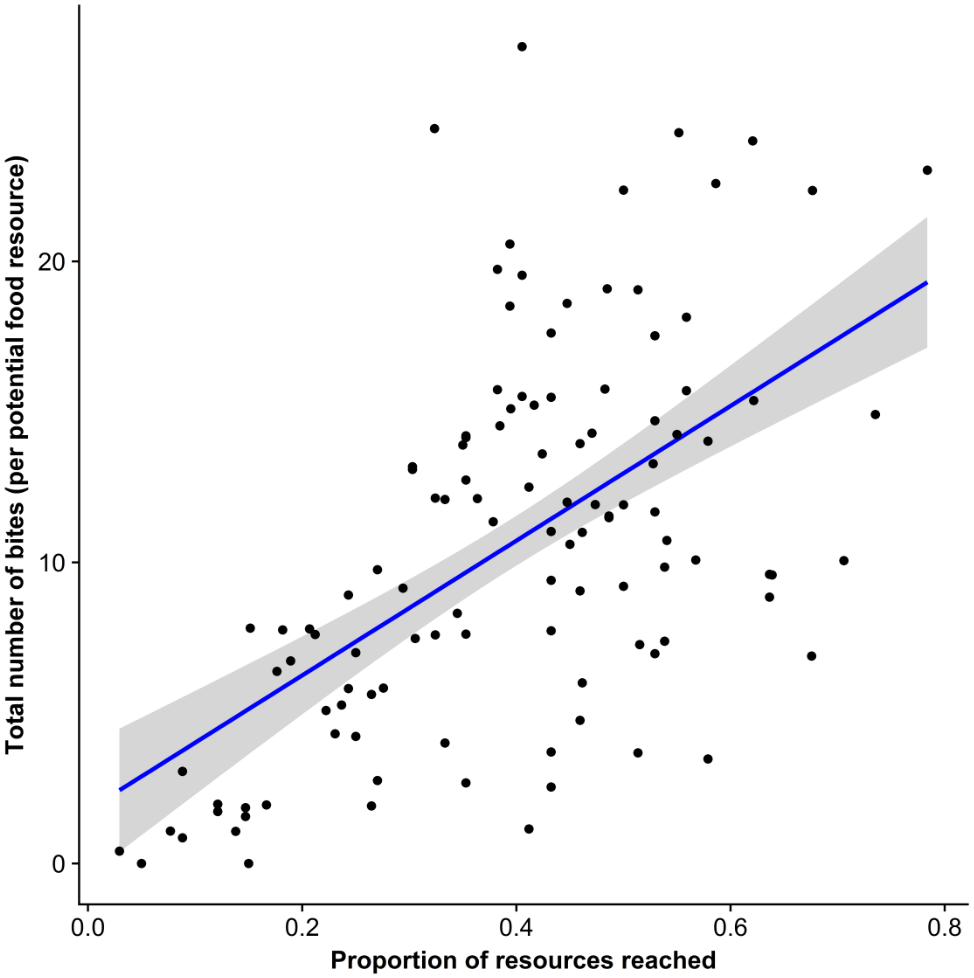
** See Supplementary Information: Additional Statistical Analysis for more information*

***Post-hoc comparisons between the sexes were all not significant*

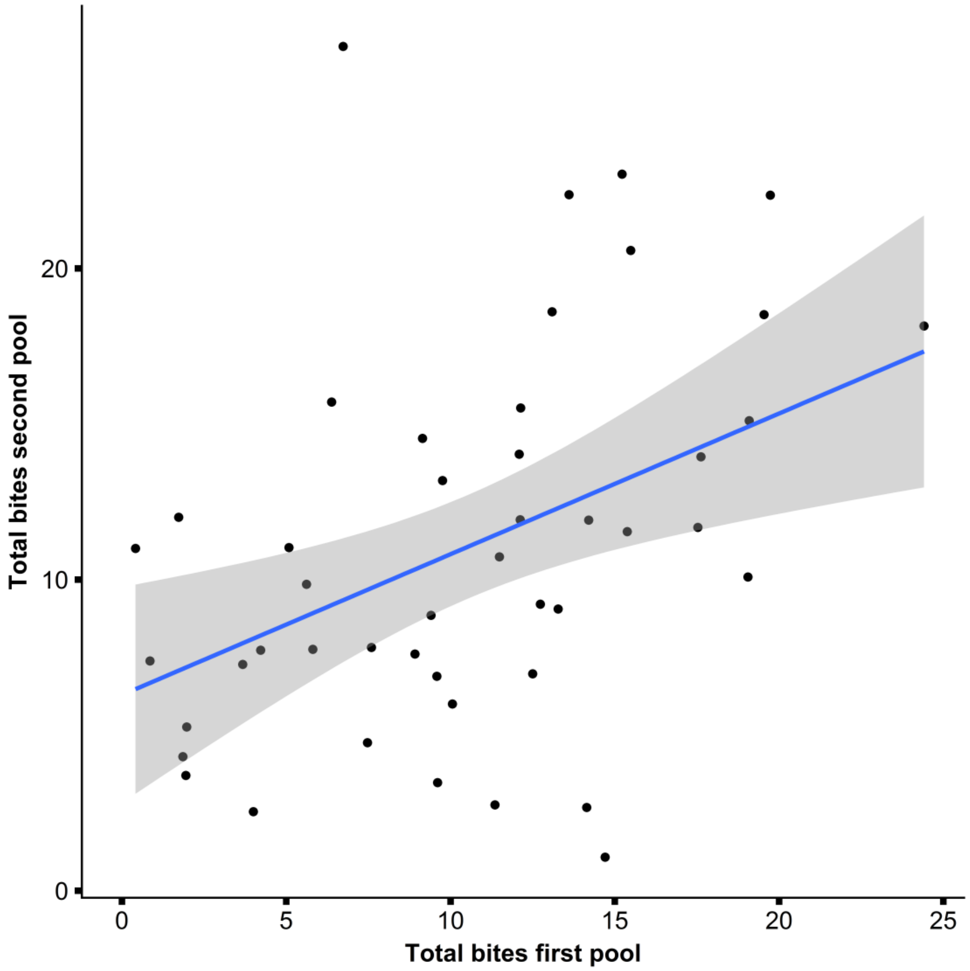
SUPPLEMENTARY FIGURES



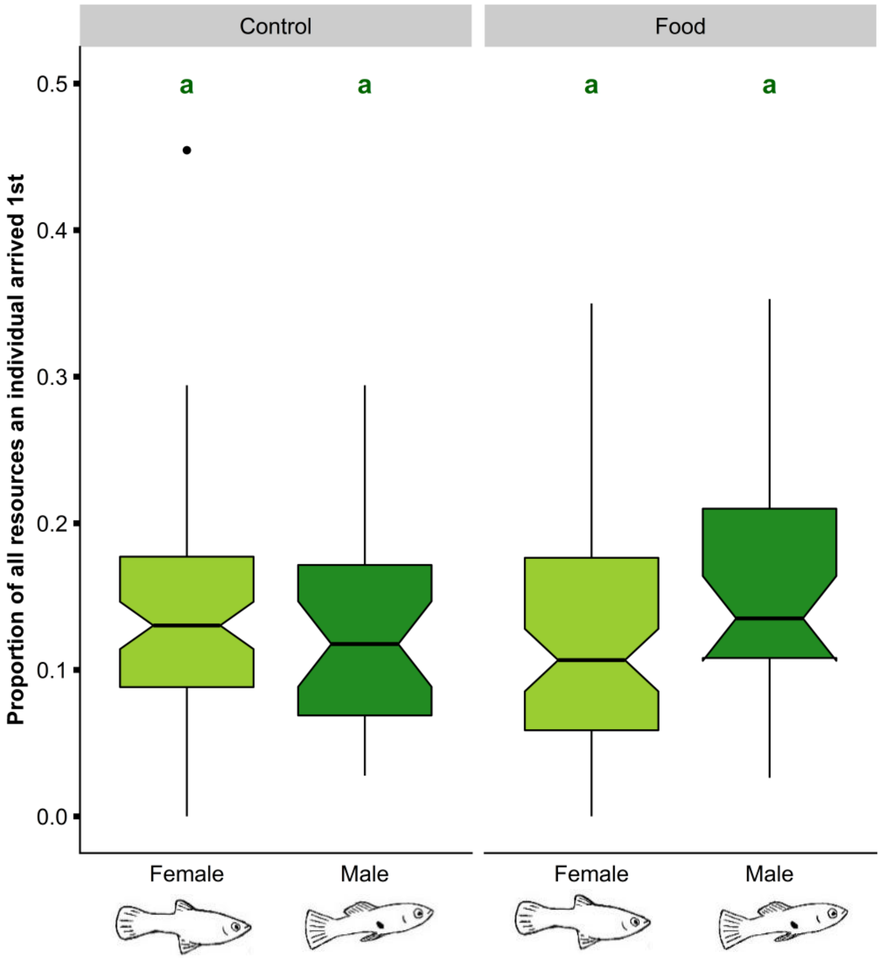
Supplementary Figure 1 | The proportion of control and food resources reached by at least one fish of the subpopulation. Overall, food resources were slightly more likely to be detected (detected = dark red fill, undetected = light red fill).



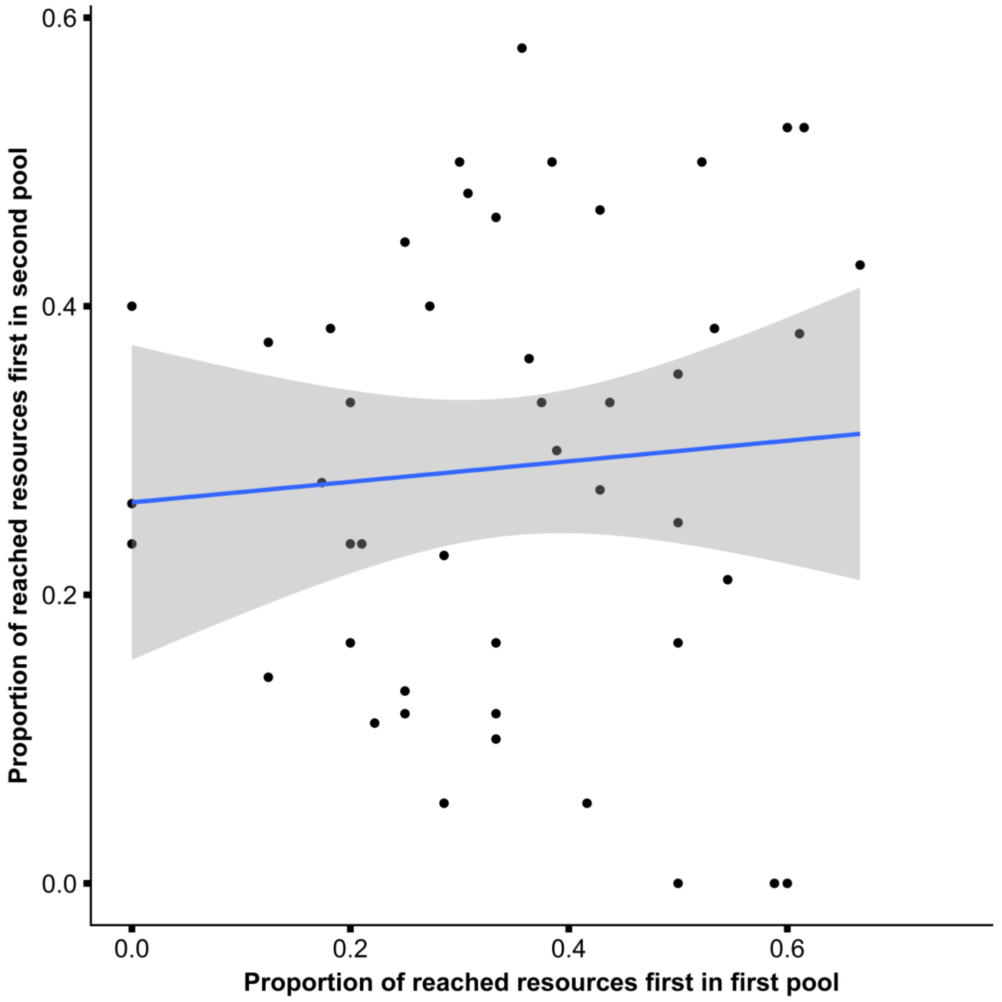
Supplementary Figure 2 | The number of bites individuals gained in relation to the proportion of resources they reached. Total number of bites acquired and proportion of resources reached are calculated relative to the total number of food resources detected per subpopulation per pool. Regression line (blue) and 95% *CI* (shaded area) based on fitted final model values.



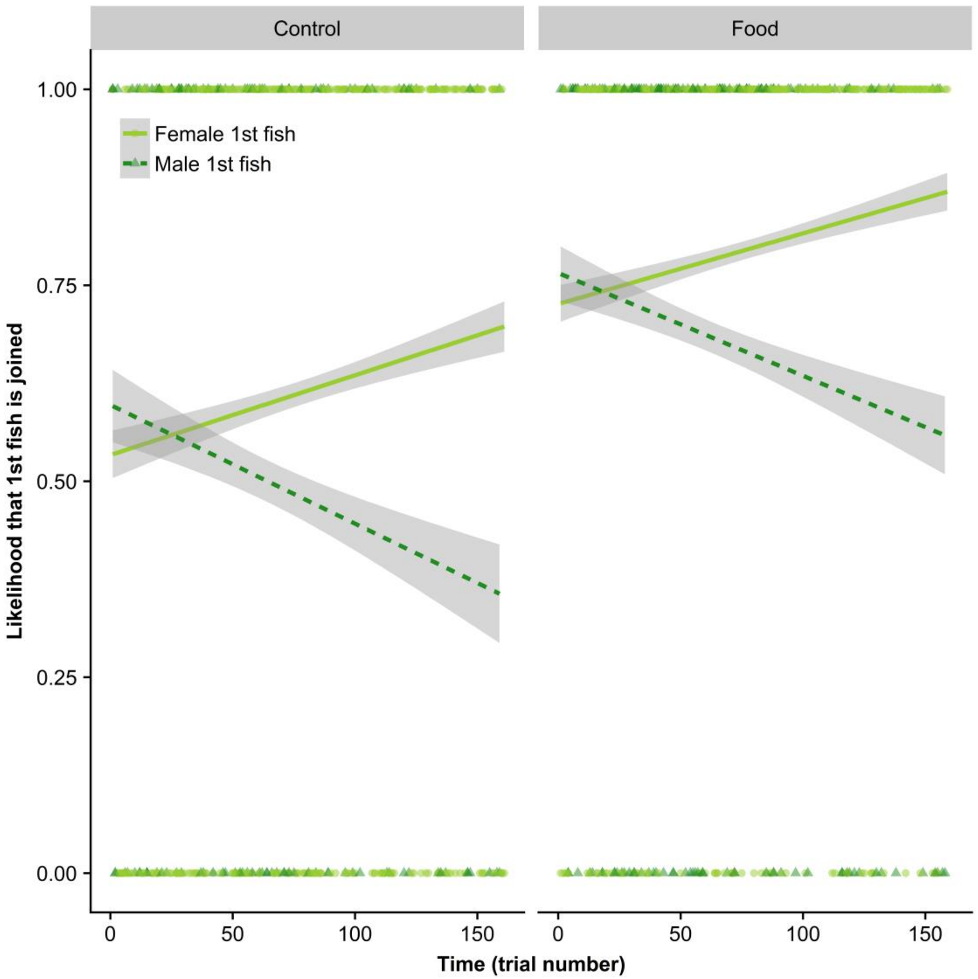
Supplementary Figure 3 | The number of bites individuals gained in the first pool compared to the second pool. Total number of bites acquired are calculated relative to the total number of food resources detected per subpopulation per pool. Regression lines and 95% *CI* (shaded area) are based on fitted values for bites acquired in the second pool against the first pool.



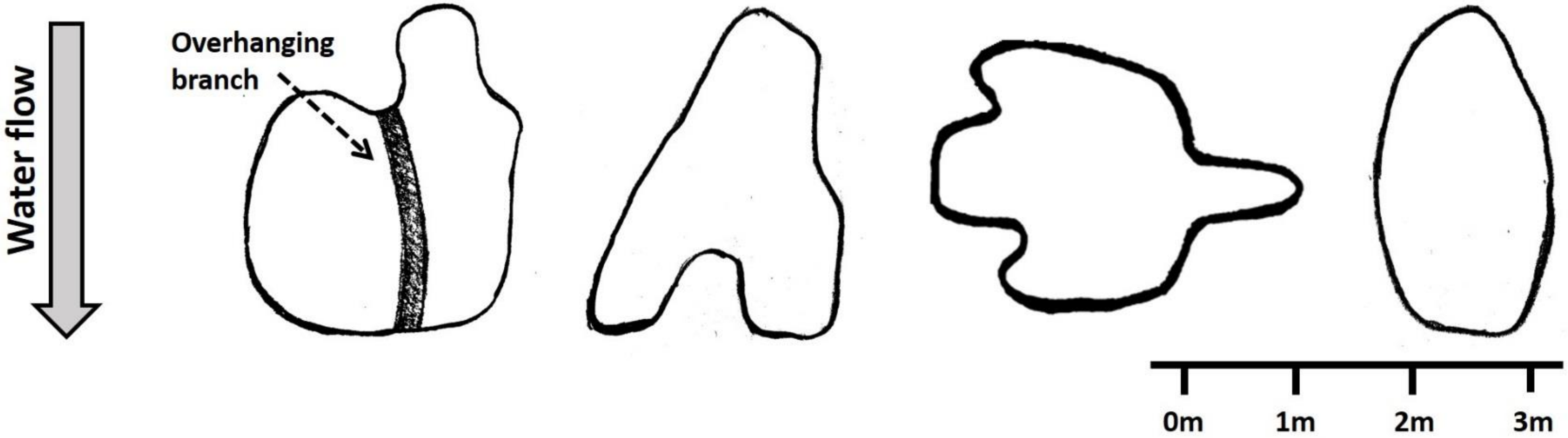
Supplementary Figure 4 | The proportion of resources at which an individual arrived first in relation to its sex. Males (dark fill) were not more or less likely than females (light fill) to be the first to arrive at a resource. Proportions are calculated relative to the total number of food or control resources detected per subpopulation per pool. Box plots show median and 25th to 75th percentiles with whiskers of 1.5 interquartile distances. Non-overlapping notches suggest a significant difference in medians. Letters ‘a’ indicate no significant differences revealed by post-hoc tests.



Supplementary Figure 5 | The proportion of resources reached first by an individual, relative to the total resources reached by the same individual, for the second pool against the first pool. Regression lines and 95% *CI* (shaded area) are based on fitted values for proportion of resources reached first in the 2nd pool against the 1st pool.



Supplementary Figure 6 | Likelihood that first arrivals are joined by subpopulation members in relation to their sex. Likelihood over time (trial number) whether a male (dark triangle, dashed line) or female fish (light circle, solid line) is joined by another fish after it was the first to arrive at a food or control resource. Over time, fish were more likely to reach a food or control resource when a female was the first to arrive than when a male was the first. Regression lines and 95% *CI* (shaded area) are based on fitted final model values.



	Pool 1	Pool 2	Pool 3	Pool 4
Max length (cm)	290	310	215	290
Max width (cm)	210	180	320	130
Avg (max) depth (cm)*	16 (21)	26 (38)	20 (25)	12 (16)
Substrate	Gravel + rocks + leaves	Completely rock + few leaves	Gravel + rocks + leaves	Gravel + rocks + leaves
Canopy	Closed	Open	Half open	Closed
Median % of food detected per batch	94.87 (*N* = 5)	97.37 (*N* = 5)	85.00 (*N* = 3)	96.25 (*N* = 2)

*Based on 5 measuring points

Supplementary Figure 7 | Pool characteristics. The four natural pools varied in shape, surface area, depth profile, substrate and canopy cover. These pool characteristics represent a substantial amount of the natural variation in pools that were present in the area, although deeper and larger as well as shallower and smaller pools also exist.