

Source-sink population structure of invasive common carp in a model Midwestern watershed: empirical evidence and notes on management

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Abstract

Effective management of invasive fishes requires a detailed understanding of the factors that influence population structure and persistence across relevant spatial and temporal scales. It has been hypothesized that the common carp (*Cyprinus carpio*) is often invasive in the North American Midwest due to its propensity to utilize shallow, predator-free basins as productive nursery habitat. Although it has been demonstrated that such basins often support extremely high abundances of young carp, the fate of these carp is unknown. To determine whether these putative nurseries serve as important sources of recruits at a watershed scale, we used mark-recapture and genetic assignment methods to investigate carp recruitment in a system of interconnected lakes, ponds, and associated wetlands in central Minnesota. Annual trap net surveys in 4 lakes and 8 ponds in the Phalen Chain watershed from 2009-2013 revealed that young-of-year carp were found exclusively in shallow pond habitats. Mark-recapture studies in 2011 and 2012 indicated that, of the 613 carp marked in one of the putative nursery ponds, ~31% of recaptured carp (25 of 80) had emigrated from the nursery pond to a connected water body. Microsatellite analysis of carp tissue samples (n=1041) from all basins throughout the watershed and from individuals moving between lakes and putative nurseries during the spawning season revealed two genetically distinct strains of carp within the watershed. The distribution and movements of genetically distinct carp revealed patterns in dispersal and colonization consistent with the carp nursery hypothesis (i.e. source-sink population structure). Additionally, there was evidence of reproductive homing by adult common carp. Our results and continued research on carp recruitment dynamics will aid in the development of population models and integrated pest management strategies to combat this highly invasive species.

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Chapter 1: An Introduction

Source-sink dynamics in aquatic systems

Source-sink theory is a well-established ecological framework that describes how local demographic rates and dispersal affect the spatial structure and persistence of populations across heterogeneous habitats (Holt 1985; Pulliam 1988; Dias 1996). A source is defined as a habitat or location with a positive rate of population growth that serves as a net exporter of individuals whereas a sink is a habitat in which local reproduction is insufficient to sustain a population in the absence of immigration (Dias 1996). Habitats can also be classified as pseudosinks which, like true sinks, are net importers of individuals, but differ in that they can sustain local populations in the absence of immigration, albeit at a lower carrying capacity (Watkinson and Sutherland 1995, Dias 1996). Although source-sink dynamics is widely recognized as one of the most important ecological processes that operates at a landscape scale (Dunning et al. 1992), empirical evidence of this phenomenon in natural systems is rare due to the inherent difficulties in measuring demographic rates and dispersal patterns across large spatial scales (see reviews in Diffendorfer 1998; Runge et al. 2006; Lipcius et al. 2011).

Identifying sources, sinks, and patterns of dispersal across heterogeneous landscapes has implications for understanding and managing populations at appropriate spatial scales. Whether management goals are to promote the recovery of vulnerable populations, to maintain populations of commercial or recreational value, or to control nuisance populations, it is important to consider habitat-specific demographic rates and the spatial arrangement of habitats of differing quality. For example, when making conservation decisions such as setting harvest restrictions or siting marine protected

areas, source habitats and dispersal pathways must be protected because subpopulations within sink habitats will not otherwise persist (e.g. Crowder et al. 2000; Novaro et al. 2005). Conversely, when attempting to eradicate nuisance populations, demographic sources must be targeted otherwise they will provide an influx of recruits to sink populations (e.g. Robertson and Gemmill 2004; Berry and Kirkwood 2010).

Although rooted in terrestrial ecology, source-sink theory is also widely applicable to both marine and freshwater systems for a variety of taxa (see reviews in Schlosser and Angermeier 1995; Sale et al. 2006; Lipcius et al. 2011). An understanding of source-sink dynamics is especially important in aquatic systems because these systems are notoriously diverse, complex, and characterized by high levels of connectivity (Amoros and Bornette 2002). Additionally, aquatic organisms often have complex life histories requiring multiple habitat types to complete their life cycles (Beck et al. 2001). Studies on source-sink dynamics within aquatic systems have largely focused on conservation efforts such as designing marine reserves (e.g. Roberts 1998; Gerber et al. 2005; Gaines et al. 2010), improving the sustainability of harvest (e.g. Hindar et al. 2004; Wilberg et al. 2008), and promoting the recovery of threatened or endangered species (e.g. Lafferty et al. 1999; Woodford and McIntosh 2010).

Interestingly, very few studies have investigated possible source-sink dynamics occurring within invasive populations, although the utility of this approach for informing effective control strategies has been suggested (Travis and Park 2004). Notable exceptions include studies by Horvath et al. (1996) who concluded that lakes serve as sources of invasive zebra mussels (*Dreissena polymorpha*) to small outflowing creeks

that otherwise would not support self-sustaining populations (i.e. sinks), Lohmeyer and Garvey (2009) who concluded that unimpounded reaches of the Upper Mississippi River System serve as sources of Asian carps (*Hypophthalmichthys* spp.), whereas impounded pools are likely sinks, and Crook et al. (2013) who concluded juvenile common carp (*Cyprinus carpio*) captured in the main channel of a large river system in Australia originated from several off-channel habitats. Although these studies provide convincing evidence of source populations or habitats, it is unclear whether the habitats identified as sinks function as true sinks or pseudosinks. This is an important distinction that warrants further investigation to inform the management of aquatic invasive species because populations in pseudosinks can still persist even if source populations have been eradicated or dispersal pathways have been disrupted.

Sources, sinks, & invasive fishes

The introduction and establishment of nonnative invasive fishes is a growing problem that poses serious threats to freshwater and marine ecosystems around the world (Kolar and Lodge 2002; Garcia-Berthou et al. 2005, Vitule et al. 2009). Because management of invasive fishes requires a detailed understanding of the factors that influence population structure and persistence, the role that source-sink dynamics may have in regulating populations should not be overlooked (Sakai et al. 2001; Travis and Park 2004). If populations of invasive fishes are exhibiting true source-sink dynamics, control efforts could be better targeted towards eliminating source habitats or disrupting dispersal pathways because populations in sink habitats would naturally tend towards extinction.

Although invasiveness can be linked to both a species' characteristics (e.g. fecundity, physiological tolerances) and local biotic and abiotic environmental factors (e.g. biotic resistance, hydrologic connectivity), many invasive fishes share similar life histories in which they are highly mobile and utilize distinctive nursery habitats. Examples include silver and bighead carps (*Hypophthalmichthys* spp.; Lohmeyer and Garvey 2009), common carp (*Cyprinus carpio*; Bajer and Sorensen 2010), Northern pike (*Esox lucius*; Koed et al. 2006), and sea lamprey (*Petromyzon marinus*; Manion and Hanson 1980). Although the use of distinctive nursery habitats is well-documented, it is unclear whether these habitats are required for population persistence or if sub-optimal habitats could also sustain local populations. Detailed information on spatially-explicit demographic rates and dispersal patterns across landscapes are required to determine the applicability of the source-sink model (Dias 1996); presently, there is a paucity of empirical evidence.

Common carp as a model invasive fish

Background

The common carp is a migratory cyprinid native to the Ponto-Caspian region of Central Asia (Kohlmann and Kersten 2013). As a result of human introductions and subsequent successful colonizations, the common carp now has a circumglobal distribution and is recognized as one of the world's one-hundred most invasive species (Balon 1995; Lowe et al. 2000). The common carp is found at extremely high densities in diverse ecosystems ranging from interconnected drainage lakes of the North American Midwest to vast river-floodplain complexes of Australia and New Zealand (Koehn 2004;

Sorensen and Bajer 2011). At high densities, the common carp can cause tremendous damage to aquatic ecosystems due to its benthivorous feeding behavior (e.g. Crivelli 1983; Drenner et al. 1997; Bajer et al. 2009). Specifically, the foraging behavior of carp has been associated with declines in rooted macrophytes, increased turbidity, and increased nutrient loading (see review in Weber and Brown 2009).

Management

Due to the remarkable ability of the common carp to invade multiple types of habitats and the extensive damage often caused, nuisance populations of carp have been the target of control efforts for several decades (e.g. Ricker and Gottschalk 1941; Cahoon 1953; Shields 1958). Traditional control strategies have relied heavily on non-selective methods such as piscicides (e.g. Weier and Starr 1950; Marking 1992), water drawdowns (e.g. Shields 1958; Verrill and Berry 1995), and physical barriers (e.g. Bulow et al. 1988; Verrill and Berry 1995). In addition to adversely impacting non-target species, these efforts have been largely unsuccessful or their successes have been short-lived due to the ability of the common carp to rapidly repopulate or recolonize disturbed habitats (Weber and Brown 2009).

More recently, progress has been made in developing control strategies that exploit species-specific behaviors exhibited by the common carp. Examples include targeting winter aggregations using under-ice seining techniques (Penne and Pierce 2008; Bajer et al. 2011) and exploiting jumping abilities using specialized traps (Stuart et al. 2006). Additionally, research has also focused on identifying species-specific attractants such as pheromones (Sorensen and Stacey 2004; Sisler and Sorensen 2008) and

deterrents such as acoustic barriers (Zielinski 2011). Integrating these techniques and tools into a holistic common carp management strategy could greatly improve the efficacy of future control efforts, but this requires a better understanding of common carp life history and the factors contributing to its invasiveness. Specifically, information on recruitment patterns and early life history is limited and of great importance for understanding common carp population dynamics.

Invasiveness & source-sink theory

Recent studies of common carp in freshwater systems of North America (Bajer and Sorensen 2010; Bajer et al. 2012; Silbernagel and Sorensen 2013) and Australia (Driver et al. 2005; Stuart and Jones 2006a; Crook et al. 2013) provide circumstantial evidence that invasive populations may exhibit source-sink dynamics. More specifically, Bajer and Sorensen (2010) hypothesized that the success of common carp in drainage lakes of the North American Upper Midwest can be explained by their ability to overcome recruitment bottlenecks by utilizing specific, high-quality nursery habitats. They found that, although common carp spawning behavior was observed in both lakes and connected peripheral shallow basins, the age structure of the population indicated that recruitment was only successful in shallow basins and only in years after harsh winters. The authors speculated that this pattern was due to a lack of predators in the peripheral shallow basins following winterkill events. Subsequent studies supported this hypothesis with evidence that young-of-year common carp were only found in large numbers in water bodies that lacked native micro-predators (Bajer et al. 2012) and that over 95% of naturally spawned common carp eggs in a normoxic lake disappeared before

hatching while large numbers of common carp eggs were simultaneously found in the stomachs of bluegill sunfish (*Lepomis macrochirus*), a native micro-predator (Silbernagel and Sorensen 2013). Silbernagel and Sorensen (2013) further demonstrated that common carp larvae were also highly vulnerable to predation by native micro-predators.

Similar to the invasive common carp populations found in interconnected lake systems of North America, common carp recruitment in large Australian river systems also seems to be restricted to specific nursery habitats that may serve as sources of immigrants to connected sink habitats (King et al. 2003; Driver et al. 2005; Stuart and Jones 2006a; Crook et al. 2013). More specifically, studies have found that the presence of larval and sub-adult common carp is correlated with high water levels, suggesting that inundation of floodplain habitats is required for successful common carp recruitment (King et al. 2003; Driver et al. 2005). In support of this hypothesis, Stuart and Jones (2006a) found that more than 99% of their total catch of larval and young-of-year common carp in the Murray River occurred at or downstream of a large riverine wetland, suggesting that it was the primary source of carp recruitment. Although the emigration of common carp from putative floodplain source habitats has not been explicitly studied, it has been demonstrated that sub-adult common carp have the ability to disperse long distances in large river systems (> 9 km; Stuart and Jones 2006b). Furthermore, Crook et al. (2013) provided indirect evidence of common carp dispersal between riverine habitats by matching elemental signatures in otoliths of larval common carp sampled in off-channel nursery habitats with those of young-of-year common carp captured in the main channel.

Although the aforementioned studies provide circumstantial evidence that source-sink dynamics may be important in regulating populations of common carp, detailed information on habitat-specific demography coupled with evidence of dispersal of recruits is lacking. The patterns of common carp emigration from established recruitment hotspots and subsequent colonization of connected habitats within large interconnected freshwater systems are presently poorly understood. In particular, evidence of true sink habitats (i.e. habitats that do not support a self-sustaining population without an influx of immigrants) is weak and cannot be confirmed without measuring habitat-specific population growth rates in the absence of immigration or identifying the natal origins of all individuals.

There are very few studies that discuss the dispersal of common carp from prospective nursery sources, all of which offer meager circumstantial evidence (Sigler 1958; Vilizzi and Walker 1999; Gilligan and Schiller 2003; King et al. 2003) or provide course-scale movement data that are difficult to interpret (Stuart & Jones 2006b). There are anecdotal accounts of mass movements of juvenile carp leaving nursery habitats in response to dropping water levels (Sigler 1958) or after they have reached a certain length (Vilizzi & Walker 1999). Gilligan and Schiller (2003) sampled thousands of larval common carp drifting in the main channel of an Australian river as the spawning season floods retreated, but the source of these larvae was unconfirmed. Similarly, the greatest density of larval and juvenile carp sampled in the Murray-Darling River in a study by King et al. (2003) was also correlated with a falling hydrograph after a major flood event. Lastly, Stuart and Jones (2006b) tagged 127 juvenile carp in floodplain habitats of the

Murray-Darling River system, but only 6 individuals were recaptured, limiting their abilities to make generalizations. Future studies are needed to systematically address the emigration of common carp from prospective nursery sources.

Methods for studying nursery contribution at a landscape scale

There are numerous methods available for studying the dispersal of recruits from putative nurseries, each with advantages and disadvantages. Traditional methods of studying fish movement rely heavily on mark-recapture techniques using artificial tags, but the utility of this approach for tracking the dispersal of recruits may be limited by a variety of factors including the small body size of individuals, high mortality rates at early life stages, and low probabilities of recapture (Thorrold et al. 2002). Furthermore, mark-recapture methods may also underestimate movement rates and the spatial extent of movement if the sampling extent or intensity is inadequate (Lucas and Baras 2000). More recently, studies of nursery contribution have moved away from tracking movements of tagged individuals and instead have utilized indirect methods such as analyzing elemental signatures in otoliths (e.g. Hobbs et al. 2010; Thorisson et al. 2011; Crook et al. 2013) or using genetic markers to infer source populations (see review in Manel et al. 2005).

Unlike otolith microchemistry, where interpretation is often complicated by a lack of spatial variation in water chemistry or too much temporal variation in water chemistry (Gillanders 2002; Swearer et al. 2003; Crook et al. 2013), genetic assignment methods are robust to environmental fluctuations. One potential approach for determining the relative contribution of nursery sources across space and time is microsatellite DNA analysis coupled with age or length data. This approach is commonly used for identifying

fish stocks of commercial or recreational value and investigating differences in stock-specific variables such as recruitment, growth, or migratory behaviors (e.g. Page et al. 2003; Tucker et al. 2009; Miller et al. 2012). Analyzing variation across microsatellite loci may also be a useful technique for studying the recruitment dynamics of invasive fishes because, like native game fish, they have often been subject to stocking or introduction histories which could result in sufficient levels of genetic differentiation (e.g. historical intentional stocking from various sources or multiple unintentional introductions). Insufficient levels of genetic differentiations may however limit the utility of this approach, especially for studies with restricted spatial scales.

Thesis overview

This thesis is comprised of two chapters and four appendices. The goal of the first chapter is to provide background information on source-sink dynamics in aquatic systems and to introduce the study organism, the common carp. The second chapter describes a set of studies designed to test the hypothesis that common carp emigration from local recruitment hotspots can explain the distribution and persistence of common carp at a watershed scale (i.e. there is source-sink population structure). Chapter 2 is written in the style of Canadian Journal of Fisheries and Aquatic Sciences (CJFAS). I intend to submit a version of this manuscript for publication in CJFAS with co-authors Loren M. Miller, Reid G. Swanson, and Peter W. Sorensen. Data collected by Chris Chizinski, Przemyslaw Bajer, and Jacob Osborne are also included in Table 1 and Figure 2 of this Chapter.

The first appendix includes the summarized mark-recapture data that were used to generate the estimates of common carp abundance reported in Table 1 of Chapter 2. The

second appendix contains all of the detailed mark-recapture data of 1,246 common carp implanted with passive integrated transponders (PIT tags) in the study lakes. A subset of these individual encounter histories was used to calculate the emigration rates reported in Study 2 of Chapter 2. The third appendix includes allele frequencies, heterozygosities, and tests of Hardy-Weinberg equilibrium for the 12 common carp microsatellite loci analyzed in Study 3 of Chapter 2. The fourth appendix includes the methods and results of computer simulations to determine the genetic classifications used in Study 3 of Chapter 2. I intend to include some or all of the aforementioned appendices in the manuscript submission as supplemental data.

Chapter 2: Mark-recapture and genetic evidence reveals source-sink population structure
of invasive common carp in a model Midwestern watershed

Chapter Summary

Effective management of invasive fishes requires a detailed understanding of the factors that influence population structure and persistence across relevant spatial and temporal scales. It has been hypothesized that the common carp (*Cyprinus carpio*) is often invasive in the North American Midwest due to its propensity to utilize shallow, predator-free basins as productive nursery habitat. Although it has been demonstrated that such basins often support extremely high abundances of young carp, the fate of these carp is unknown. To determine whether these putative nurseries serve as important sources of recruits at a watershed scale, we used mark-recapture and genetic assignment methods to investigate carp recruitment in a system of interconnected lakes, ponds, and associated wetlands in central Minnesota. Annual trap net surveys in 4 lakes and 8 ponds in the Phalen Chain watershed from 2009-2013 revealed that young-of-year carp were found exclusively in shallow pond habitats. Mark-recapture studies in 2011 and 2012 indicated that, of the 613 carp marked in one of the putative nursery ponds, ~31% of recaptured carp (25 of 80) had emigrated from the nursery pond to a connected water body. Microsatellite analysis of carp tissue samples (n=1041) from all basins throughout the watershed and from individuals moving between lakes and putative nurseries during the spawning season revealed two genetically distinct strains of carp within the watershed. The distribution and movements of genetically distinct carp revealed patterns in dispersal and colonization consistent with the carp nursery hypothesis (i.e. source-sink population structure). Additionally, there was evidence of reproductive homing by adult common carp. Our results and continued research on carp recruitment dynamics will aid in the development of population models and integrated pest management strategies to combat this highly invasive species.

Introduction

The introduction and establishment of nonnative invasive fishes is a growing problem that poses serious threats to freshwater and marine ecosystems around the world (Kolar and Lodge 2002; Garcia-Berthou et al. 2005; Vitule et al. 2009). Management of invasive fishes requires a detailed understanding of the factors that influence population structure and persistence across relevant spatial and temporal scales. In complex landscapes, such as large river systems or interconnected drainage lakes, there is often considerable variation in the quality of habitats as well as the degree of connectivity between habitat patches. Such heterogeneity across the landscape may lead to spatially explicit demographic rates (e.g. natality, mortality) resulting in some habitats serving as net sources of recruits and others as net sinks (Pulliam 1988; Dias 1996). Identification of possible sources, sinks, and dispersal pathways for invasive fish populations can have far-reaching management implications.

Source-sink theory defines sources as habitats with positive population growth rates that serve as net exporters of individuals whereas sinks are defined as habitats in which local reproduction is insufficient to sustain a population in the absence of immigration (Dias 1996). Because populations in sink habitats tend towards extinction without an influx of recruits from source habitats, dispersal between sources and sinks is essential for population persistence at the landscape scale (Figueira and Crowder 2006). Despite its many applications to the management of rare, vulnerable, or commercially important aquatic species (e.g. Roberts 1998; Wilberg et al. 2008; Woodford and McIntosh 2010), source-sink theory has rarely been applied to invasive populations

although the utility of this approach has been suggested (Travis and Park 2004). If invasive fish populations exhibit source-sink dynamics, management efforts could be better targeted towards locations where they would have the greatest adverse impact on population viability (i.e. source habitats or dispersal pathways).

Although it has been hypothesized that source-sink population dynamics often regulate species' abundance, distribution, and population viability (Dunning et al. 1992), empirical evidence of source-sink dynamics in natural systems is rare due to the difficulties associated with measuring both demographic rates and dispersal patterns across large spatial scales (see reviews in Diffendorfer 1988; Runge et al. 2006; Lipcius et al. 2011). The importance of local recruitment hotspots as sources of recruits across broader spatial scales is commonly assumed, but evidence of dispersal from putative nurseries to connected habitats is often lacking (see review in Beck et al. 2001). To our knowledge, source-sink population structure has never been fully demonstrated for any invasive fish population, although circumstantial evidence has been presented for invasive populations of common carp (*Cyprinus carpio*; e.g. Driver et al. 2005; Stuart and Jones 2006a; Bajer et al. 2012) and bigheaded carp (*Hypophthalmichthys* spp.; Lohmeyer and Garvey 2009). The aforementioned studies clearly demonstrated habitat-specific differences in reproductive success, but did not directly examine dispersal of recruits between putative source and sink habitats. Crook and Gillanders (2006) and Crook et al. (2013) did however provide strong indirect evidence that local recruitment hotspots made significant contributions to the overall recruitment of invasive common

carp in a large river system, but it remains unclear whether emigration from source habitats controlled population persistence at a landscape scale.

The common carp, a large cyprinid native to Eurasia (Kohlmann and Kersten 2013), serves as an excellent model to investigate source-sink dynamics because it is highly mobile and is known to utilize distinctive nursery habitats (Brown et al. 2005; Bajer and Sorensen 2010; Sorensen and Bajer 2011). Additionally, it is one of the world's most pervasive and damaging invasive fishes (Lowe et al. 2000; Zambrano et al. 2006; Weber and Brown 2009). It has been hypothesized that the remarkable success of the common carp can be attributed to its utilization of localized productive habitats that subsequently function as nurseries across large spatial scales within diverse freshwater systems such as chains of lakes in Midwestern North America (Bajer and Sorensen 2010; Bajer et al. 2012; Silbernagel and Sorensen 2013) and large river systems in Australia (King et al. 2003; Stuart and Jones 2006a; Crook et al. 2013). Although localized recruitment hotspots for common carp have been identified and it has been demonstrated that juvenile carp have the ability to move long distances (Stuart and Jones 2006b), the patterns of dispersal and colonization of recruits across interconnected freshwater systems are poorly understood.

In this study, we used spatially explicit demographic data coupled with information on movement patterns to test the hypothesis that dispersal from local recruitment hotspots determines the distribution, abundance, and persistence of common carp across a model Midwestern watershed. Our objectives were three-fold: 1) to identify putative sources and sinks of common carp across a watershed by determining the

distribution and relative abundance of young-of-year carp, 2) to document emigration of common carp recruits from putative sources using mark-recapture methods, and 3) to quantify the relative contribution of common carp sources across a watershed using genetic assignment methods. We hypothesized that one or more locations within the watershed would account for a disproportionately high amount of common carp reproductive output relative to other locations and that there would be evidence of emigration of carp recruits from each of these putative sources to less productive sink habitats. This study presents the first empirical evidence of source-sink dynamics regulating the persistence of an invasive fish population.

Methods

Study Site

This study took place in the Phalen Chain watershed located in Ramsey County, Minnesota, USA (45° 0' 30" N, 93° 3' 36" W; Figure 1). The Phalen Chain watershed is an urban watershed that spans 6,100 hectares and contains four connected lakes ranging in size from 29 to 95 ha with maximum depths between 2.5 and 27.7 m. The system has two major inflows (Kohlman and Gervais Creeks) which each drain a series of shallow (maximum depth <2.0 m) ponds and wetlands. The Phalen Chain watershed eventually drains to the Mississippi River, but fish passage from the river to the chain of lakes is prevented by physical barriers. There has been extensive urban development in the Phalen Chain watershed over the past century that has significantly altered the hydrology of system. Notably, two major interstate highways that pass through the Gervais Creek

subwatershed over Gervais Creek were constructed in the 1970s and two stormwater retention basins (Markham Pond and Upper Basin) were constructed along Kohlman Creek in the 1970s and 1990s respectively (Figure 1). This system of interconnected lakes, ponds, and wetlands is representative of many freshwater systems located in previously glaciated regions of the Midwestern United States and elsewhere around the world.

The common carp population in the Phalen Chain watershed has been extensively studied and is well-suited for an investigation of source-sink dynamics for a variety of reasons. The Sorensen Lab Group at the University of Minnesota has been collecting routine data on the distribution and abundance of common carp in the Phalen Chain watershed since 2009. This information has revealed that although common carp are present in large numbers throughout much of the watershed (Table 1; Appendix 1), the production of young-of-the-year (YOY) common carp is seemingly restricted to shallow, predator-free basins (Bajer et al. 2011), suggesting there are habitat-specific demographic rates. A study by Osborne (2012) confirmed that there were habitat-specific differences in reproductive success in the Phalen Chain watershed by estimating that there were between 2,700 and 5,400 YOY carp per hectare in two of the shallow ponds (i.e. Markham and Casey) in 2010 despite not sampling any YOY carp in the four study lakes. Additionally, a pilot study examining common carp genetic diversity in regional lakes documented the presence of at least two distinct genetic strains of common carp within the Phalen Chain watershed (Loren M. Miller, Personal Communication, February 2012). The presence of genetic differentiation at the subwatershed level may enable the

use of genetic assignment tests to identify the natal sources of recruits and infer their dispersal patterns across the watershed.

Study 1: Identifying sources and sinks

To identify putative demographic sources and sinks of common carp, we assessed whether there were spatially explicit reproductive rates by comparing the relative abundance of YOY carp in all water bodies of the Phalen Chain known to support common carp populations (Table 1). Surveys for YOY common carp were conducted each August for 5 years from 2009 to 2013 using trap nets, a passive sampling gear designed for sampling littoral fishes (Hubert 1996). Relative abundance was measured as the catch-per-unit-effort (CPUE = number per net night) of YOY common carp (total length <150 mm; Osborne 2012) sampled during standardized trap net surveys. Specifically, in each water body, five trap nets (13 mm square mesh, 10 m lead, 1.8 m x 0.9 m frame) were set perpendicular to shore at approximately equidistant locations and fished for approximately 24 hours. All common carp were counted, measured to the nearest millimeter, and released at the location of capture.

Study 2: Documenting common carp emigration from a putative source

To test the hypothesis that common carp emigrate from putative sources, the movement of common carp recruits out of Markham Pond was assessed using mark-recapture methods from May 2012 to November 2013. A recruit was defined in its broadest sense, as any individual that could potentially join a population in a sink habitat, regardless of age or size (Nichols and Pollock 1990). Markham Pond is a small (6.5 ha), shallow (maximum depth 1.8 m) pond within the Kohlman Creek subwatershed of the

Phalen Chain watershed (Figure 1); it was chosen as a study site because it supports extremely high densities of young carp (Osborne 2012), is readily accessible with sampling gear, and because fish movement out of the system is restricted to one outflowing creek. Common carp were sampled via boat electrofishing (5–12 A, 80–150 V, 20% duty cycle, 120-pulse frequency), sexed, measured to the nearest millimeter, implanted with individually-coded 23 mm passive integrated transponder (PIT) tags (Oregon RFID, Portland, Oregon), and released at the point of capture. Common carp less than 150 mm total length were not implanted with PIT tags due to their small body size relative to tag size.

Throughout the study, Markham Pond and the pond roughly 1 km downstream (Upper Kohlman Basin: 4.3 ha, maximum depth 2 m) were sampled via boat electrofishing approximately once every two weeks during the open water season (May–November). All common carp sampled were inspected for PIT tags and released at the point of capture. Emigration was documented when common carp originally tagged in Markham Pond were recaptured in Upper Kohlman Basin. Emigration rates were estimated by calculating the percentage of all recaptured fish that were recaptured in Upper Kohlman Basin. Estimates should be considered conservative because tag loss, mortality, and emigration beyond Upper Kohlman Basin were not systematically accounted for due to logistical constraints. All common carp captured in the other study lakes during the study period as part of unrelated sampling efforts were however inspected for marks.

Study 3: Determining patterns of nursery contribution across a watershed

Sample collection

To quantify nursery contribution and determine patterns of dispersal and colonization at a watershed scale, we assessed the genetic variation and genetic structure of common carp sampled across the Phalen Chain watershed. We collected tissue samples (fin clip) from common carp captured in the main lakes (i.e. Lakes Kohlman, Gervais, Keller, and Phalen), in all putative source habitats in the Kohlman Creek subwatershed, and in all putative source habitats in the Gervais Creek subwatershed (Table 2). We also collected separate spawning season (May-June) samples from common carp spawning in three isolated areas of the watershed (the main lakes, Kohlman Creek, and Gervais Creek; Table 2). Fish were sampled via electrofishing, seining, trap nets, and baited traps between February 2011 and October 2013. All tissue samples were referenced to capture location and sample date and stored in 95% ethanol for future analysis.

To elucidate any temporal trends in nursery contribution, we aged a random subset of common carp captured in the main lakes that also had genetic data ($n = 141$). We aged the fish following established protocols for common carp outlined in Bajer and Sorensen (2010). Briefly, asterisci otoliths were extracted, embedded in epoxy, and sectioned transversely through the primordium region. Annuli were counted using a compound microscope and transmitted light by three independent observers; only the samples in which at least 2 of the 3 observers agreed on age were used in subsequent analyses.

Microsatellite analysis

Genetic variation at 12 microsatellite DNA loci previously established for common carp was assessed following the procedures outlined by Miller et al. (2009), except the starting tissue was 4 mm² fin tissue. DNA was extracted from each sample using 5% Chelex (Sigma Chemical Co. St. Louis, MO) and amplified via polymerase chain reaction (PCR) using *Taq* polymerase (Promega, Madison, WI) and forward and reverse locus-specific primers. To select microsatellite loci, we initially screened the 14 loci used by Haynes et al. (2009) to describe genetic structure of invasive common carp in Australia. Because many of these loci had little to no variation in initial tests of 16-24 individuals, we also screened all of the Crooijmans et al. (1997) loci. Twelve loci from Crooijmans et al. (1997) and Yue et al. (2004) were chosen based on their variation, scorability, and size compatibility for joint analysis (Table 3). PCR products were electrophoresed on an ABI Prism 3130xl Genetic Analyzer (Applied Biosystems, Foster City, CA) and alleles were scored using the software GeneMapper version 4.1 (Applied Biosystems). Observed and expected heterozygosities were estimated for each locus in each sample. Conformance with Hardy–Weinberg expectations and tests for linkage disequilibrium were performed in GENEPOP version 3.4 (Raymond and Rousset 1995). Significance was evaluated at P-values <0.05 and after adjustments for multiple testing within samples using sequential Bonferroni procedures (Rice 1989).

Analysis of genetic structure

To confirm genetic structuring of the common carp population(s) sampled across the watershed and relate this information to nursery function, multilocus allele frequency

data from all samples were analyzed using the Bayesian clustering method in STRUCTURE version 2.3.4 (Pritchard et al. 2000). This approach estimates the number of genetically distinct clusters (K) in the dataset with no *a priori* assumptions about population membership using a Markov chain Monte Carlo algorithm. We executed the algorithm with a burn-in of 50,000 followed by a run length of 200,000 for five replications at each K value ranging from 1-5. The most likely value of K was determined based on when $-\log P(X/K)$ plateaued and based on the Evanno delta K method (Evanno et al. 2005) implemented in STRUCTURE HARVESTER (Earl and VonHoldt 2012). After determination of K , individuals were assigned percent ancestry derived from each genetically distinct cluster or ‘strain’ identified.

After assigning ancestry to individual carp, we calculated the proportion of individuals of each distinct genetic strain sampled in the various locations within the watershed (i.e. Kohlman Creek subwatershed, Gervais Creek subwatershed, and each of the main lakes). We also assessed whether the genetic composition of the common carp population in the main lakes remained constant over time by analyzing the genetic assignment of individuals of known ages. Additionally, in order to look for mechanisms that would sustain genetic structuring at the subwatershed level, we analyzed the genetic composition of each spatially separated spawning group (i.e. spawning migrations in Kohlman Creek, spawning migrations in Gervais Creek, and common carp spawning in the main lakes). Using this information we determined whether one or more of the putative source habitats consisted of genetically distinct common carp whose dispersal

and colonization could be tracked throughout the watershed to demonstrate source-sink population structure.

Results

Study 1: Identifying sources and sinks

Catch rates of YOY common carp across the Phalen Chain watershed were variable between years and locations and ranged from 0.0 to 173.0 carp/net (Figure 2). Several of the shallow ponds consistently had higher catch rates of YOY carp relative to other locations within the watershed, indicating that there were habitat-specific differences in carp reproductive success. Specifically, YOY common carp were sampled in 3 of the 4 shallow ponds in the Kohlman Creek subwatershed (Casey, Markham, and Upper Kohlman Basin) each year surveyed (mean CPUE = 5.0, 44.3, and 4.1 carp/net respectively), but no YOY carp were sampled in any of the four main lakes over all 5 years. In the Gervais Creek subwatershed, sampling efforts were limited by accessibility, but YOY carp were sampled in 3 of the 4 basins (Interstate, Owasso Basin, and Gervais Mill) at least one year over the 5 year period (CPUE = 23.0, 6.3, and 1.0 respectively).

Study 2: Documenting common carp emigration from a putative source

Between May 2012 and July 2013, 613 common carp ranging in size from 151 to 894 mm total length (mean = 328 mm TL) were captured and implanted with individually coded PIT tags in Markham Pond, a putative source habitat. By November 2013, 80 of the 613 common carp (13.1%; TL: 183-723 mm; mean: 350 mm) had been recaptured in either Markham Pond or Upper Kohlman Basin, the pond located 1km downstream. Of

those recaptured, 25 common carp (31.3%; TL: 304-628 mm; mean: 360 mm) were recaptured in Upper Kohlman Basin, indicating that they had emigrated from Markham Pond. Movement downstream of Upper Kohlman Basin was not systematically addressed although movement of common carp between Upper Kohlman Basin and the main lakes is common (personal observation). Furthermore, seven carp originally tagged in Upper Kohlman Basin as part of a related study were later recaptured in one of the main lakes (Justine Koch, unpublished data, Appendix 2).

Study 3: Determining patterns of nursery contribution across the watershed

Genetic variation

Genetic variation at all twelve microsatellite loci from common carp ($n = 1\ 041$) collected throughout the Phalen Chain watershed was substantial (Appendix 3). Numerous tests indicated deviations from Hardy-Weinberg and linkage equilibrium across all samples (Hardy-Weinberg results reported in Appendix 3), but three samples were of particular importance because they should not be susceptible to strain mixing that could affect these test results. These samples from the most isolated ponds in the Kohlman Creek subwatershed (Casey and Markham Ponds have barriers to upstream fish movement) had only three Hardy-Weinberg tests with P-values < 0.05 and only two significant after adjustment for multiple testing. The significant tests occurred in a sample of older fish from Casey pond while tests for the same loci were not significant in a sample of YOY from the same pond. Additionally, only 3 to 5 of 66 locus pairs per sample had indications of linkage at $P < 0.05$, but none after adjustment and no pair was significant in all three samples. These results indicate that the loci satisfy the genetic

equilibrium assumptions for STRUCTURE analysis of population structure and ancestry. Genotyping was repeated for 51 individuals and allele scoring error averaged 1.2% across loci, with all errors involving just one of the two alleles in a genotype.

Genetic structure

Bayesian clustering analysis in STRUCTURE revealed two genetically distinct strains of common carp within the watershed as indicated by values of $-\log P(X/K)$ plateauing at $K = 2$ and strong support for $K = 2$ from the rate of change of the likelihood function (i.e., Evanno method). We chose to refer to these genetic strains as ‘Type A’ and ‘Type B’. We then classified individuals as either ‘Type A’, ‘Type B’, or hybrid crosses between strains (‘A x B’) using criteria based on STRUCTURE assignments of simulated genotypes for pure individuals and hybrids (Appendix 4). Because the classification of some individuals was uncertain, we created a fourth category ‘Type A or A x B’, to indicate that individuals belonged to one of these two categories, but were unlikely Type B.

Spatial patterns of genetic composition

The genetic composition of the common carp populations inhabiting the putative source habitats (shallow ponds of the Kohlman Creek and Gervais Creek subwatersheds) and putative sink habitats (each of the main lakes) were very different (Figure 3). Of the 523 carp sampled in the main lakes combined, both genetic strains and their hybrids were well-represented (19.1% Type A, 61.4% Type B, 15.7 % hybrids, and 3.8% either A or A x B), whereas each putative nursery region only contained a subset of the genetic strains (Figure 3). More specifically, of the 209 common carp sampled in the ponds of the

Kohlman Creek subwatershed (Casey, Markham, and Upper Kohlman Basin), the majority (84.7%) were Type A. The remaining individuals were classified as either Type A or A x B (13.4%), with only 4 individuals (1.9%) classified as hybrids (A x B). No individuals captured in the Kohlman Creek subwatershed were classified as Type B. Conversely, of the 70 carp sampled in the nursery ponds of the Gervais Creek subwatershed (Interstate and Gervais Mill), only 1 (1.4%) individual was classified as Type A. The majority of the potential recruits in the Gervais Creek subwatershed were hybrids (78.6%) or possible hybrids (12.9% Type A or A x B) and the remaining individuals (7.1%) were the only pure Type B common carp sampled in a putative source habitat.

Temporal patterns of genetic structure

Of the 141 common carp collected for age determination, agreement by 2 of the 3 independent observers was reached for 127 (90.1%) of the samples. Ages ranged widely from 3 to 64 years (median = 35 yrs, mean = 31 yrs). Based on the genetic assignment results of the carp of known ages, the genetic composition of the carp population in the main lakes was not stable over time (Figure 4a). Younger carp were predominately assigned as Type A or hybrids, whereas older carp were predominately Type B. No carp older than 33 years old was classified as Type A. Reanalyzing the dataset by including only individuals 33 years old or younger to reflect the more recent recruitment dynamics of the system resulted in a dramatic shift in the genetic composition of the common carp inhabiting the main lakes. Compared to the genetic composition across all age groups (19.1% Type A; 61.4% Type B; 15.7 % A x B; 3.8% A or A x B), common carp 33 years

old and younger were predominately classified as Type A (56.7%) instead of Type B (21.7%; Figure 4b).

Dispersal and colonization of recruits across the watershed

Because our aging results indicated the Phalen Chain watershed only contained one genetic strain (Type B) of common carp prior to 1979 (33 years before 2012; Figure 4b), we were able to infer the dispersal and colonization of Type A individuals across the watershed against the existing background of Type B ancestry. The distribution of Type A individuals across the watershed was consistent with individuals originating at a point source located in the Kohlman Creek subwatershed. Specifically, as the distance from the Kohlman Creek subwatershed increased, the proportion of Type A individuals decreased from 0.41 in Lake Kohlman, to 0.16 in Lake Gervais, to 0.10 in Lake Keller, and finally to 0.03 in Lake Phalen (see Figure 3).

Genetic composition of spawning groups

In May 2013, we observed common carp actively spawning or preparing to spawn in three spatially separated locations within the Phalen Chain watershed. We captured 40 individuals actively spawning in the littoral areas of the main lakes and we also intercepted individuals making synchronized spawning migrations up both Kohlman Creek ($n = 147$) and Gervais Creek ($n = 52$). The genetic composition of the carp spawning in the main lakes (27.5% Type A; 55.0% Type B; 15.0% A x B; 2.5% A or A x B) resembled that of the residents in the main lakes (19.1% Type A; 61.4% Type B; 15.7% A x B; 3.8% A or A x B), whereas the carp that made spawning migrations from the main lakes up either of the inflowing creeks consisted of distinct subsets of the carp

population inhabiting main lakes. In fact, the genetic composition of these migrating carp resembled that of the resident populations within each respective subwatershed that they were migrating towards (Figure 5). Specifically, the spawning migration up Kohlman Creek consisted primarily of Type A (83.0%), hybrid (4.1%), or either Type A or A x B (8.5%) individuals, with only 5 (3.4%) individuals classified as Type B. The spawning migration in Gervais Creek was dominated by hybrid individuals (51.9%), but also contained individuals of both pure types (19.2% Type A; 23.1% Type B).

Discussion

The results of this study support our hypothesis that dispersal from local recruitment hotspots explains the distribution, abundance, and persistence of common carp at a watershed scale. This study provides the first empirical evidence of an invasive fish population exhibiting source-sink dynamics. We demonstrated not only that there are habitat-specific demographic rates across the Phalen Chain watershed, but also that there is dispersal of common carp recruits between source and sink habitats. We conclude that shallow ponds serve as sources whereas lakes are demographic sinks. More specifically, Study one revealed that common carp reproductive success was restricted to shallow pond habitats despite five years of sampling lake habitats for YOY carp. Study two confirmed that shallow ponds serve as sources by documenting emigration of common carp from Markham Pond to Upper Kohlman Basin. Specifically, the 31.3% of our recaptured carp that were recaptured in Upper Kohlman Basin over the two-year study period represents roughly 348 emigrants per year from Markham Pond alone given its

estimated carp population size of 2,224. This rate of emigration would be more than enough to sustain a sizeable carp population in the main lakes given the longevity of common carp in this system (up to 64 years). Additionally, the results of Study three also supported the source-sink hypothesis because the spatial and temporal patterns in genetic composition across the watershed were consistent with dispersal of recruits from shallow ponds of the Kohlman and Gervais Creek subwatersheds.

Because there was no evidence of YOY common carp in any of the main lakes and there were genetically distinct subpopulations of common carp in each subwatershed, we were able to assign common carp recruits sampled in the main lakes to their respective natal sources. It follows that Type A individuals originated from the nursery ponds in the Kohlman Creek subwatershed and Type B individuals originated from the Gervais Creek subwatershed. Although likely hybrids (A x B) and potential hybrids (A or A x B) were sampled in both subwatersheds, the proportion of individuals classified as likely hybrids in the Kohlman Creek subwatershed (1.9%) was within the range of possible misassignment error whereas likely hybrids made up the majority of the Gervais Creek subwatershed samples (78.5%). It is therefore reasonable to assume that most, if not all, of the hybrid individuals sampled in the main lakes also originated from the Gervais Creek subwatershed. The decreasing proportion of Type A individuals as distance from the Kohlman Creek subwatershed increased provides further evidence in support of recruits emigrating from the shallow ponds of Kohlman Creek to colonize lake habitats.

The present study adds to the growing body of literature seeking to explain common carp invasiveness and inform effective control strategies. Previous research suggested that the invasiveness of common carp could be attributed to recruitment hotspots that serve as nurseries across large spatial scales in both lake systems of North America as well as river systems of Australia (e.g. Bajer and Sorensen 2010; Stuart and Jones 2006a; Crook et al. 2013). Subsequent studies lent support to this hypothesis by providing evidence that common carp recruitment is controlled by native egg and larval predators in portions of their invasive range, but that optimal spawning habitats that lack predators often exist as part of the landscape mosaic (Bajer et al. 2012; Silbernagel and Sorensen 2013). These studies speculated that such localized predator-free habitats have been serving as common carp nurseries by supplying recruits to connected waters, but did not provide any direct evidence. Our findings support this hypothesis with both mark-recapture and genetic evidence of common carp dispersal between source and sink habitats, emphasizing the importance of localized predator-free nursery habitats for population persistence at the landscape scale. These results suggest that traditional management efforts such as mass harvesting of adults in lake habitats or in main channel habitats of rivers may not be sustainable for reducing or eradicating invasive populations of common carp. Instead, management efforts should first be directed towards eliminating source populations or habitats and blocking dispersal pathways between sources and sinks.

Although our study only provides evidence of source-sink population structure in one invasive fish population, it is likely that source-sink dynamics also regulate the

populations of many other invasive fishes in diverse aquatic habitats. Of particular relevance may be invasive fishes that share similar life history strategies with the common carp such as the utilization of distinctive nursery habitats within complex heterogeneous systems. The bigheaded carps, for example, exhibit long-distance spawning movements in open river systems of the Mississippi River Basin and utilize flooded backwaters as nursery habitats for larvae and juveniles (Schrank et al. 2001; Lohmeyer and Garvey 2009). Similarly, invasive populations of northern pike (*Esox lucius*) in lentic and lotic systems of western North America have been shown to use backwater habitats and floodplain ponds as spawning and nursery habitats (Hill 2004). Additionally, the invasive sea lamprey (*Petromyzon marinus*) in the Laurentian Great Lakes has specific nursery requirements, utilizing select tributaries for spawning (Manion and Hanson 1980). Future studies are needed to determine the applicability of source-sink population models to additional invasive fishes to inform new sustainable control strategies.

In addition to providing novel insights on common carp recruitment dynamics, our study also demonstrates the potential utility of genetic assignment methods for investigating source-sink dynamics in invasive fish populations. Although previous studies have used genetic assignment methods to infer pathways and processes of aquatic invasive species introductions (e.g. Herborg et al. 2007; Darling and Folino-Rorem 2009; Brown and Stepien 2010), these studies were mostly carried out across very large spatial scales (e.g. continental), limiting their management applications. In contrast, our study demonstrates genetic structuring at a subwatershed scale, although such fine-scale genetic

structuring may or may not be typical of other invasive fish populations. In the Phalen Chain watershed, our ageing and genetic assignment results revealed that Type B carp were present for at least 64 years whereas Type A carp first showed up in the 1970s, indicating that the high level of genetic differentiation was likely caused by multiple introductions of genetically distinct common carp. These findings make sense given the historical changes to the hydrology of the system. Specifically, Markham Pond did not exist prior to the 1970s and may have been stocked with common carp upon its construction. Additionally, the shift in genetic composition from predominately Type B ancestry to predominately Type A ancestry could be explained by reduced connectivity between the main lakes and the proposed source habitats of the Gervais Creek subwatershed due to construction of the interstate highway system in the 1970s. Because many populations of invasive fishes are established by intentional stocking practices (Garcia-Berthou et al. 2005), the presence of several distinct genetic strains of a particular invasive fish within a given aquatic system may not be uncommon. Analysis of microsatellite variation has in fact been a useful tool in determining the recruitment dynamics of fish populations with a history of stocking for commercial or recreational purposes (e.g. Page et al. 2003; Wollebaek et al. 2010; Miller et al. 2012). Further investigation of genetic diversity and structure within interconnected freshwater systems may be useful for determining trends in invasive fish recruitment across space and time.

Another important finding of our study is the discovery of stock-specific differences in common carp spawning behavior. The genetic compositions of adult common carp sampled migrating from the main lakes towards the Kohlman Creek and

Gervais Creek subwatersheds represented distinct subsets of the resident population in the main lakes. The striking resemblance between the genetic compositions of each spawning run to those of the respective resident populations found in each subwatershed suggests that common carp exhibit reproductive site fidelity. Although intra-annual spawning site homing by common carp has been previously documented (Bonneau and Scarnecchia 2002), this is the first evidence in support of interannual reproductive homing. Furthermore, our results are consistent with natal homing because the genetic differentiation that has persisted in the Phalen Chain watershed over several generations would require ongoing reproductive isolation strong enough to prevent genetic homogenization over time (Miller et al. 2001).

Remarkably, even though the mouths of Gervais and Kohlman Creeks are less than 2 km apart, our estimated straying rates of < 4% Type B individuals attempting to spawn in the Kohlman Creek subwatershed are comparable to rates reported for species of salmonids notorious for homing behavior (see review in Quinn 1993). The management implications of homing by common carp will depend on how universal this behavior is and whether it is facultative or obligatory. For example, if the site fidelity is obligatory, targeted management actions such as installing barriers to block migrating adults or destroying particular spawning habitats could result in reproductive failure of an entire spawning population. Future research on the cues and mechanisms associated with common carp migratory behavior are warranted; such discoveries could lead to the development of targeted management strategies such as pheromone attractants which

have been utilized in the control of other invasive fishes such as the sea lamprey (Sorensen et al. 2005; Wagner et al. 2006; Meckley et al. 2012).

Understanding the factors that influence population structure and persistence at relevant spatial and temporal scales is paramount for effectively managing invasive fishes. This study provides the first empirical evidence of source-sink population structure in an invasive fish population, highlighting the potential importance of habitat heterogeneity and connectivity in regulating fish metapopulation dynamics. Future research is needed to identify sources, sinks, and dispersal pathways for additional invasive fish populations and to better understand how source-sink structured populations can be most effectively controlled. We advocate for the development of adaptive, integrated pest management strategies that target species-specific vulnerabilities across multiple life stages at a landscape scale.

Tables

Table 1. Abundance (mean Schnabel mark-recapture estimate) of adult and subadult common carp in each study site at the onset of the study period. Abundance estimates do not include young-of-year carp (< 150mm TL) because they were not recruited to the sampling gear used.

Location	Site	Area (ha)	Year sampled	Common carp abundance
Kohlman Creek subwatershed	Willow	42.5	2011	NA
	Casey	4.7	2011	5,799 ¹
	Markham	6.5	2011	2,224 ¹
	Upper Kohlman Basin	4.3	2011	618 ¹
Gervais Creek subwatershed	Interstate	2.2	2011	NA
	Owasso Basin	3.1	2011	NA
	Savage	12.2	2011	NA
	Gervais Mill	3.1	2011	NA
Main Lakes	Kohlman	29.9	2010	827 ²
	Gervais	94.5	2010	2,613 ²
	Keller	29.0	2010	802 ²
	Phalen	76.6	2010	2,316 ^{a,2}

NA indicates study sites in which abundance estimates were not available

^aabundance was estimated using boat electrofishing catch rates

¹J. D. Koch, unpublished data (Appendix 1)

²Bajer et al. (2012)

Table 2. Location, sample size, and sample date of common carp tissue samples collected across the Phalen Chain watershed for genetic analyses.

Location	Site	Sample size	Sample year(s)
Kohlman Creek subwatershed	Casey	93	2011
	Markham	39	2011, 2012
	Upper Kohlman Basin	77	2012, 2013
Gervais Creek subwatershed	Interstate	63	2013
	Owasso Basin	5	2013
	Gervais Mill	2	2013
Main Lakes	Kohlman	94	2012
	Gervais	347	2011, 2012, 2013
	Keller	52	2013
	Phalen	30	2012, 2013
Spawning Groups	Kohlman Creek	147	2013
	Gervais Creek	52	2013
	Main Lakes	40	2013

Table 3. Details of the primers used to analyze 12 common carp microsatellite loci.

Name	Allele range	Source
Cca67	233-309	Yue et al. 2004
MFW1	167-221	Crooijmans et al. 1997
MFW11	200-212	Crooijmans et al. 1997
MFW24	219-239	Crooijmans et al. 1997
MFW25	273-325	Crooijmans et al. 1997
MFW26	124-154	Crooijmans et al. 1997
MFW29	163-223	Crooijmans et al. 1997
MFW31	274-318	Crooijmans et al. 1997
MFW32	268-290	Crooijmans et al. 1997
MFW4	134-150	Crooijmans et al. 1997
MFW6	134-170	Crooijmans et al. 1997
MFW7	188-277	Crooijmans et al. 1997

Figures

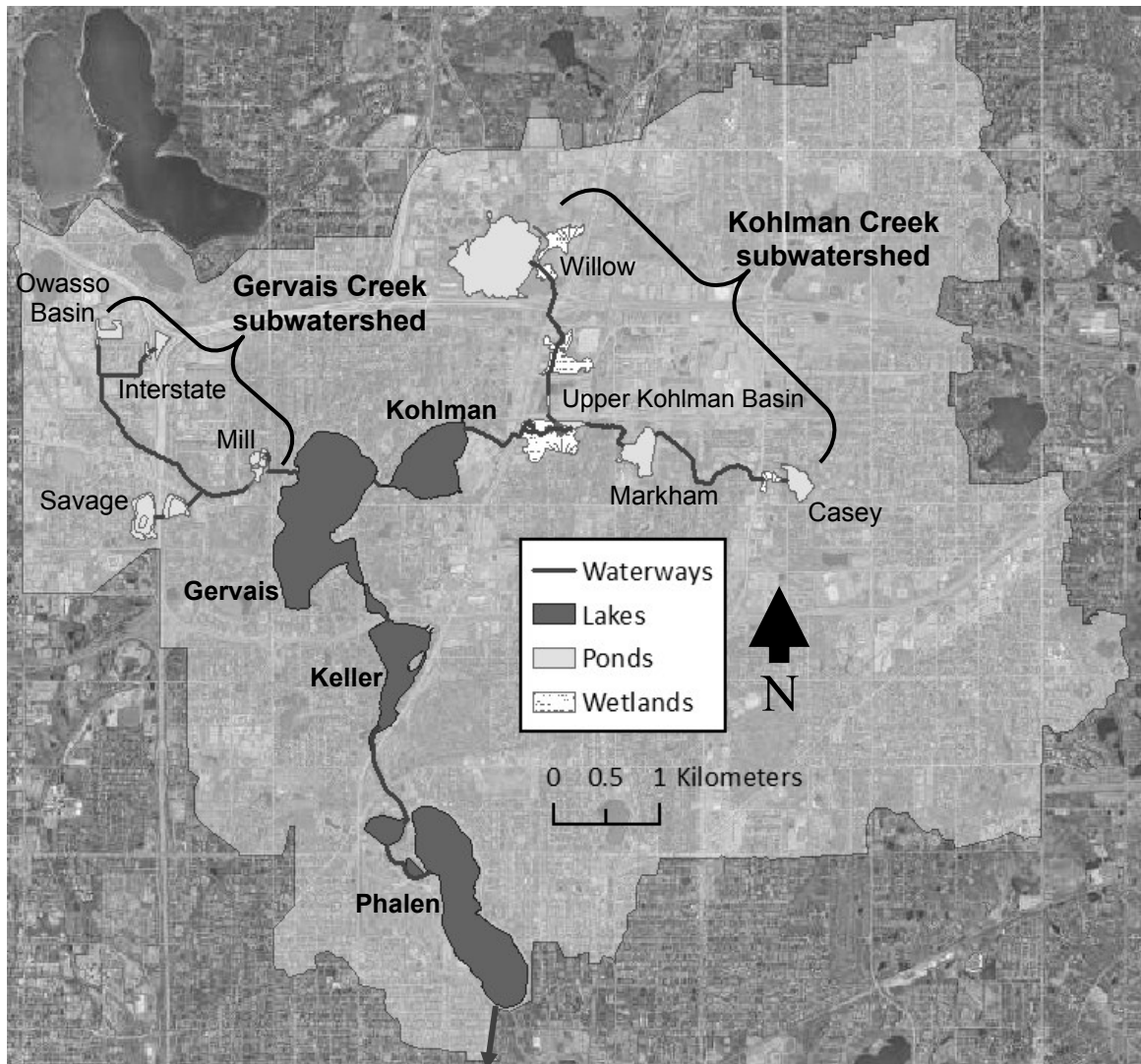


Figure 1. Map of the study sites in the Phalen Chain watershed (Ramsey County, Minnesota, USA). Water flows from north to south and eventually outlets to the Mississippi River.

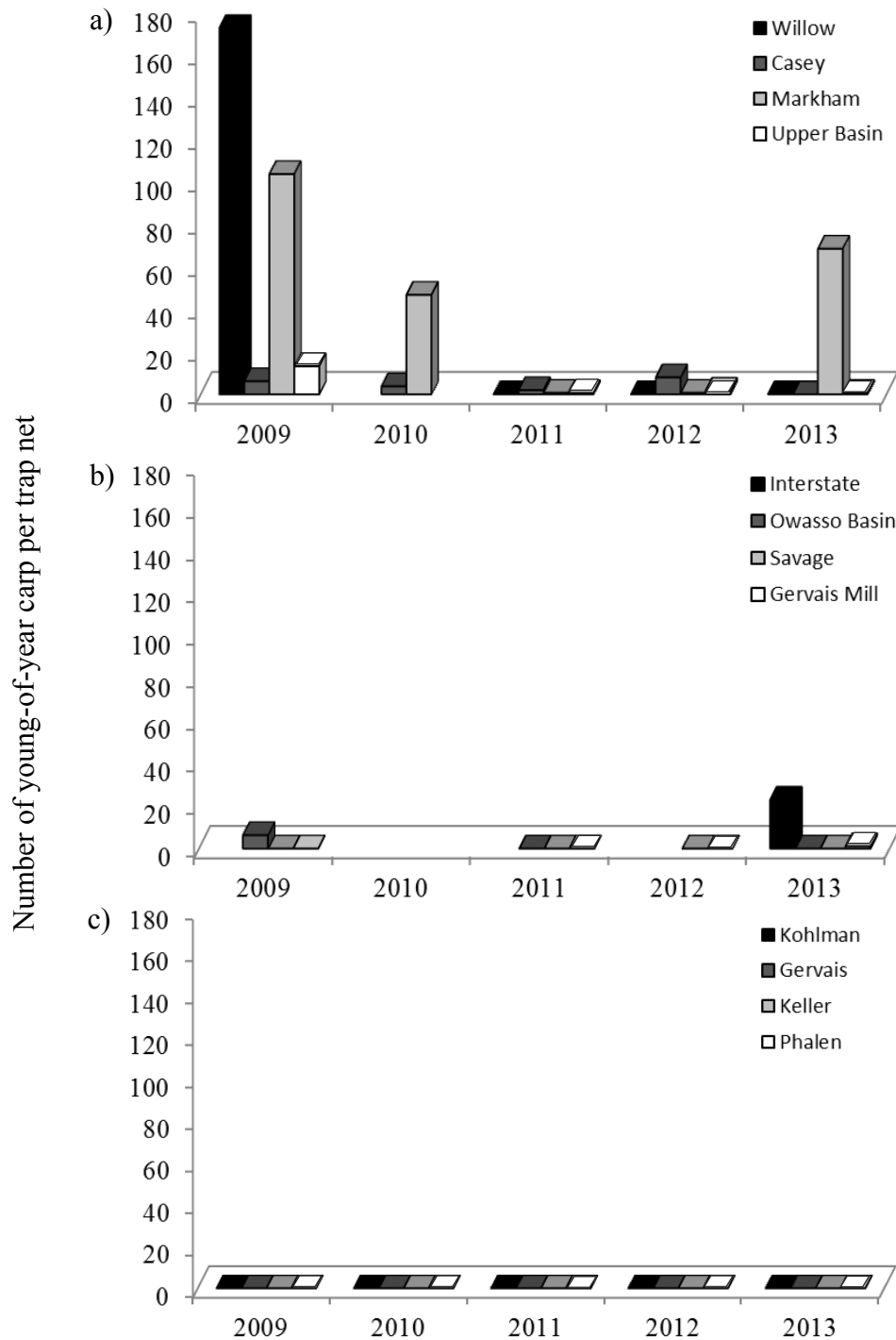


Figure 2. Catch rates of young-of-year common carp (< 150 mm TL) sampled during annual trap net surveys from 2009-2013 in the Phalen Chain watershed: a) shallow ponds of the Kohlman Creek subwatershed, b) shallow ponds of the Gervais Creek subwatershed, and c) the main lakes. Blank columns denote sites that were not sampled that year. Catch rates from 2009 and 2010 are from Osborne (2012).

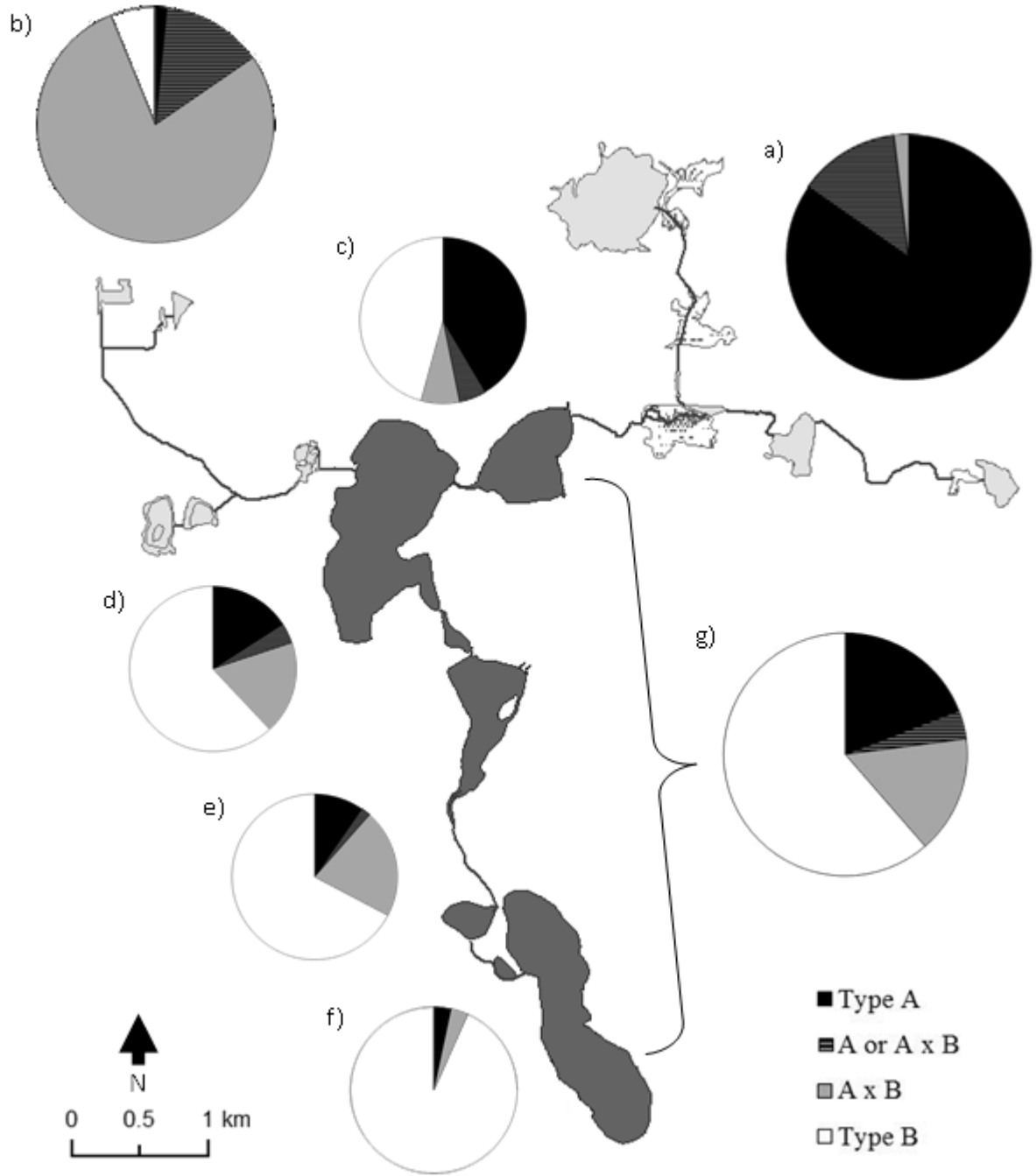


Figure 3. The genetic composition of common carp sampled in water bodies of the Phalen Chain watershed: a) shallow ponds of the Kohlman Creek subwatershed (n = 209), b) shallow ponds of the Gervais Creek subwatershed (n = 70), c) Kohlman Lake (n = 94), d) Gervais Lake (n = 347), e) Keller Lake (n = 52), f) Phalen Lake (n = 30), and g) the main lakes combined (n = 523).

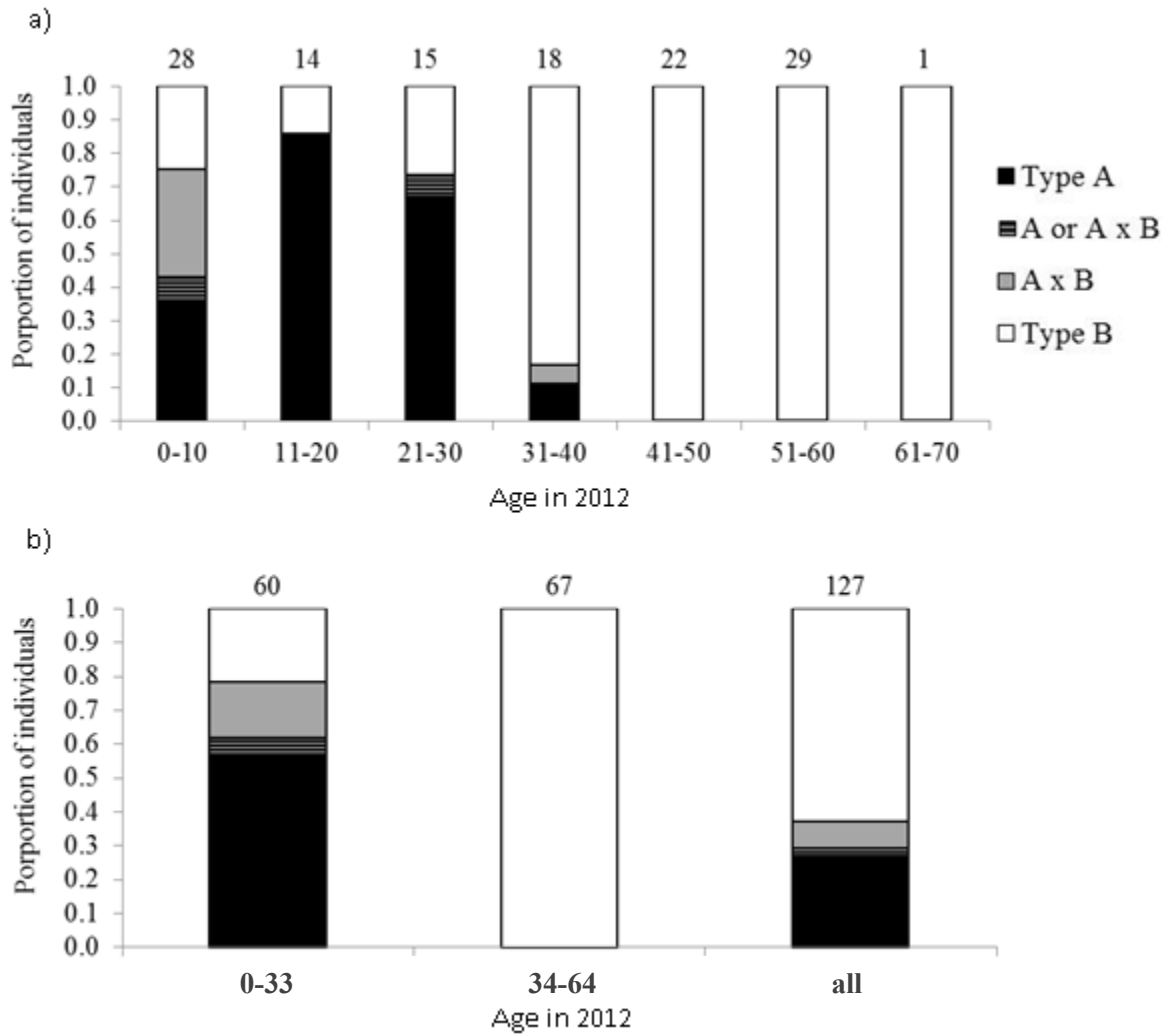


Figure 4. The genetic composition of a random subset of common carp ($n = 127$) sampled in lakes Kohlman, Gervais, Keller, and Phalen of the Phalen Chain watershed by age group; sample size is indicated above each bar. The lower panel shows the genetic composition of the same carp combined and split into two age categories (< 34 year old and ≥ 34 years old).

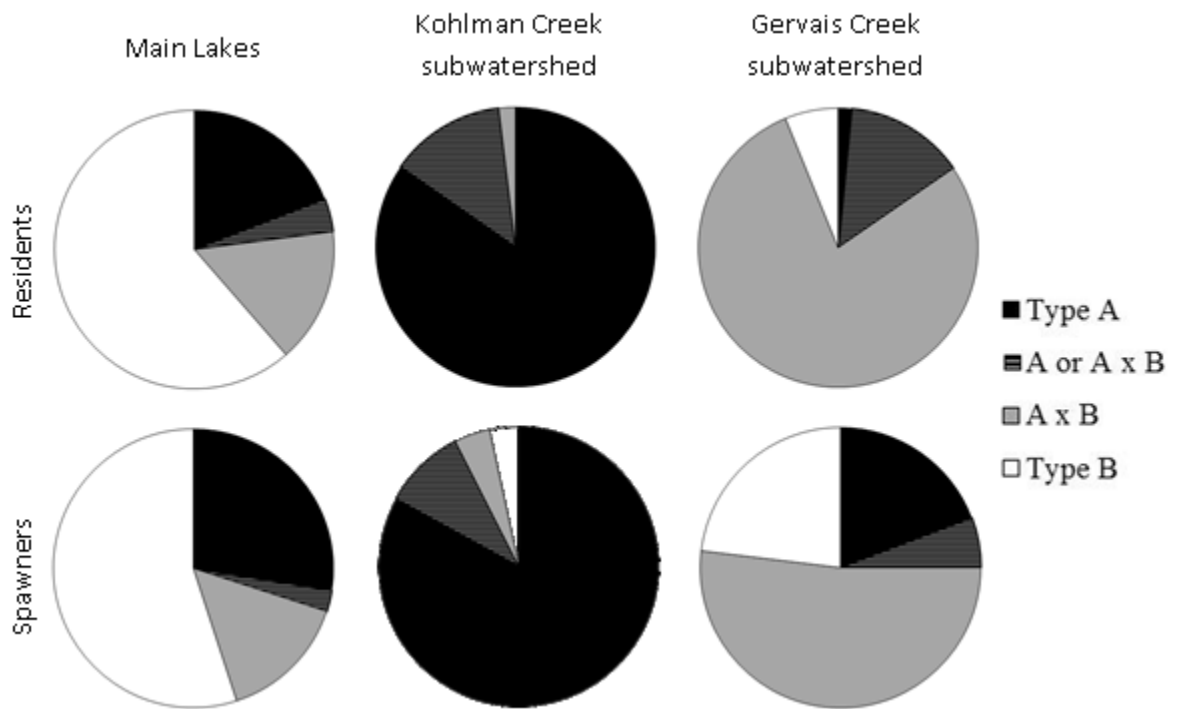


Figure 5. The genetic composition of common carp resident subpopulations and spawning groups in 3 spatially separated regions of the Phalen Chain watershed: the Kohlman Creek subwatershed, the Gervais Creek subwatershed, and the main lakes (Lakes Kohlman, Gervais, Keller, and Phalen).

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Appendix 1: Summarized mark-recapture data and population estimates

This appendix contains a summary of mark-recapture data and Chapman-modified Schnabel population estimates for the nursery ponds of the Kohlman Creek subwatershed reported in Table 1 of Chapter 2. Estimates were calculated using the following equations¹:

$$N = \Sigma(M_i C_i) / [\Sigma(R_i) + 1]$$

$$95\% \text{-interval (low)} = \Sigma(M_i C_i) / [R_U + 1]$$

$$95\% \text{-interval (high)} = \Sigma(M_i C_i) / [R_L + 1]$$

Where:

M_i : total previously marked at the start of the i th sampling period

C_i : total number sampled during the i th sampling period

R_i : number of recaptures sampled during the i th sampling period

R_u : upper limit Poisson value of ΣR

R_l : lower limit Poisson value of ΣR

¹Ricker, W. E., 1975. Computation and interpretation of biological statistics of fish populations. Bull. Fish. Res. Board Can. 191.

A1.1. Summary of mark-recapture data and the Chapman-modified Schnabel estimate of common carp in Casey Lake in 2011. Young-of-year carp (<150mm TL) are not included.

Date	Examined (C _i)	Marked	Total previously marked (M _i)	M _i *C _i	Recaptured (R _i)
7/26/2011	122	122	0	0	0
8/9/2011	10	10	122	1220	0
8/30/2011	80	78	132	10560	2
9/14/2011	70	68	210	14700	2
9/28/2011	72	67	278	20016	5
10/21/2011	151	144	345	52095	7
				$\Sigma(M_i * C_i) = 98591$	$\Sigma(R_i) = 16$ R _L = 9.2 R _U = 26

$$N = \Sigma(M_i C_i) / [\Sigma(R_i) + 1] = 5,799$$

$$95\% \text{-interval (low)} = \Sigma(M_i C_i) / [R_U + 1] = 3,652$$

$$95\% \text{-interval (high)} = \Sigma(M_i C_i) / [R_L + 1] = 9,665$$

A1.2. Summary of mark-recapture data and the Chapman-modified Schnabel estimate of common carp in Markham Pond in 2011. Young-of-year carp (<150mm TL) are not included.

Date	Examined (C _i)	Marked	Total previously marked (M _i)	M _i *C _i	Recaptured (R _i)
7/29/2011	22	22	0	0	0
8/10/2011	4	4	22	88	0
9/2/2011	17	16	26	442	1
9/21/2011	48	47	42	2016	1
9/30/2011	33	32	89	2937	1
10/18/2011	13	6	121	1573	0
11/9/2011	67	64	127	8509	3
				$\Sigma(M_i * C_i) = 15565$	$\Sigma(R_i) = 6$ R _L = 2.2 R _U = 13.1

$$N = \Sigma(M_i C_i) / [\Sigma(R_i) + 1] = 2,224$$

$$95\% \text{-interval (low)} = \Sigma(M_i C_i) / [R_U + 1] = 1,104$$

$$95\% \text{-interval (high)} = \Sigma(M_i C_i) / [R_L + 1] = 4,864$$

A1.3. Summary of mark-recapture data and the Chapman-modified Schnabel estimate of common carp in Upper Kohlman Basin in 2011. Young-of-year carp (<150mm TL) are not included.

Date	Examined (C _i)	Marked	Total previously marked (M _i)	M _i *C _i	Recaptured (R _i)
7/13/2011	39	39	0	0	0
7/27/2011	30	30	39	1170	0
8/11/2011	3	3	69	207	0
8/29/2011	22	21	72	1584	1
9/23/2011	19	14	93	1767	5
10/19/2011	2	1	107	214	1
				$\Sigma(M_i * C_i) = 4942$	$\Sigma(R_i) = 7$ R _L = 2.8 R _U = 14.4

$$N = \Sigma(M_i C_i) / [\Sigma(R_i) + 1] = 618$$

$$95\% \text{-interval (low)} = \Sigma(M_i C_i) / [R_U + 1] = 321$$

$$95\% \text{-interval (high)} = \Sigma(M_i C_i) / [R_L + 1] = 1,301$$

Appendix 2: Mark-recapture encounter histories of all common carp

A2.1. Encounter histories of individually-tagged common carp (n=1,246) in the Phalen Chain watershed. Sampling periods occurred at two to three-week intervals during the open water seasons (May-November) of 2012 and 2013. An “a” denotes an individual that was encountered in Markham Pond, a “b” denotes an individual that was encountered in Upper Kohlman Basin, and a “0” denotes an individual that was not encountered during that sampling period. All individuals that were encountered outside of the study region (in the main lakes downstream) are identified by a “Y” in the “Main Lakes?” column. Sex (m = 1, f = 0, unknown = 0.5) and total length (mm) are recorded for each individual as well as length upon subsequent recapture(s) if applicable.

Fish ID	2012 Sampling Periods													2013 Sampling Periods										Main Lakes?	Sex (m=1)	TL_0 (mm)	TL_1 (mm)	TL_2 (mm)	TL_3 (mm)
	1	2	3	4	5	6	7	8	9	10	11	12	13	1	2	3	4	5	6	7	8	9	10						
2260050208	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	252			
2260050292	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	205			
2260050224	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	248			
2260050271	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		1	262			
2260050249	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	232			
2260050294	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	244			
2260050275	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	224			
2260050212	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		1	257			
2260050217	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		1	222			
2260050281	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	205			
2260050201	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	536			
2260050254	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	655			
2260050202	b	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		1	595	590		
2260050199	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	372			
2260050260	b	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		1	482	485	505	
2260050204	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	235			
2260050203	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0.5	263			

2260050206	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	279			
2260050198	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	423			
2260050272	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	395			
2260050244	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	257			
2260050276	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	290			
2260050213	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	260			
2260050253	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	285			
2260050252	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	249	374		
2260050269	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	245			
2260050257	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	367			
2260050210	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	150			
2260050230	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	350			
2260050211	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	367			
2260050205	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	601			
2260050282	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	591	598		
2260050232	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	600			
2260050286	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	473			
2260050283	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	576			
2260050279	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	229			
2260050236	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	211			
2260050226	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	220			
2260050289	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	246			
2260050277	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	255			
2260050227	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	237			
2260050265	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	230	300		
2260050195	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	240			
2260050235	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	207			
2260050267	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	245			
2260050278	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	235			
2260050218	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	253			
2260050270	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	259			
2260050285	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	233			
2260050220	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	235			

2260050256	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	243				
2260050216	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	235			
2260050241	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	250				
139224902	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	280				
139225288	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	476				
139224953	0	b	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	415	419			
139225527	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	383				
139224960	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	356				
139224957	0	b	0	0	0	0	b	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	455	482	492	494	
139225438	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	410				
139224956	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	480				
139224926	0	b	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	445	453			
180598705	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	308				
180598703	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	284				
180598701	0	0	b	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	573	589			
180598700	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	611				
180598699	0	0	b	0	0	0	0	0	0	0	0	0	0	b	b	0	0	0	0	0	0	0	0	0	0	0	0	1	615	609	615		
180598698	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	565				
180598697	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	545				
180598696	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	453				
180598695	0	0	b	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	444	451			
180598694	0	0	b	0	0	b	0	0	0	0	0	b	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	413	416	439	438	
180598693	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	631				
180598692	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	604				
180598691	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	471				
180598690	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	1	584	595			
180598689	0	0	b	0	0	b	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	590	590	594		
180598688	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	241				
180598687	0	a	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	416	479			
180598686	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	272				
180598685	0	a	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	247	262			
180598684	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	247				
180598683	0	a	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	b	0	0	0	0	0	0	0	0	0	0.5	254	317	358		

180598682	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	255					
180598681	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	176					
180598680	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	273					
180598679	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	250					
180598678	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	322					
180598677	0	0	0	b	b	0	0	0	0	0	0	0	b	0	b	0	0	0	0	0	0	1	590	590	601	597		
180598676	0	0	0	b	0	0	0	0	0	0	0	0	0	b	b	0	0	0	0	0	0	Y	0	665	671	662	.	
180598674	0	0	0	b	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	309	385			
180598673	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	1	311	412				
180598672	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	1	300	388				
180598671	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310					
180598670	0	0	0	b	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	481	519			
180598669	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	613					
180598665	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	294					
180598664	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	225					
180598663	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	205					
180598662	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	456					
180598661	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	194					
180598660	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	169					
180598659	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	243					
180598658	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	270					
180598657	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	277					
180598656	0	0	a	0	0	0	0	0	0	0	0	0	0	b	b	0	0	0	0	0	0	0	0	270	326	325		
180598655	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	247					
180598654	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	279					
180598653	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	285					
180598652	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	286					
180598651	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	172					
180598650	0	0	a	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	311	320				
180598649	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	277					
180598648	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	507					
180598647	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	272					
180598646	0	0	a	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0.5	302	356				

180598645	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	276			
180598644	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	381			
180598643	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	276			
180598642	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	184			
180598641	0	0	a	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	174	183		
180598640	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	262			
180598639	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	245			
180598638	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	274			
180598637	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	268			
180598635	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	296			
180598636	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	305			
180598634	0	0	a	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	314	344		
180598633	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	261			
180598632	0	0	a	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	1	450	470		
180982904	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	265			
180982905	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	263			
180982906	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	272			
180982907	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	271			
180982908	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	319			
180982909	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	276			
180982910	0	0	a	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	264	285		
180982911	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	269			
180982912	0	0	a	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	292	331		
180982913	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	310			
180982914	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	265			
180982915	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	184			
180982916	0	0	a	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	262	306		
180982918	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	252			
180982917	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	315			
180982919	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	384			
180982920	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	290			
180982921	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	285			
180982922	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	280			

180982923	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	266			
180982924	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	249			
180982925	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	285			
180982927	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	285			
180982926	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	275			
180982928	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	290			
180982929	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	285			
180982930	0	0	a	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	313	339		
180982931	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	270			
180982932	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	266			
180982933	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	269			
180982934	0	0	a	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0.5	289	308		
180982935	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	295			
180982936	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	348			
180982937	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	292			
180982938	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	599			
180982939	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	317			
180982941	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	480			
180982940	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	625			
180982942	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	335			
180982943	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	610			
180982944	0	0	0	0	b	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	547	525		
180982945	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	580			
180982946	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	609			
180982947	0	0	0	0	b	b	0	0	0	0	0	0	0	0	b	0	0	0	0	0	618	613	613	
180982948	0	0	0	0	b	0	b	0	0	0	0	0	0	0	0	0	0	0	0	1	605	605		
180982949	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	611			
180982950	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	318	400		
180982952	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	390			
180982953	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	1	300	391		
180982954	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	300			
180982958	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	326			
180982955	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	295			

180982956	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	296				
180982957	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	303				
180982959	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	282				
180982960	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	316				
180982961	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	316				
180982962	0	0	0	a	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	287	304	315		
180982963	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	267				
180982964	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	331				
180982965	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	269				
180982966	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	280				
180982967	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	291				
180982968	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310				
180982969	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	202				
180982970	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	293				
180982971	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	294				
180982972	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	240				
180982973	0	0	0	0	a	0	0	0	0	0	0	0	0	a	0	a	0	0	0	a	0	0	301	310	314	350
180982974	0	0	0	0	a	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0.5	279	307			
180982975	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	289				
180982976	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	295				
180982977	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	288				
180982978	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	256				
180982979	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	365				
180982980	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	287				
180982981	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	319				
180982982	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	280				
180982983	0	0	0	0	a	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	278	289			
180982984	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	316				
180982985	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	313				
180982986	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	346				
180982987	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	327				
180982988	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	363				
180982989	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0.5	276	369			

180982990	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	240			
180982991	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	291			
180982992	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	196			
180982993	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	300			
180982994	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	288			
180982995	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	264			
180982996	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	267			
180982997	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	275			
180982998	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	269			
180982999	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0.5	305	361		
180983000	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	304			
180983001	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	300			
180983002	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	286			
180983003	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	305			
180983004	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	270			
180983005	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	271			
180983006	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	288			
180983007	0	0	0	0	a	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	1	288	288		
180983008	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	290			
180983009	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	339			
180983010	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	326			
180983011	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	295			
180983012	0	0	0	0	a	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	1	281	428		
180983013	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	288			
180983014	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	289			
180983015	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	273			
180983028	0	0	0	0	0	b	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	463	473		
180983029	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	275			
180983030	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	307			
180983016	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	627			
180983017	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	592			
180983018	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	621			
180983019	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	516			

180983020	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	620			
180983021	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	304			
180983022	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	610			
180983026	0	0	0	0	0	b	0	b	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	656	647	650	
180983023	0	0	0	0	0	b	0	0	b	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	1	725	710	718	
180983024	0	0	0	0	0	b	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	1	637	630		
180983025	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	679			
180983027	0	0	0	0	0	b	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	1	635	634		
180983031	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	300			
180983032	0	0	0	0	0	a	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	296	310		
180983033	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	267			
180983034	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	296			
180983035	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	340			
180983036	0	0	0	0	0	a	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	310	319		
180983037	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	492			
180983038	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	314			
180983039	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	289			
180983040	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	1	317	385		
180983041	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	318			
180983042	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	503			
180983043	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	317			
180983044	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	303			
180983045	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	344			
180983046	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	1	305	343		
180983047	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	315			
180983048	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	292			
180983049	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	1	534	540		
180983050	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	295			
180983051	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	344			
180983052	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	298			
180983053	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	297			
180983054	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	222			
180983055	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	281			

180983091	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	1	313			
180983092	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	615			
180983090	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	1	565			
180981344	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	289			
180981233	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	292			
180981222	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	304			
180981291	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	360			
180981323	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	311			
180981379	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	330			
180981269	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	234			
180981391	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	b	1	325	392		
180981193	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	263			
180981095	0	0	0	0	0	0	a	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	330	327		
180981205	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	306			
180981127	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	318			
180981362	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	325			
180981179	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	305			
180981365	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310			
180981310	0	0	0	0	0	0	a	0	0	0	0	0	0	0	a	a	0	0	0	0	0	301	350	354	
180981128	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	304			
180981188	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	346			
180981184	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	320			
180981164	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	283			
180981298	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	319			
180981299	0	0	0	0	0	0	a	0	0	0	0	0	a	0	0	0	0	0	0	0	0.5	325	300		
180981374	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	284			
180981220	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	312			
180981326	0	0	0	0	0	0	a	0	0	0	0	0	0	0	a	0	0	0	0	0	0	305	335		
180981363	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	1	308			
180981142	0	0	0	0	0	0	a	0	0	0	0	0	0	a	0	0	0	0	0	0	1	309	308		
180981301	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	300			
180981383	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	291			
180981743	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	325			

180981202	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	313			
180981111	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	287			
180981332	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	363			
180981388	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	319			
180981340	0	0	0	0	0	0	0	0	a	0	0	0	a	0	0	0	0	0	0	0	0	0	0	1	275	275		
180981153	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	308			
180981380	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	311			
180981086	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	334			
180981331	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	350			
180981236	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310			
180981341	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310			
180981211	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	337			
180981158	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	326			
180981271	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	215			
180981103	0	0	0	0	0	0	0	0	a	0	0	0	0	a	0	0	0	0	0	0	0	0	0	1	300	310		
180981092	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	300			
180981098	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	300			
180981XX2	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	316			
180981151	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	310			
180981399	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	304			
180981177	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	351			
180981317	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	323			
180981393	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	282			
180981240	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	309			
180981338	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	342			
180981249	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	302			
180981182	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	321			
180981290	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	350			
180981181	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	440			
180981122	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	334			
180981189	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	340			
180981149	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	276			
180981094	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	378			

181177351	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	305				
181177510	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	320				
181177381	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	283				
181177295	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	342				
181177600	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	332				
181177465	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	b	0	0	0	0	0	0	0	0	308	319		
181177310	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	91				
181177293	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	a	b	0	0	0	0	0	0	0	319	345	375	374
181177560	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	92				
181177396	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	82				
181177531	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	425				
181177316	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	104				
181177598	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	105				
181177454	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	89				
181177489	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	85				
181177516	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	94				
181177501	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	97				
181177348	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	335				
181177582	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	132				
181177370	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	88				
181177324	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	83				
181177543	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	104				
181177388	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	93				
181177470	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	89				
181177434	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	99				
181177551	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	83				
181177584	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	357				
181177XX3	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	430				
181177438	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	336				
181177528	0	0	0	0	0	0	0	0	0	0	a	0	0	a	0	0	0	0	0	0	0	0	0	0	486	490	496	
181177593	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	1	529				
181177443	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	340				
181177315	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	542			

181177360	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	348						
181177591	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	387						
181177291	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	86						
181177288	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	84						
181177512	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	112						
181177493	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	104						
181177331	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	99						
181177477	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	92						
181177337	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	93						
181177294	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	100						
181177576	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	94						
181177407	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	82						
181177412	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	296	302					
181177546	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	99						
181177307	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	105						
181177549	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	101						
181177308	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	104						
181177492	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	82					
181177583	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	93					
181177523	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	117					
181177410	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	102					
181177550	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	492						
181177433	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	471	486			
181177459	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	358					
181177538	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	393			
181177350	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	382					
181177509	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	352					
181177344	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	383					
181177447	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	350					
181177356	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	341					
181177346	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	237					
181177301	0	0	0	0	0	0	0	0	0	0	0	b	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	338	342				
181177432	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	629					

181177362	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	139			
181177319	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	285			
181177602	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	420				
181177320	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	324				
181177332	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	306				
181177389	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	294				
181177498	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	288				
181177333	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	312				
181177327	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	120				
181177496	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	408				
181177478	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	267				
181177571	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	324				
181177314	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	111				
181177517	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	102				
181177292	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	120				
181177589	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	279				
181177442	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	108				
181177597	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	111				
181177297	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	114				
181177359	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	108				
181177532	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	117				
181177460	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	126				
181177495	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	108				
181177439	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	111				
181177601	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	111				
181177305	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	117				
181177559	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	435				
181177304	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	230				
181177357	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	240				
181177468	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	265	373	387		
181177490	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	265				
181177330	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	110				
181177575	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	240	320			

181177756	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0.5	100				
181177737	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0.5	85				
181177567	0	0	0	0	0	0	0	0	0	0	0	a	a	0	0	0	0	0	0	0	0	0	0	0	0.5	240	291			
181177561	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0.5	117				
181177289	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	632				
181177426	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	b	0	0	0	0	0	0	0	1	611	609			
181177506	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	686				
181177302	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	543				
181177336	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	471				
181177526	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	491				
181177435	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	588				
181177317	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	b	b	b	0	0	0	0	0	0	0	536	534	540	540
181177341	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	545				
181177380	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	440				
181177XX4	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	389				
181177390	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	638				
181177369	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	567				
181177518	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	567				
181177530	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	495				
181177383	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	618				
181177555	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	609				
181177467	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	499				
181177298	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	b	b	0	0	0	0	0	0	0	0	0	579	576	581	
181177363	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	0	0	0	0	0	0	0	0	1	583	584			
181177463	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	535				
181177525	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	518				
181177290	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0.5	540				
181177450	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	b	b	0	b	0	0	0	0	0	1	401	400	410	415	
181179278	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	b	0	0	0	0	0	0	304	350		
181179279	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	295				
181179280	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	475				
181179281	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	112				
181179282	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0.5	138				

181179283	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	513														
181179284	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	234													
181179285	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	518													
181179286	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	305													
181179287	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	301													
181179288	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	352													
181179289	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	295													
181179290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	302													
181179291	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	299													
181177386	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	361													
181177541	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	310	336													
181177577	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	351													
181177486	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	122													
181177448	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	316													
181177563	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	274													
181177401	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	140													
181177374	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	255													
181177399	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	366	364									
181177536	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	260													
181177473	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	291													
181177415	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	133													
181177385	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	b	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	290	315													
181177547	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	493											
181177365	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	417										
181177552	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	366										
181177309	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	367										
181177529	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	555										
181177595	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	354							
181177311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	333								
181177408	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	275								
181177482	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	348						
181177484	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	320				
181177421	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	559				

181179009	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0		1	289				
181179010	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0	0		0	299				
181179011	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	314					
181179012	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	339					
181179013	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	a	0	0	0	0	0	0	0		1	371	381				
181179014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0	330					
181179015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0	538					
181179016	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	392					
181179017	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	328					
181179018	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0	457					
181179019	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	323					
181179020	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	274					
181179021	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0	326					
181179022	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	a	0	0	0	0	0	0	0		0	279	291				
181179023	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	355					
181179024	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		1	294					
181179025	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	282					
181179026	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	124					
181179027	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	111					
181179028	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	114					
181179029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	96					
181179030	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0	0	0	0	0	0	0	0		0.5	113					
181179041	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		1	495					
181179042	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	0	b	0	0	0	0		1	594	586	594			
181179043	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		1	339					
181179044	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		0	390					
181179045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	b		0	377	434				
181178963	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		1	581					
181178964	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	b	b	0	0	0	0	0	0	0		1	404	394	401			
181178965	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	b	0	0	0	0	0		0	380	393				
181178966	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		0	154					
181178971	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0	Y	0	259	254				
181178972	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0	0	0	0	0	0		1	412					

181179067	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	399	398		
181179068	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	320			
181179069	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	348			
181179070	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	330			
181179071	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	379			
181179072	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	894			
181179073	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0.5	335	372		
181179074	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	311			
181179075	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	312			
181179076	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	375			
181179077	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	362			
181179078	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	298	305		
181179079	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	322			
181179080	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0.5	325	365		
181179081	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	422			
181179082	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	321			
181179083	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	313			
181179084	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	331			
181179085	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	305			
181179086	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	330			
181179087	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	364			
181179088	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	313			
2260051261	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	157			
2260051247	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	104			
2260051235	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	155			
2260051250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	135			
2260051296	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	115			
181179089	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	578			
181179090	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	578			
181179091	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	561			
181179092	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	320			
181179093	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	728	723		
181179094	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	534			

183585892	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0		0.5	154				
183585893	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0	0		0.5	166				
183585996	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	360			
183585995	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	283			
183585994	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	258			
183585993	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	580			
183585992	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	244			
183585991	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	b	0		0.5	390	393		
183585990	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	614			
183585989	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0	728			
183585988	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	b	0	0	0		1	370	363		
183585987	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	174			
183585986	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	b	0	0	0		0	373	363		
183585985	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	514			
183585984	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	406			
183585983	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	b	0	0	0		0	346	352		
183585982	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	0		0.5	241	284		
183585981	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	350			
183585980	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	b	0		1	369	387		
183585979	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0	362			
183585978	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	0		1	340	365		
183585977	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	b	0	0		0.5	235	244		
183585976	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	239			
183585974	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	390			
183585973	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	257			
183585970	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		1	353			
183585969	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	231			
183585968	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	357			
183585967	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	222			
183585966	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0	0		0.5	166			
183586848	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	b	b	0		0	490	483	488	
183586851	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0		0	391			
183586782	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0	0	0		1	308			

183585931	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0		0.5	105			
183585930	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0		0.5	108			
183585936	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	a	0		0.5	426			
183585929	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	194			
183585928	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	215			
183585927	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	131			
183585925	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	128			
183585924	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	650			
183585923	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	385			
183585922	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	363			
183585921	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	436			
183585920	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	433			
183585919	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	387			
183585918	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	395			
183585917	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	362			
183585916	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	184			
183585915	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	166			
183585914	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	153			
183585913	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	177			
183585912	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	184			
183585911	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	170			
183585910	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	173			
183585909	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		1	711			
183585908	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0	585			
183585907	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	234			
183585906	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	338			
183585905	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	251			
183585904	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		1	360			
183585903	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		1	355			
183585902	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	169			
183585901	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	239			
186585998	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	276			
186585999	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b	0		0.5	266			

183586028	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	233			
183586029	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		1	315			
183586030	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	214			
183586031	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		1	300			
183586032	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	203			
183586097	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	248			
183586096	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	265			
183586095	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	b		0.5	537			

Appendix 3: Genetic variation across the 12 microsatellite loci assayed for common carp

In order to assess whether the microsatellite markers assayed for common carp met the assumptions for STRUCTURE, tests for Hardy-Weinberg equilibrium and linkage equilibrium were carried out in GENEPOP. The results of Hardy-Weinberg equilibrium tests along with allele frequencies and observed and expected heterozygosities are reported for each loci for each sample (Table 1).

Sample abbreviations and details are as follows:

- CSY1: Casey Lake young-of-year, 2011 (n = 46)
- CSY2: Casey Lake year 1+, 2011 (n = 47)
- MRK: Markham Pond, 2011 (n = 39)
- UKB1: Upper Kohlman Basin, 2012 (n = 45)
- UKB2: Upper Kohlman Basin, 2013 (n = 32)
- KHL: Lake Kohlman, 2013 (n = 94)
- GRV1: Lake Gervais, 2011 (n = 120)
- GRV2: Lake Gervais, 2012 (n = 70)
- GRV3: Lake Gervais, February 2013 (n = 113)
- GRV4: Lake Gervais, October 2013 (n = 44)
- KEL: Lake Keller, 2013 (n = 52)
- PHA: Lake Phalen, 2013 (n = 30)
- INT1: Interstate Pond year 1+, 2013 (n = 14)
- INT2: Interstate Pond young-of-year, 2013 (n = 49)
- SPW: Spawners in the main lakes, 2013 (n = 33)
- KC: Spawners in Kohlman Creek, 2013 (n = 147)
- GC: Spawners in Gervais Creek, 2013 (n = 52)

A3.1. Allele frequencies and heterozygosities for 12 microsatellite loci across 17 samples of common carp. Also shown are observed (H obs) and expected (H exp) heterozygosities, with H exp in bold indicating significant deviation from Hardy-Weinberg expectations at $P < 0.05$ and bold-italics indicating significance following sequential Bonferroni correction for multiple testing.

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
Cca67																	
235	0.02	0.02	-	-	-	0.03	0.01	0.03	0.01	0.06	0.09	-	-	-	0.02	0.01	0.02
237	-	-	-	-	-	0.01	-	-	-	0.01	-	0.02	-	-	-	0.00	-
241	0.27	0.21	0.49	0.28	0.27	0.32	0.23	0.31	0.32	0.26	0.31	0.34	0.31	0.50	0.20	0.26	0.40
243	0.31	0.37	0.28	0.27	0.35	0.17	0.12	0.04	0.10	0.02	0.02	-	0.23	0.08	0.17	0.28	0.18
245	-	-	-	-	-	-	-	-	0.01	-	-	-	-	0.01	-	0.00	-
247	0.02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	-
249	0.06	0.11	0.08	0.14	0.15	0.06	0.03	0.02	0.05	0.01	-	-	0.19	0.18	0.03	0.20	0.05
257	0.17	0.12	0.04	0.10	0.06	0.02	0.03	0.01	0.04	-	0.03	-	0.04	-	0.02	0.07	0.06
259	0.03	0.01	0.04	0.03	-	0.25	0.42	0.36	0.27	0.34	0.32	0.38	0.19	0.11	0.31	0.05	0.23
261	-	0.01	0.01	0.06	0.03	0.10	0.14	0.19	0.18	0.29	0.21	0.27	0.04	0.11	0.25	0.03	0.04
263	-	-	-	-	-	0.01	-	-	-	-	-	-	-	-	-	-	-
265	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-	-	-
273	0.03	0.03	0.03	-	0.02	0.01	-	0.01	0.00	-	-	-	-	-	-	0.01	0.01
299	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	-
303	-	0.01	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-
309	0.09	0.11	0.04	0.11	0.11	0.03	0.02	0.01	0.02	-	0.01	-	-	-	-	0.07	-
H obs	0.88	0.79	0.74	0.70	0.65	0.61	0.68	0.71	0.73	0.80	0.76	0.71	0.77	0.82	0.56	0.70	0.76
H exp	0.80	0.79	0.68	0.81	0.77	0.80	0.74	0.73	0.79	0.74	0.75	0.68	0.81	0.69	0.78	0.80	0.75
MFW1																	
167	0.43	0.44	0.60	0.33	0.58	0.29	0.27	0.27	0.28	0.36	0.19	0.29	0.75	0.74	0.45	0.41	0.51
209	0.19	0.28	0.08	0.30	0.23	0.26	0.27	0.22	0.26	0.15	0.31	0.16	0.07	0.11	0.24	0.28	0.15
215	0.11	0.06	0.11	0.08	0.09	0.22	0.24	0.35	0.24	0.30	0.30	0.38	0.07	0.13	0.18	0.11	0.23
217	0.23	0.18	0.21	0.27	0.09	0.13	0.06	0.02	0.09	0.02	0.02	-	0.11	-	0.06	0.19	0.07
219	-	0.01	-	0.01	-	0.10	0.17	0.14	0.13	0.16	0.18	0.18	-	0.01	0.06	0.01	0.04

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
221	0.03	0.03	-	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-
H obs	0.59	0.60	0.61	0.78	0.66	0.78	0.74	0.79	0.69	0.81	0.69	0.64	0.36	0.35	0.61	0.64	0.60
H exp	0.72	0.70	0.59	0.73	0.60	0.78	0.77	0.74	0.78	0.74	0.75	0.73	0.43	0.42	0.71	0.71	0.66
MFW11																	
200	0.14	0.11	0.25	0.09	0.13	0.18	0.16	0.19	0.17	0.12	0.23	0.23	0.35	0.28	0.26	0.15	0.20
202	0.01	0.01	-	-	0.02	0.19	0.32	0.33	0.27	0.38	0.36	0.41	0.23	0.33	0.14	0.03	0.30
204	0.36	0.47	0.42	0.61	0.55	0.46	0.40	0.41	0.41	0.47	0.36	0.34	0.35	0.40	0.44	0.50	0.42
206	0.28	0.24	-	0.11	0.11	0.08	0.05	0.03	0.06	0.02	0.03	-	0.04	-	0.08	0.11	0.02
208	0.21	0.17	0.33	0.18	0.20	0.09	0.07	0.04	0.09	0.02	0.01	0.02	0.04	-	0.09	0.20	0.06
210	-	-	-	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-
212	-	-	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-
H obs	0.63	0.72	0.50	0.63	0.69	0.71	0.72	0.76	0.62	0.55	0.73	0.61	0.77	0.73	0.82	0.66	0.62
H exp	0.74	0.69	0.71	0.58	0.64	0.71	0.71	0.69	0.72	0.63	0.69	0.67	0.73	0.67	0.72	0.68	0.69
MFW24																	
219	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.02	-	-
223	0.01	0.01	0.05	0.01	0.06	0.09	0.08	0.18	0.12	0.14	0.14	0.14	0.18	0.11	0.06	0.00	0.13
225	0.28	0.34	0.53	0.51	0.45	0.43	0.47	0.44	0.45	0.47	0.49	0.41	0.36	0.38	0.59	0.48	0.43
227	-	-	-	-	-	-	0.00	0.01	0.00	-	-	-	-	-	-	0.00	-
231	0.24	0.29	0.14	0.17	0.28	0.10	0.09	0.02	0.08	0.03	0.04	-	0.29	0.30	0.08	0.17	0.12
233	-	-	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-
235	0.46	0.36	0.28	0.31	0.20	0.38	0.36	0.35	0.34	0.36	0.33	0.43	0.18	0.21	0.26	0.34	0.32
237	-	-	-	-	-	0.01	-	-	-	-	-	-	-	-	-	-	-
239	0.01	-	-	-	-	-	-	-	-	-	-	0.02	-	-	-	-	-
H obs	0.74	0.53	0.58	0.66	0.59	0.57	0.59	0.70	0.67	0.64	0.57	0.55	0.86	0.82	0.39	0.64	0.76
H exp	0.66	0.68	0.63	0.62	0.68	0.66	0.64	0.65	0.66	0.63	0.64	0.63	0.75	0.72	0.58	0.62	0.69
MFW25																	
273	0.24	0.26	0.11	0.18	0.23	0.30	0.26	0.25	0.22	0.27	0.33	0.38	0.09	0.13	0.23	0.23	0.24
277	-	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
279	-	0.02	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
281	-	-	-	-	-	-	0.00	-	0.00	-	-	-	-	-	-	-	-
299	-	-	-	-	-	-	0.00	-	0.01	-	-	-	-	-	-	0.00	-
303	0.03	0.02	-	-	-	0.01	0.00	-	0.00	-	0.01	-	0.05	-	-	0.00	0.01
305	0.07	0.06	0.05	0.03	0.02	0.15	0.21	0.14	0.17	0.19	0.15	0.23	0.36	0.47	0.10	0.03	0.24
307	0.49	0.51	0.77	0.63	0.62	0.46	0.44	0.48	0.50	0.44	0.45	0.33	0.18	0.14	0.52	0.59	0.41
309	0.02	0.02	0.04	-	0.02	0.02	0.01	0.02	0.01	0.01	-	-	0.27	0.12	0.02	0.04	0.05
311	-	-	-	-	-	-	0.01	0.01	0.00	-	-	0.02	0.05	0.07	0.02	0.00	0.04
313	0.13	0.10	0.04	0.13	0.10	0.03	0.03	0.02	0.02	0.01	0.01	0.02	-	0.01	0.03	0.09	0.01
315	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.02	-	-
317	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
321	0.01	-	-	0.03	0.02	0.03	0.03	0.07	0.05	0.07	0.05	0.02	-	0.06	0.07	0.01	-
H obs	0.68	0.64	0.43	0.61	0.50	0.57	0.54	0.74	0.62	0.77	0.72	0.63	0.91	0.74	0.73	0.63	0.63
H exp	0.69	0.67	0.40	0.56	0.56	0.68	0.70	0.68	0.67	0.69	0.68	0.71	0.78	0.73	0.67	0.59	0.72
MFW26																	
124	0.09	0.12	0.08	0.08	0.08	0.03	0.03	-	0.02	-	0.01	0.02	-	-	0.05	0.12	0.01
128	0.12	0.12	0.04	0.06	0.05	0.04	0.01	0.01	0.02	0.03	-	-	-	0.01	-	0.03	0.06
130	0.02	0.03	0.04	0.05	-	0.03	-	-	0.02	-	-	-	-	-	-	0.06	0.03
136	-	-	-	-	-	0.03	0.04	0.05	0.02	0.01	0.05	0.12	-	-	-	0.00	0.01
142	0.02	0.03	-	0.02	0.03	0.01	-	0.01	0.01	-	-	-	-	-	-	0.05	-
146	0.04	0.02	0.06	0.01	0.06	0.06	0.10	0.13	0.08	0.13	0.15	0.12	0.12	0.11	0.08	0.05	0.08
148	-	0.02	-	0.01	-	0.19	0.24	0.24	0.22	0.17	0.33	0.33	0.15	0.24	0.14	0.02	0.23
150	0.70	0.66	0.78	0.76	0.78	0.61	0.56	0.56	0.59	0.67	0.46	0.41	0.73	0.63	0.73	0.67	0.57
152	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-	-	0.01
154	0.01	-	-	0.01	-	-	0.03	0.01	0.00	-	-	-	-	-	0.02	0.00	-
H obs	0.46	0.57	0.36	0.42	0.41	0.57	0.62	0.57	0.59	0.56	0.71	0.69	0.46	0.53	0.52	0.49	0.56
H exp	0.50	0.54	0.38	0.42	0.38	0.59	0.62	0.62	0.59	0.52	0.66	0.70	0.45	0.53	0.45	0.52	0.62
MFW29																	
163	0.63	0.64	0.68	0.56	0.69	0.65	0.72	0.71	0.63	0.70	0.73	0.72	0.86	0.98	0.56	0.61	0.75
171	-	0.03	-	-	-	-	0.02	-	0.00	0.03	-	-	-	-	0.02	0.01	-

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
173	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	-
177	0.03	0.04	0.11	0.16	0.13	0.07	0.03	0.03	0.05	0.03	-	-	-	-	0.03	0.10	0.05
181	0.07	0.09	0.05	0.08	0.03	0.07	0.02	0.01	0.05	0.01	0.01	-	0.04	0.02	0.06	0.06	0.02
185	0.05	0.08	0.01	0.03	0.02	0.11	0.15	0.20	0.17	0.15	0.20	0.26	0.04	-	0.20	0.04	0.06
223	0.22	0.12	0.14	0.17	0.13	0.10	0.06	0.05	0.09	0.09	0.07	0.02	0.07	-	0.14	0.18	0.13
H obs	0.53	0.59	0.47	0.57	0.55	0.48	0.45	0.54	0.55	0.50	0.48	0.38	0.29	0.04	0.58	0.57	0.40
H exp	0.56	0.56	0.50	0.64	0.49	0.55	0.46	0.45	0.56	0.48	0.43	0.42	0.27	0.04	0.63	0.58	0.42
MFW31																	
276	0.01	-	-	-	-	-	0.01	-	-	-	-	-	-	-	0.02	-	-
282	0.36	0.45	0.38	0.41	0.45	0.40	0.40	0.48	0.47	0.40	0.38	0.42	0.43	0.30	0.45	0.42	0.47
286	-	-	-	-	-	0.01	-	-	-	-	-	0.02	-	-	-	-	-
296	0.07	0.03	0.09	0.07	0.13	0.04	0.01	0.02	0.04	0.02	-	0.02	-	0.01	-	0.05	0.02
298	-	-	-	-	-	-	-	-	-	-	-	-	0.04	-	-	0.00	-
300	0.17	0.12	0.10	0.09	0.06	0.07	0.04	0.02	0.04	-	0.03	-	0.04	-	0.02	0.14	0.02
302	0.33	0.34	0.35	0.39	0.28	0.31	0.31	0.26	0.27	0.36	0.35	0.19	0.43	0.62	0.28	0.29	0.40
306	0.06	0.07	0.05	0.03	0.02	0.02	0.01	0.01	0.01	0.01	-	0.04	-	-	0.03	0.06	-
312	-	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-	-	-
314	0.01	-	0.03	0.01	0.06	0.16	0.22	0.19	0.18	0.20	0.24	0.31	0.07	0.07	0.20	0.04	0.09
318																	
H obs	0.64	0.63	0.79	0.60	0.66	0.64	0.65	0.63	0.72	0.60	0.76	0.69	0.57	0.53	0.66	0.65	0.70
H exp	0.74	0.68	0.72	0.68	0.70	0.72	0.70	0.67	0.68	0.67	0.68	0.70	0.65	0.53	0.68	0.72	0.62
MFW32																	
268	-	-	-	-	-	0.03	0.04	0.06	0.03	0.05	0.02	0.05	-	0.07	0.06	0.00	0.03
270	0.02	-	-	-	-	-	-	-	0.01	-	-	-	-	-	-	0.00	-
272	0.03	0.01	0.06	0.03	0.10	0.02	0.00	0.01	0.02	-	-	-	-	-	0.02	0.03	-
276	0.87	0.94	0.83	0.85	0.74	0.92	0.87	0.91	0.85	0.95	0.97	0.95	1.00	0.92	0.88	0.84	0.91
278	-	-	-	-	-	-	-	0.01	-	-	-	-	-	0.01	-	0.01	-
282	0.01	-	-	-	-	-	0.04	-	-	-	-	-	-	-	-	-	-
290	0.06	0.05	0.11	0.13	0.16	0.04	0.04	0.01	0.08	-	0.01	-	-	-	0.05	0.12	0.06

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
H obs	0.19	0.09	0.23	0.30	0.52	0.14	0.23	0.18	0.22	0.09	0.06	0.10	0.00	0.16	0.18	0.24	0.10
H exp	0.24	0.12	0.30	0.27	0.42	0.16	0.24	0.17	0.27	0.09	0.06	0.10	0.00	0.15	0.23	0.28	0.17
MFW4																	
134	-	-	0.04	0.04	-	0.14	0.21	0.17	0.19	0.24	0.17	0.13	0.14	0.12	0.08	0.05	0.15
138	0.21	0.32	0.35	0.30	0.34	0.38	0.44	0.46	0.41	0.44	0.44	0.68	0.25	0.16	0.47	0.28	0.41
142	0.17	0.23	0.14	0.11	0.16	0.13	0.19	0.22	0.16	0.14	0.23	0.12	0.54	0.56	0.18	0.19	0.22
144	0.26	0.16	0.23	0.22	0.24	0.08	0.07	0.01	0.11	0.03	0.02	0.02	-	0.02	0.12	0.17	0.13
146	0.36	0.29	0.24	0.30	0.26	0.26	0.09	0.13	0.13	0.15	0.14	0.05	0.07	0.13	0.15	0.31	0.08
148	-	-	-	0.02	-	0.01	-	-	0.00	-	-	-	-	-	-	0.01	-
H obs	0.76	0.76	0.82	0.80	0.61	0.70	0.73	0.71	0.70	0.66	0.83	0.53	0.71	0.59	0.67	0.71	0.73
H exp	0.74	0.74	0.76	0.76	0.75	0.75	0.72	0.69	0.75	0.71	0.71	0.51	0.65	0.63	0.71	0.76	0.74
MFW6																	
138	0.60	0.62	0.58	0.56	0.66	0.48	0.48	0.43	0.44	0.33	0.45	0.43	0.43	0.60	0.50	0.61	0.50
140	0.01	-	-	-	-	-	0.00	0.01	0.00	0.01	-	-	-	-	0.03	-	-
142	-	-	-	-	0.02	-	0.00	-	-	-	-	-	-	-	-	-	-
146	0.32	0.32	0.28	0.20	0.13	0.27	0.33	0.36	0.33	0.32	0.30	0.41	0.32	0.27	0.28	0.22	0.25
148	-	-	-	-	-	-	-	-	-	-	0.01	-	-	-	0.03	-	-
150	-	-	-	-	-	0.11	0.14	0.17	0.15	0.31	0.22	0.16	0.25	0.12	0.13	0.02	0.21
154	-	-	-	-	-	-	-	-	-	0.01	-	-	-	-	-	-	-
170	0.07	0.06	0.14	0.24	0.20	0.13	0.05	0.04	0.07	0.01	0.02	-	-	0.01	0.03	0.15	0.05
H obs	0.59	0.57	0.55	0.68	0.50	0.62	0.69	0.67	0.61	0.64	0.84	0.66	0.71	0.51	0.50	0.59	0.57
H exp	0.54	0.52	0.58	0.60	0.52	0.67	0.65	0.66	0.67	0.70	0.67	0.63	0.67	0.56	0.66	0.56	0.65
MFW7																	
188	0.30	0.36	0.36	0.33	0.34	0.22	0.14	0.08	0.13	0.05	0.06	0.02	0.32	0.23	0.09	0.38	0.16
192	0.54	0.47	0.54	0.52	0.53	0.57	0.53	0.54	0.56	0.73	0.55	0.67	0.61	0.66	0.56	0.44	0.62
196	-	-	-	-	-	-	-	0.01	-	-	0.01	-	-	-	-	-	-
250	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01	-	-	-
254	0.15	0.17	0.10	0.14	0.13	0.21	0.33	0.38	0.30	0.22	0.38	0.32	0.07	0.09	0.34	0.17	0.21
258	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-	-	-

Locus & Alleles (bp)	Allele frequencies by sample																
	CSY1	CSY2	MRK	UKB1	UKB1	KHL	GRV1	GRV2	GRV3	GRV4	KEL	PHA	INT1	INT2	SPW	KC	GC
268	-	-	-	-	-	-	-	-	0.00	-	-	-	-	-	-	-	-
H obs	0.50	0.43	0.58	0.64	0.69	0.57	0.57	0.66	0.59	0.36	0.49	0.43	0.57	0.55	0.59	0.58	0.53
H exp	0.60	0.63	0.57	0.60	0.59	0.59	0.59	0.57	0.58	0.42	0.56	0.46	0.54	0.50	0.57	0.63	0.55

Appendix 4: Simulations to determine genetic classifications of common carp

For each common carp analyzed, STRUCTURE estimated the proportion of ancestry derived from each genetic strain. Based on these estimates, we attempted to classify each individual as a pure Type A, pure Type B, or hybrid cross between strains. The accuracy of such classifications can be assessed using simulated genotypes of pure baseline populations but these were unavailable in our study. Instead, we used STRUCTURE results and other information to identify baseline populations. To represent Type A we used a sample from Casey Lake in the Kohlman Creek subwatershed, which is isolated from both upstream and downstream movement and had an average assignment of 0.94 to Type A. To represent Type B, we used a subset of older fish (>33 years) in the main lakes samples that had an average assignment of 0.98 to Type B. The older fish apparently represent a population of Type B fish present prior to the introduction of the distinct Type A strain in the 1970s.

To conduct the simulations of classification power, we simulated genotypes for each pure carp population and two generations of hybrids crosses between strains [F1, F2 (F1xF1) and backcrosses to each pure type (F1xType A; F1xType B)] in Hybridlab¹. For three replications, we created 100 individual genotypes for each cross type, added them to our real data, and ran STRUCTURE at K=2 as outlined for our real data set. We then determined classification error between simulated Type A, Type B, and hybrid crosses based on different criteria of ancestry assignment (Table 1).

¹Nielsen, E. E., Bach, L. A. and Kotlicki, P. 2006. Hybridlab (version 1.0): a program for generating simulated hybrids from population samples. *Molecular Ecology Notes* 6: 971–973.

We chose classification criteria to balance potential error among categories. Individuals with estimated Type B ancestry > 0.9 were classified as Type B. At this criterion, $> 98\%$ of true Type B individuals would be correctly classified. Individuals with Type B ancestry < 0.15 were classified Type A. Only 87% of Type A individuals would be correctly classified at this criterion, but $> 98\%$ would be classified Type A or fall in the uncertain Type A or A x B category. Only a small percentage of hybrids would be expected to be incorrectly classified as pure types (0-4%), except for backcrosses. As many as 20% of backcrosses would be misclassified as the pure type to which they backcrossed (e.g., backcrosses to Type A classified as Type A). These simulations only included first-generation backcrosses. Increased error would be expected if advanced-generation backcrosses were present, however, based on the old age of the common carp and relatively short time since the strains have been mixed, there should have been relatively few advanced-generation hybrids in the population.

A4.1. Simulation results used to establish criteria for classifying individuals as Type A, Type B or hybrid crosses (A x B). Shown are cumulative percentages of simulated individuals of pure and hybrid crosses that have estimated Type B ancestry at increments of 0.05. Individuals with Type B ancestry > 0.9 were classified as Type B, those < 0.15 were classified as Type A, and those 0.35-0.90 were classified as hybrids. Individuals with Type B ancestry from 0.15 to 0.35 were classified as Type A or A x B due to high uncertainty in assignment between these two categories.

Proportion of Type B ancestry	Cumulative % of simulated individuals of each type						Classification
	Type B	Type A	F1	BCxB	BCxA	F2	
0.95	79.7	0.0	1.0	8.3	0.0	0.7	"Type B"
0.90	98.3	0.0	2.3	20.3	0.0	3.7	
0.85	99.3	0.0	2.3	32.3	0.0	6.0	
0.80	100.0	0.0	6.7	45.7	0.7	8.7	
0.75	100.0	0.0	12.3	61.7	0.7	14.0	"A x B"
0.70	100.0	0.0	17.7	72.0	1.3	21.7	
0.65	100.0	0.0	28.3	78.7	3.3	29.3	
0.60	100.0	0.0	38.3	88.0	3.7	41.3	
0.55	100.0	0.0	48.7	93.0	6.3	53.0	
0.50	100.0	0.0	62.3	95.0	10.3	61.0	
0.45	100.0	0.3	71.3	96.7	17.0	69.0	"A x B or A"
0.40	100.0	0.7	79.7	98.7	24.3	77.7	
0.35	100.0	0.7	87.3	99.7	33.3	84.0	
0.30	100.0	1.7	91.3	100.0	44.7	91.7	
0.25	100.0	3.7	94.3	100.0	58.3	96.0	"Type A"
0.20	100.0	6.7	96.3	100.0	69.7	97.0	
0.15	100.0	12.7	98.0	100.0	79.0	98.0	"Type A"
0.10	100.0	21.7	99.3	100.0	87.3	99.0	
0.05	100.0	51.7	100.0	100.0	95.7	100.0	
0.00	100.0	100.0	100.0	100.0	100.0	100.0	