

**Combining Ability of Channel Catfish, *Ictalurus punctatus*, Females and Blue
Catfish, *I. furcatus*, Males for Early Growth, Growth Variation,
Disease Resistance, and Carcass Yield of their Progeny**

by

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Abstract

The hybrid between channel catfish (*I. punctatus*) females and blue catfish (*I. furcatus*) males is considered the best catfish genotype for commercial catfish farming due to their faster growth rate, better survival rate, disease resistance, better carcass yield and seinability. However, the hybrid is not a panacea, and genetically improved hybrids might be developed by improving the parent species, especially by selecting for female channel catfish and male blue catfish that have increased combining abilities. Reciprocal recurrent selection for the parent species could be conducted to improve traits of the hybrid progeny, however estimation of general combining ability (GCA) and specific combining ability (SCA) is necessary to determine the feasibility and the best approach to the reciprocal recurrent selection.

Twenty channel catfish females and twelve blue catfish males were crossed in a 20 x 12 factorial mating design, but an unbalanced design resulted as only 40 families had adequate hatch. The 40 hybrid families were evaluated for their early performance traits in three different rearing systems at two ages. The body weight, weight gain, coefficient of variation (CV) in body weight, survival rate from natural *Aeromonas hydrophila* infection, and dressout percentage were analyzed to estimate genetic component variances.

The estimates for variance of combining ability showed that variance for early growth of hybrid catfish in all the three rearing systems at two ages was significantly ($P < 0.05$) affected by the additive gene actions attributable to the channel catfish female parent. The genetic effects controlling the CV in body weight when hybrids were reared in flow-through system was

additive gene actions. However, when the hybrids were further reared in recirculating system, the CV became attributable to dominant gene actions. The resistance of hybrid catfish to *Aeromonas hydrophila* was significantly affected by the additive gene effects of the blue catfish male parent. The dressout percentage of hybrid catfish was affected by the dominant gene actions attributable to the specific cross of channel and blue catfish parents. Overall, the combining abilities indicate that reciprocal recurrent selection for early traits appears to have potential to improve the performance of F1 hybrid catfish.

Dedication

To my dearest Ama and Ina

My sibs: Rajia, Jehan, Riaz, Hanie, and Nizhar

My little angels: Jannan, Rheanor, Jibran, Rashdan, and Razana

Odin and Yusop Family

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List of Abbreviations

AU	Auburn University
GCA	General Combining Ability
SCA	Specific Combining Ability
REML	Restricted Estimation of Maximum Likelihood
BLUP	Best Linear Unbiased Prediction
LHRHa	Luteinizing Hormone Releasing Hormone analogue

CHAPTER ONE

General Introduction and Literature Review

Aquaculture has always been considered as a sustainable food producing sector that can address the increasing demand for food of the increasing human population. The world aquaculture production continued to grow in 2015, reaching 106 million tonnes (live weight) with an estimated value of US\$157 billion, contributing 45.3 percent (%) of the total world fish production (Zhou 2017). Although there is an overall increase in the aquaculture production, which can be attributed to the increasing demand for food fish from around the world, the production in developed countries such as the USA, Japan, Korea, and various European countries has declined the past few years. The importation of fish from developing countries where production costs are relatively low is seen as a major reason for this decline.

The channel catfish (*Ictalurus punctatus*), which is mostly produced in the southern parts of the United States, accounted for up to 68% of the total aquaculture production in the USA at its peak in 2003. Since that time, the US industry has been greatly affected by the importation of catfish from other countries (NOAA 2016). The cheaper price, \$1.50-\$2 per pound, of the imported catfish than the American variety of catfish is attracting most of the US consumers. The imports account for 80% of all U.S. sales of frozen catfish and catfish-like fillet products. Over the last 10-13 years, the US catfish industry has declined to more than 50% of its production (Hanson and Sites, 2015). During the past decade, the 40% of the catfish farms were lost. Factors that can be considered to have contributed to this crisis in the catfish industry are competition

with cheap imports, which now have more than 50% of the US catfish market, increasing production costs and fish disease control (Wagner et al. 2002, FAO 2011).

The current levels of aquaculture production of important food fish like catfish have been attained through improved hatchery and grow-out culture techniques, disease diagnosis and treatments and application of genetics and biotechnology. Several genetic enhancement programs for catfish have been examined such as strain selection, intraspecific crossbreeding, mass selection, and interspecific hybridization (Yant et al. 1975; Green et al. 1979; Dunham and Smitherman 1984). The hybrid between channel catfish females and blue catfish (*I. furcatus*) males was found to have exceptional heterotic growth (Giudice 1966) and at commercial densities, its growth, feed conversion ratio (FCR) (Yant et al. 1976; Li et al. 2004), survival, disease resistance (Ella 1984; Wolters et al. 1996; Dunham et al. 2008; Arias et al. 2012), dressout percentage and fillet yield (Yant 1975; Chappell 1979; Huang et al. 1994; Argue et al. 2003; Bosworth et al. 2004; Bosworth 2012) and seinability (Yant et al. 1976; Chappell 1979; Dunham and Argue 1998) were found to be superior to that of the channel and blue catfish (Dunham 2011). The Auburn University has played an important role in developing the farming techniques for hybrid catfish in the US (Dunham and Perera 2014). An increasing number of catfish farmers are utilizing hybrid catfish, which has been a key component that has allowed the catfish industry to survive and perhaps becomes stronger in the future. In 2014, about 200 million hybrid catfish fry were produced and now the industry has shifted to a majority hybrid catfish industry with 50-70% of all production and processing accounted to hybrid catfish (Multistate Research Project 2015).

Current Status of the Catfish Industry

Catfish growers of food fish, stockers, and fingerlings and fry in the US had sales of US\$361 million in 2015 which is 3% higher than in previous year, and 96% of these catfish were produced in Mississippi, Alabama, Arkansas, and Texas (National Agricultural Statistics Service (NASS) 2016). The total food size sales also increase to 4% during 2015 from its previous year and 95.9% of these were directly sold to processors. The sales of stockers in 2015 was US\$8.20 million which was 8% lower than the previous year while the sales of fingerlings and fry in 2015 was US\$7.69 million, which was 25% lower than 2014. The direct sales of stockers to other catfish grow-out producers decreased by 3% in 2015 from the previous year. The number of broodfish was down 10%, production and survival of fingerlings and stockers declined almost 30% from 2015-2016, resulting in a decrease in total hectares used for production of broodfish, fingerlings, and stockers and a decrease in sales of fingerlings and stockers (NASS 2016)

Seed production is an important component of hybrid catfish industry. It is vital that attention be given to boosting the production of quality broodfish, and quality fingerlings and stockers to augment catfish sales and strengthen the industry.

Quantitative Genetics and Its Application to Catfish Production

Geneticists have been successful in producing and improving performance traits of plants and animals through selective breeding. Traits which are of economic importance include growth performance, survival, disease resistance, tolerance to myriad of environmental stressors, harvestability, and processing characteristics. Such traits are usually controlled by actions of multiple genes. The work of Galton and Pearson in 1880-1900 resulted in many of the basic statistical tools (such as regression and correlation) that led to the development of methods for

the analyses of important quantitative traits (Stanton 2001). The formal beginning of this field started with the treatment of the inheritance of quantitative characters, which showed how explicit Mendelian genetic models of inheritance could account for the resemblance in continuous traits between relatives (Fisher 1918). Fisher's findings introduced the powerful statistical method of analysis of variance (ANOVA), which is now applied widely even outside the field of quantitative genetics. Thus, many of the basic statistical tools we used today were first introduced and developed for quantitative genetics.

The important performance and production traits of catfish which, are usually recorded per individual and are referred to as phenotype are the bases of quantification of the multiple genes for the desired traits. Information from such records are statistically analyzed to select for the best performing fish in a breeding program. Breeding programs require data collection and data analysis to determine if the phenotypic goal can be achieved through selection or crossbreeding and hybridization (Tave 1993).

Quantitative phenotypes exhibit continuous variation, requiring analyses and partitioning of phenotypic variance into independent components. Phenotypic variance (V_P) reflects the sum of genetic variance (V_G), environmental variance (V_E), and the genetic environmental interaction variance ($V_{G \times E}$).

$$V_P = V_G + V_E + V_{G \times E}$$

The V_G , V_E , and $V_{G \times E}$ are equally important and critical from a commercial stand point. Partitioning of phenotypic variation into genetic and environmental components permits breeders to make decisions for resource allocation and response to selection (Hallauer and Miranda 1981; Hill et al. 1998). A breeding program is designed to exploit and maximize available genetic

variance through the use of its main components: additive variance (V_A), dominance variance (V_D), and epistatic variance (V_I).

$$V_G = V_A + V_D + V_I$$

Because of the difficulty to exploit and measure the epistatic variance, breeders assume its non-existence. And so, V_A and V_D are considered the two most important genetic components. Additive variance is attributed to additive effects which are related to the heritability of various traits and consequently are the basis for selection (Tave 1993). When additive effects influence a continuous trait, choosing those organisms presenting the best performing traits as broodstock should result in the overall improvement of the offspring (Lutz 2001). Dominance variance (V_D) describes the variance associated with dominance genetic effects, which are expressed based on combinations of specific alleles, or combinations of individuals, strains or species that carry those alleles. Dominance effects are the basis of genetic improvement from hybridization and crossbreeding and are expressed as heterosis, commonly described as hybrid vigor, increased performance of hybrids or crossbred individuals over that of the parental lines (Hallauer and Miranda 1988).

Other genetic components, such as maternal and strain effects include both additive and dominance effects. Maternal effect is the source of variance attributed to the maternal genotype and phenotype and the environment it provides for the offspring (Falconer and McKay 1996). It can therefore be both environmental and genetic in origin. It reflects the differences in either environment or genetic merit of the female parent on the performance of her progeny (Wilham 1980). In fish and shellfish, maternal effects are related to variation in egg size and quality, which results in variation in hatching and survival during the early stage of growth and development. In channel catfish, egg size was found to affect its early growth rate (Reagan and

Conley 1977). Maternal effects on growth of brown trout, *Salmo trutta fario* (Vandeputte et al. 2002), rainbow trout, *Onchorhynchus mykiss* (Henryon et al. 2002), hybrid striped bass, *Morone chrysops* × *Morone saxatilis* (Wang et al. 2006) and Atlantic cod, *Gadus morhua* (Tosh et al. 2010) decline as the progeny age.

The strain effects of parents on a myriad of traits such as body weight, growth rate, survival, reproduction traits, sexual maturity, immunological parameters and disease resistance of their progeny have been reported in aquaculture species like salmonids (Kanis et al. 1976; Refstie et al. 1977; Gunnes and Gjedrem 1978; Jonasson 1996; Unwin et al. 2003), rainbow trout (Kincaid 1981; Okamoto et al. 1993; Overturf et al. 2003; Quinton et al. 2004), striped bass, *Morone saxatilis* (Jacobs et al. 1999), tilapia, *Oreochromis niloticus* (Eknath et al. 1993; Macaranas et al. 1997), common carp, *Cyprinus carpio* L. (Vandeputte et al. 2004), rohu, *Labeo rohita* (Reddy et al. 2002) and catfish (Dunham and Smitherman 1984; Smitherman and Dunham 1985; Dunham et al. 1987; Rezk et al. 2003; Bosworth et al. 2004; Dunham et al. 2014a, 2014b).

Quantitative genetics research has greatly impacted production of other farm animals through improved breeding since the 1930s until today (Wolters and Tiersch 2004). Channel catfish genetics and breeding began in the late 1960s and early 1970s (Dunham and Smitherman 1987). The realized response to selection in fish has been much higher than in farm animals (Gjerde 1986; Dunham et al. 2001). Catfish genetic improvement has been projected to be larger than other farm animals in terms of potential for increased food production efficiency from 2000 to 2030 (Smith 1991).

Selective breeding programs have been conducted for channel catfish to improve its growth as length and weight, time of spawning, viability, disease resistance, dressout percentage (El-Ibiary et al. 1976; El-Ibiary and Joyce 1978; Reagan 1979; Dunham 1981; Bondari 1983,

Dunham and Smitherman 1983, 1985; Dunham et al. 1987; Rezk 1993; Dunham and Brummett 1999; Rezk et al. 2003; Small 2005; Gima et al. 2014). The initial genetic enhancement programs conducted for catfish were strain selection, intraspecific crossbreeding, mass selection, and interspecific hybridization (Yant et al. 1976; Green et al. 1979; Dunham and Smitherman 1983a, 1983b).

Dunham and Smitherman (1984) first documented the origin, history, breeding and performance traits of various channel catfish strains used by university, state, federal, and private hatcheries in the US. During 80's, channel catfish, blue catfish, white catfish (*I. catus*), and flathead (*Pylodictus olivaris*) and the major catfish species in the US. The channel catfish was the primary species propagated because it has superior culture traits. This species grows faster and has more disease resistance than other species. They are native to the Mississippi-Missouri river system southward into northeastern Mexico, but their range has been expanded through introductions to almost all parts of North America where there are suitable waters. The blue catfish has relatively uniform growth and body conformation, high dressing percentage, and high vulnerability to seining. They native to the main channels of the Mississippi River and its major tributaries from Minnesota and South Dakota southward into Mexico. The white catfish have poor bacterial resistance and poor dressout percentage and are more difficult to catch during seining. They are native to lower reaches of coastal streams from Delaware and New Jersey south into Florida, including a few streams entering the Gulf of Mexico. The flathead catfish which are native to large rivers of the Mississippi, Missouri, and Ohio basins, and south into Mexico were only used for sport fishing before.

A strain is a population of fish within a single species that has the same history, the same origin and has at least one trait or a suite of traits that make it unique or make it different from other strains (Dunham 2011). The National Fish Strain Registry for catfish contains important and substantial information on the broodfish strains of channel catfish, blue catfish, and white catfish and their history, origin, behavior, reproduction, disease resistance, availability and other important traits (Kincaid et al. 2000). Strain evaluation and selection is the first step to any genetic improvement program (Dunham 2011). Basically, the best performing domestic strains of catfish are selected. In channel catfish, variation in strains was reported for growth, disease resistance, body conformation, dressing percentage, vulnerability to angling and seining, age of maturity, time of spawning, fecundity and egg size (Dunham and Smitherman 1984; Smitherman and Dunham 1985). Strains have a major impact on the success and ultimate outcome of all genetic enhancement programs. Channel catfish strains affected the production, meat yield and quality traits of channel catfish female x blue catfish male hybrids (Bosworth et al. 2004). In addition, the strain of parent species was also reported to affect the level of heterosis/ performance for growth (Dunham et al. 1987; Dunham et al. 2014a), vulnerability to angling (Dunham et al. 1986), survival and sexual dimorphism (Dunham et al. 2014a) and tolerance to low dissolved oxygen (Dunham et al. 2014b) observed in channel catfish x blue catfish hybrids. Variability in production of hybrid catfish due to the strain effects of channel and blue catfish parents used was also observed for growth rate and processing yield traits (Bosworth et al. 1998).

Selection is the classical method of screening, selecting, and breeding of better performing individuals and/or groups to improve desirable quantitative or production traits. The two basic types of selection are individual or mass (where individuals are selected based on their own performance) and family selection (where individuals are selected based on the mean

performance of their family). Combined selection can also be done where best performing individuals are selected from the best performing families. Realized response to selection in fish is generally very high compared with what has been obtained in farm animals (Gjerde 1986; Dunham et al. 2001). Like in other fish species, selection was also reported to improve growth rate in catfish (Dunham and Perera 2014). Selection has improved the body weight of channel catfish by 12–20% with one or two generations of mass selection (Bondari 1983; Dunham and Smitherman 1983a; Smitherman and Dunham 1985; Dunham and Brummet 1999;). Selection has been successful in all eight lines of channel catfish that were evaluated, and the fastest growing strains yielded the fastest-growing select lines (Smitherman and Dunham 1985). The best select line grew twice as fast as average strains of channel catfish (Burch 1986). Responses to one generation of selection in Rio Grande, Marion, and Kansas strains of channel catfish were reported to improve body weight of catfish by 17%, 18%, and 12%, respectively (Dunham and Smitherman 1983a, 1983b), suggesting the importance of strain effects in selective breeding programmes. After three generations of selection, growth rate of channel catfish was improved by 20–30% when grown in ponds (Rezk 1993) and four generations of selection in Kansas strain resulted in a 55% improvement in growth rate (Padi 1995). The selective breeding research made a larger impact in the 1990s through the mid-2000s by commercial farms taking the results and applying them to their own brood stock rather than through release of improved germplasm from research institutions (USDA 2003; Steeby and Wagner 2006; Dunham and Perera 2014). Improved selected lines were developed. Some farmers have employed their own crossbreeding programs to enhance performance or to avoid inbreeding. By 2005, 70% of the catfish industry was utilizing selected fish that were a result of Auburn research or were developed following the program demonstrated by Auburn (Dunham and Perera 2014).

Intraspecific crossbreeding is the mating of unrelated individuals of the same species (Dunham 2011). Dunham and Smitherman (1985) reported the effects of crossbreeding between the two channel catfish strains to increase their growth and reproductive performance. The goal of crossbreeding and hybridization is to produce progeny that performs better than the existing parents. The two selection programs in crossbreeding and hybridization with little genetic issues are recurrent selection (which is selection of purebred parental line based on its performance) and reciprocal recurrent selection (which is selection of parents based on the hybrid progeny performance) (Bosworth and Waldbieser 2014).

Another genetic enhancement program with the goal of producing heterosis is interspecific hybridization. Hybrids between the seven-major species of North American catfish (*Ictalurids*) were first evaluated in 1966 (Giudice 1966; Dupree and Green 1969; Chappell 1979; Dunham and Smitherman 1984; Masser and Dunham 2012). Giudice (1966) indicated that the cross between channel catfish female and blue catfish male showed increased growth and production compared to channel catfish. This hybrid has shown superior characteristics (heterosis) for many traits such as faster growth 20 - 100% (Giudice 1966; Dunham et al. 1987, 1990; Dunham and Brummet 1999; Argue et al. 2003; Brown et al. 2011), especially at high densities, 15-20% better feed conversion (Yant et al. 1976; Li et al. 2004), 50- 100% higher tolerance to low oxygen levels (Dunham and Smitherman 1984), increased resistance to many common diseases, especially bacterial (Ella 1984; Wolters et al. 1996; Dunham et al. 2008; Arias et al. 2012), higher dress-out percentage (Yant 1975; Bosworth et al. 2004; Bosworth 2012) and increased harvestability by seining (Dunham and Argue 1998) and vulnerability to angling (Tave et al. 1981; Dunham et al. 1986).

Combining Ability: Concepts and Principles

Combining ability is defined as the estimation of the genetic value of the parents/cross on based on the performance of their progeny in some definite mating design (Allard 1960). Since this is measured by progeny testing it can be used in reciprocal recurrent selection. This concept was introduced in 1942, and was originally developed and applied in corn breeding (Sprague and Tatum 1942). This has also been widely adopted in plant breeding to determine genetic components influencing agronomic traits. Combining ability has also been adopted in aquaculture species like hybrid striped bass (*Morone chrysops* × *Morone saxatilis*) (Wang et al. 2006), sea bass (*Dicentrarchus labrax* L.) (Saillant et al. 2006), common carp (Vandeputte et al. 2004; Su et al. 2013), blunt snout bream, *Megalobrama amblycephala* (Luo et al. 2014), channel catfish (Wolters and Johnson 1995), hybrid catfish (Bosworth and Waldbieser 2014; Drescher 2017) and tilapia (Lutz et al. 2016).

There are two types of combining ability. The first is the general combining ability (GCA) which measures the additive genetic effects of the parent. This is simply the breeding value of a parent. The second is the specific combining ability (SCA), which measures the dominance genetic effect of the cross. This is the genetic value of a cross. Sprague and Tatum (1942) defined GCA as the average performance of an individual parent in a series of hybrid combinations. They defined SCA as those cases in which certain hybrid combinations perform better or poorer than would be expected on the basis of the average performance of the parental inbred lines. Parents showing a high average combining ability in crosses are considered to have good GCA, while if their potential to combine well is bounded to a particular cross, they are considered to have good SCA.

From a statistical point of view, the GCA is a main effect and the SCA is an interaction effect (Kulembeka et al. 2012). Based on Sprague and Tatum (1942), GCA is the activity of genes which are largely additive in their effects as well as additive \times additive interactions (Griffing 1956). Specific combining ability is regarded as an indication of loci with dominance variance (non-additive effects) and all the three types of epistatic interaction components if epistasis were present. They include additive \times dominance and dominance \times dominance interactions.

The concept of GCA has been effectively used in crop and livestock breeding for more than 70 years (Sprague and Tatum 1942; Shikano et al. 2000; Adebambo 2011; Wang et al. 2014). This is an effective tool used in selection of elite parents based on the performance of their progenies, usually the F1 but it has also been used in F2 and later generations (Fn) (Fasahat et al. 2016). A low GCA value, positive or negative, shows that the mean of a parent in crossing with the other does not vary largely from the population mean. In contrast, a high GCA value shows that the parental mean is superior or inferior to the population mean. This indicates a potent evidence of desirable gene flow from parents to offspring at high intensity and represents information regarding the concentration of predominantly additive genes (Franco et al. 2001). A high GCA estimate indicates higher heritability and less environmental effects. It may also result in less gene interactions and higher achievement in selection (Topal et al. 2004; Chigeza et al. 2014). One of the main features of the elite parent with high GCA effect is its large adaptability. A parent good in per se performance may not necessarily produce better hybrids when used in hybridization (Allard 1960; Shukla and Pandey 2008). One parent of the worst combination could make the best combination if the other parent was selected properly (Bao et al. 2009).

The impact of SCA is decreased when genetically broad testers or increased number of testers are used in a mating design (Hallauer and Miranda 1988). Selection of parents based only on the SCA effect have limited value in breeding programs. Therefore, SCA effect should be used in combination with a high performing hybrid, favorable SCA estimates, and involving at least one parent with high GCA estimates (Franco et al. 2001; Joshi et al. 2004; Makanda et al. 2010).

The varying patterns of performance of crosses based on SCA have also revealed the gene actions involved in the expression of the traits. High SCA effects resulting from crosses where both parents have good GCA estimates may be ascribed to additive \times additive gene action (Dey et al. 2014). The high SCA effects derived from crosses of parents with good \times poor GCA estimates (Milić et al. 2011; Dey et al. 2014) may be attributed to favorable additive effects of the parent with good GCA and epistatic effects of parent with poor GCA. High SCA effects manifested by both parents having poor \times poor GCA (Dey et al. 2014) may be due to dominance \times dominance type of non-allelic gene interaction producing over dominance. Predominance of non-additive effects has been reported for inheritance of pod yield and related traits in groundnut under salinity stress in which there were cross combinations with high SCA effects arising from parents with high and low GCA, and another set of crosses with high SCA effects arising from both parents with good GCA effects (Azad et al. 2014).

Among the three commonly used mating designs/techniques (diallel, line \times tester, and North Carolina design) for estimation of combining ability, the North Carolina (NC II) designs proposed by Comstock and Robinson (1952), which is defined as a class of factorial mating designs or schemes where certain groups of parents are designated male (factor 1) and others female (factor 2) in crosses could be the most appropriate technique for estimating GCAs in hybrid catfish since

the parents are interspecific. Hence, the GCA of individual maternal and paternal parent should be estimated. Hallauer (2007) suggested the NC II as a preferable design, which can make use of a larger number of parents resulting in a fewer crosses generated than a diallel mating design. The NC II mating design is a factorial experiment that measures the variance of male and female main effects and male \times female interaction effects (Comstock and Robinson 1952). According to Hallauer & Miranda (1988), male and female main effects, and the male \times female interaction effects in a NC II mating design are equivalent to the GCA and the SCA effects in a diallel. The main difference between a diallel and NC II is that there are two independent estimates for the GCA effects in the NC II, which is an advantage of the NC II over the diallel. Two independent estimates of GCA allow determination of maternal effects and calculation of heritability based on male variance, which is free from maternal effects. Another advantage is that the NC II can handle more parents and produce fewer crosses than the diallel. This is achieved by dividing parents into sets as described by Hallauer and Miranda (1988). Because fish species exhibit reproduction singularities especially, high fecundity, easy in vitro fertilization in many species, NC II is an efficient mating design can be used for inference of genetic parameters. In fact, this design has been applied in fish species (Dupont-Nivet et al. 2002; Dupont-Nivet et al. 2006; Bosworth and Waldbieser 2014), hybrid striped bass (Wang et al. 2006), sea bass, *Dicentrarchus labrax L.* (Saillant et al. 2006), and carp (Vandeputte et al. 2004). This design has also been used to increase effective number of breeders in fish hatcheries (Busack and Knudsen 2007). Since catfish have high fecundity and have external fertilization which allows access and handling of gametes from male and female parents, the use of NC II mating design to estimate additive (GCA) and dominance (SCA) genetic effects is possible.

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CHAPTER TWO

Introduction

Catfish has been the leading aquaculture commodity in the US for 3-4 decades. However, in the past years few years, US catfish production has suffered decline because of increased production costs and failure to compete with imported cheap catfish, resulting in a significant decrease in the number of catfish farms and US catfish sales (USDA 2013).

The hybrid catfish from crossing the channel catfish female and blue catfish male (C×B) can help address the problems of the ailing catfish industry. The hybrid catfish is preferred for its faster growth (Giudice 1966; Yant et al. 1976; Dunham et al. 1987, 1990, 2008; Dunham and Brummett 1999; Argue et al. 2003; Li et al. 2004; Brown et al. 2011), better FCR (Yant et al. 1976; Li et al. 2004), tolerance to low dissolved oxygen (Dunham et al. 1983), increased bacterial disease resistance diseases (Ella 1984; Wolters et al. 1996; Dunham et al. 2008; Arias et al. 2012), uniformity in size and shape (Yant et al. 1976; Dunham et al. 1982; Brooks et al. 1982a, 1982b), high dressout percentage and fillet yield (Yant 1975; Chappell 1979; Huang et al. 1994; Argue et al. 2003; Bosworth et al. 2004; Bosworth 2012), increased harvestability (Yant et al. 1976; Chappell 1979; Dunham and Argue 1998), and angling vulnerability (Tave et al. 1981; Dunham et al. 1986).

Currently, approximately 70% of catfish production and processing is hybrid catfish in the US catfish industry (Nagaraj Chatakondi, USDA-ARS, personal communication). However,

the performance of hybrid catfish varies due to parental strain and individual genetic effects (Dunham et al. 1987; Bosworth et al. 1998; Bosworth et al. 2004; Dunham et al. 2014a, 2014b).

Currently, a small number of catfish hatcheries produce most of the hybrid fingerlings, which are sold to numerous independent grow-out catfish farmers (Bosworth and Waldbieser, 2014). The hybrid catfish is not a panacea, and the early performance of the F1 C×B hybrid catfish during the fry and fingerling stage can be affected by infectious diseases and parasites (Silverstein et al. 2008; Beecham et al. 2011; Griffin et al. 2014). The early growth of the F1 C×B hybrid fingerlings has production implications. The ultimate goal is to grow fry to fingerlings and fingerlings to food fish as quickly as possible, preferably within a year for a single-batch cropping. Tucker and Robinson (1990) suggested that the optimum fingerling size for single-batch cropping in the case of channel catfish is a 30-40 g per fish. Pomerleau and Engle (2005) reported that stocking larger fingerlings significantly ($P < 0.05$) increased the total yield, net yield, final weight, final length and FCR of catfish. Larger fingerlings grow faster to market-size. However, these fingerlings are more expensive as they require more space and time to produce. Hence, production of an F1 C×B hybrid catfish fingerling with a desirable early growth performance traits would be an important goal for selective breeding programs.

Reciprocal recurrent selection which is the selection of purebred parents based on the hybrid progeny performance offers great promise to genetically improve the desirable traits of hybrid catfish. To achieve this purpose, information about the combining ability of the parents and their performance in hybrid combination is a prerequisite to develop the most efficient and effective breeding plans (Salem and Ali 2012). Griffing (1956) proposed the partition of the total genetic variation into general combining ability (GCA) of the parents and specific combining ability (SCA) of the crosses. Sprague and Tatum (1942) defined GCA as the average

performance of the parental lines in hybrid combinations while SCA as the performance of a combination of parents in a specific cross. The estimation of GCA and SCA has been widely used for developing the corn breeding program and has been applied to various breeding programs for plants and animals including fish (Wolters and Johnson 1995; Vandeputte et al. 2004; Saillant et al. 2006; Wang et al. 2006; Lutz et al. 2010; Su et al. 2013a; Bosworth and Waldbieser 2014; Luo et al. 2014; Drescher 2017).

However, there are very few analyses of GCA and SCA for economic traits of catfish such as growth and carcass yield of market size F1 hybrid catfish (Bosworth and Waldbieser 2014), oxygen tolerance (Drescher 2017) and resistance to enteric septicemia in channel catfish (Wolters and Johnson 1995).

Bosworth and Waldbieser (2014) reported that GCA of the parental dam was more important in controlling the carcass yield and harvest weight of F1 hybrids. Similarly, GCA was also found important in the expression of traits pertaining to the tolerance of hybrid catfish to low dissolved oxygen (Drescher 2017) and resistance to enteric septicemia in Norris and Marion x Kansas strains of channel catfish (Wolters and Johnson 1995). These results suggest the potential of combining ability estimation for selection to improve the desired traits of catfish.

Combining ability estimation is considered useful indirect criterion for selecting elite parents. With this, general and specific combining abilities are important indicators for expressing the potential value of catfish parents that can produce consistently better performing F1 hybrid catfish. The GCA and SCA variances provide estimation for additive and non-additive gene action, respectively (Falconer 1989). The exploration and estimation of such gene actions can be used to select for elite parent lines and produce improved F1 hybrid catfish.

Although, the channel blue hybrid catfish is genetically superior to the parent species, it could be further improved for growth rate, disease resistance and dressout percentage. Additionally, a recent industry problem is variable growth by hybrids and a partial solution to that problem could be from genetic selection. To determine the potential for genetically improving these traits for hybrid catfish, the combining abilities of the parent species must be estimated. No research has been conducted yet to determine and estimate the combining abilities for early performance traits of F1 hybrid catfish. In the current study, the GCA and SCA effects of parental channel catfish and blue catfish to the performance of their F1 hybrid progeny was estimated following NC II factorial mating design of Hallauer (2007).

The objectives of this research were to estimate the GCA and SCA for the early performance traits of channel catfish female x blue catfish male F1 hybrid progeny such as: a) body weight, and body weight gain; b) coefficient of variation in body weight; c) resistance to *Aeromonas hydrophila*, and; d) dressout percentage. Additionally, the individual combining abilities of the parents were determined. The genetic variance components for early performance traits of hybrids during an initial 311 days of tank rearing in a flow-through system, and after an additional 245 days of tank rearing in a recirculating system and communal rearing in split-pond were determined. The best parental genotypes with high GCA and best parental cross with high SCA that produce superior performing hybrid catfish were identified. This research will be beneficial to improving the selection and breeding programs for hybrid catfish production.

Materials and Methods

Experimental fish

Twenty females from nine strains of channel catfish were crossed with twelve males from four strains of blue catfish to produce F1 C×B hybrid catfish progeny. The nine strains of female channel catfish were Tishomingo, AR, Kansas Select, Kansas Random, ARMK, Kansas × Thompson, Rio Grande, Thompson, and mixed strains. The four strains of male blue catfish were D&B, Rio Grande, D&B × Rio Grande, and Tombigbee. These fish were maintained at the Fish Genetics Unit, E.W. Shell Fisheries Research Center, Auburn University, Alabama. All procedures involving the handling and treatment of fish in this study were approved by the Auburn University Institutional Animal Care and Use Committee (AU-IACUC).

The twenty channel catfish females (dams) were from nine strains. The strains used included Kansas Random which originated from Ninnescah River in 1911, and is the oldest domestic strain of channel catfish (Dunham and Smitherman 1984). This strain was randomly bred and has the traits increased resistance to disease, rapid growth, and late sexual maturity. Kansas Select, a line derived from Kansas random that has been selected for body weight for eight generations. AR line which was derived from the crossbreeding of Auburn and Rio Grande strains followed by 6 generations of mass selection for body weight. Traits of this line include spawning late in the season. ARMK, was initiated by producing a 4-way crossbreed (Auburn X Rio Grande) X (Marion X Kansas) followed by 6 generations of mass selection, these fish are also late spawners. Thompson strain originated from the Yazoo River, MS, and on-farm selection was conducted for several traits including body size, disease resistance, and early spawning. Tishomingo strain originated from the Tishomingo federal hatchery in Oklahoma. Kansas X Thompson was a F1 crossbreed between Kansas random females and Thompson males. Rio

Grande a single surviving wild female of a collection of 50 fish from the Rio Grande River, Texas. Traits of individuals of this strain collected 40 years ago included high dress out percentage, susceptibility to disease, slow growth, large sexual dimorphism for body weight, high fecundity, small egg size, and maturity at two years of age. Mix strain was initiated by the mixing of multiple strains.

The twelve blue catfish males (sires) were from four strains. These included: Tombigbee (TBB), which originated from the Tombigbee River. Rio Grande was from the Rio Grande River in Texas, and has distinctive spots on the entire body. D&B originating from D&B Fish Farms in Crockett, TX and, were selected for small head size (Dunham and Smitherman 1984). D×R was an F1 crossbreed between D&B females and Rio Grande males.

Matings

Twenty channel catfish females were crossed with twelve blue catfish males following a complete factorial mating design in May 2015. Maternal half-sib, paternal half-sib, and full-sib families of F1 C×B hybrid catfish progeny were produced. However, due to poor survival of some crosses, 40 families were obtained resulting in an unbalanced design (Fig. 2.1).

Spawning procedures

Sexually mature male blue catfish with large muscular heads were selected and sacrificed by cranial percussion. The testes were surgically excised and macerated in 0.9% salt solution to produce sperm suspensions. The suspensions were stored in plastic tubes and refrigerated.

		Blue Catfish Male (Sire)												
		1	2	3	4	5	6	7	8	9	10	11	12	
Channel Catfish Female (Dam)	1													
	2													
	3													
	4													
	5													
	6													
	7													
	8													
	9													
	10													
	11													
	12													
	13													
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	15													
	16													
	17													
	18													
	19													
	20													

Figure 2. 1 Lay-out of factorial mating design used to cross twenty channel catfish (*I. punctatus*) females with twelve blue catfish (*I. furcatus*) males. The 40 hybrid families obtained are highlighted with red.

The females with the classic signs of readiness for spawning, including a soft, distended belly and a genital opening that is red and swollen (Dunham and Masser 2012; Su et al. 2013b) were selected for hormone induced ovulation. These females were injected with luteinizing hormone analog (LHRHa) at 100 µg/kg via intraperitoneal implants and were placed in spawning bags (the same as ¼-inch mesh laundry bags) suspended in holding vats with flow-through water and aeration. The dissolved oxygen was maintained above 5 mg/L and the water temperature at 26-30°C. The females were checked for ovulation (presence of eggs released and sticking in their bags) about 36-72 hours after hormone injection. Females that had ovulated were anesthetized with 150 parts per million (ppm) of buffered 100ppm tricaine methane sulfonate (MS-222),

rinsed with hatchery water, and dried with towel. Through application of abdominal pressure, the eggs were hand stripped and placed into a stainless pan coated with vegetable oil to prevent the eggs from sticking to the pan. Eggs from each female were divided equally into aliquots based on the number of males for the factorial mating design and placed in a pan coated with vegetable oil. Sperm solution from each male was mixed with each aliquot of eggs. Hatchery water was then added to activate the fertilization. The fertilized egg masses were moved to a trough to allow them to water harden for 15-20 minutes. After this, the eggs were moved to another trough with egg baskets and fry catchers. Fry catchers made of fine mesh nylon netting were used to prevent the newly hatched fry from escaping outside the basket.

Fish husbandry

After the eggs hatched, 210 fry from each family were stocked in three replicate 60cm x 30cm x 50cm glass aquaria at a stocking density of 70 fry per aquarium with flow-through water and aeration. The water quality parameters were maintained at flow rate of 4 L/minute, water temperature at 26 – 28°C and dissolved oxygen at >5 mg/L with the use of air diffusers. Each aquarium was labeled with the family information. The fry were initially fed the Purina® AquaMax® powdered starter diet containing 50% protein until they reached 2.5cm in size. From 2.5-3.8 cm the fish were fed Purina® AquaMax® 100 diet containing 50% protein, from 3.8-5 cm they were fed Purina® AquaMax® 200 containing 50% protein, and from 5-7.6 cm Purina® AquaMax® 300 containing 50% protein. Fish were fed *ad libitum* daily. After 311 days of separate tank rearing in flow-through system, all fish were injected individually with a PIT tag (model MiniHPT8, 8.4mm, 132.2 kHz ISO FDX-B; Biomark, Boise, Idaho) into the mid-section of the abdomen.

For the next 245 days of rearing, 50% of the fish from each family were stocked and reared in a communal split-pond system with total area of 526 square-meter, depth of 1.5 meter, and volume of 789 cubic-meter. The remaining 50% of the fish from each family were kept in their original separate aquaria tank. The flow-through aquaria system was then converted into a recirculating aquaria system to allow additional 245 days rearing of fish in separate tanks. The fish in separate tanks were fed with Purina® AquaMax® 300 containing 50% protein while the fish in communal split-pond were fed *ad libitum* with 32% protein floating catfish pellets from Alabama Catfish Feedmill, LLC for 245 days.

Dissolved oxygen, ammonia, nitrite, pH, hardness, alkalinity and temperature were monitored and recorded throughout the two phases of the experiment period. Water quality parameters were maintained at their optimum levels, whereas, DO was >5mg/L, ammonia was <1 mg/L, nitrite was <0.05 mg/L, pH was between 6 and 7, hardness was between 40 and 70 mg/L, alkalinity was between 40 and 80 mg/L.

Natural infection from Aeromonas hydrophila

A natural *Aeromonas hydrophila* infection occurred during the second month of the initial 311-day rearing in the flow-through system, and lasted for 20 days. During that infection period, mortality was observed across the hybrid families. The causative agent for this infection was confirmed to be the non-virulent strain (AL-01) of the *Aeromonas hydrophila* following PCR analysis of the putative *Aeromonas* isolates obtained from the moribund fish samples.

Data gathering and analyses

After 311 days of separate tank rearing in flow-through system, data pertaining to early growth in terms of final body weight and body weight gain, coefficient of variation in size in

terms of body weight, and survival from *A. hydrophila* natural infection were gathered and recorded. After 245 days of additional tank rearing in the recirculating system and the communal split-pond rearing, body weight, weight gain, and dressout percentage in the communal split-pond system were measured. All data were analyzed to estimate the general and specific combining ability for the early performance traits of the hybrids in three different intensive rearing systems.

The following formulas were used to calculate the performance traits:

- a) Weight Gain (GW) = Final body weight (W_f) – initial body weight (W_i);
- b) Specific Growth Rate (SGR) = $[(\ln W_f - \ln W_i) / \text{no. of days}] \times 100$
- c) Coefficient of Variation (CV) = (Standard deviation of W_f / mean W_f) x 100

(Note: The calculation of the CV in size was only possible for hybrid catfish families that were reared in separate tanks which served as replicate units in the flow-through and recirculating system and not for those hybrids reared in only one communal split-pond.)

- d) Survival (%) = (Number of surviving fish / initial number of fish) x 100
- e) Actual dressout percentage ($DrO_A\%$) = (Dressout weight/Body weight) x 100
- f) Corrected dressout percentage ($DrO_C\%$) = $DrO_A\% - [(body\ weight - mean\ weight\ per\ family) \times b\text{-value between } DrO_A\% \text{ and body weight based on sex per family}]$

(Note: The *b*-value mentioned above was calculated using LINEST function in Microsoft Excel 2016).

In this study, the dressout weight is the weight of the gutted fish without the head, fins, and tail. The early dressout percentage of the F1 C×B hybrid catfish was corrected for the effects of gender and family variability. Patterns of sexually dimorphic growth and carcass yield have

been reported for hybrid catfish (Argue et al. 2003; Bosworth 2012), and channel catfish and blue catfish (Argue et al. 2003; Bosworth et al. 2004). The calculation of the *b*-value was done following the syntax for LINEST function in Microsoft Excel below:

$$b\text{-value} = \text{LINEST} (y_values, x_values)$$

Where, *y*_values is the dressout percentages of hybrids based on sex per family, *x*_values is the body weight of hybrids based on sex per family.

The statistical model I used as a genetic relationship matrix for the analysis of the early performance traits is stated below as suggested by Becker (1984) for factorial mating designs:

$$Y_{ijk} = \mu + S_i + D_j + (S \times D)_{ij} + e_{ijk}$$

Where, Y_{ijk} is the trait value for the m^{th} hybrid progeny, μ is the overall mean, S_i is the random effect of the i^{th} sire, D_j is the random effect of the j^{th} dam, $(S \times D)_{ij}$ is the random effect of the cross between the i^{th} sire and j^{th} dam, and e_{ijk} is the random error.

The variance components are stated below following the genetic model II of Becker (1984):

$$\sigma^2_S = \text{COV}_{\text{hs}(S)}$$

$$\sigma^2_D = \text{COV}_{\text{hs}(D)}$$

$$\sigma^2_{SD} = \text{COV}_{\text{fs}} - (\text{COV}_{\text{hs}(S)} + \text{COV}_{\text{hs}(D)})$$

$$\sigma^2_e = \sigma^2_T - \text{COV}_{\text{fs}}$$

Where, the variance components of sire (σ^2_S) and dam (σ^2_D) are equal to the covariance of half sibs (hs) of the sire groups and dam groups, respectively. The dam component also contains the maternal effect. The component for the cross (σ^2_{SD}) is the covariance of the full sibs (fs) minus the sum of the half sibs covariance from dams and sires. The variance for random error (σ^2_e) contains the remainder of the genetic variance and environmental variance.

Given that this experiment had unbalanced data with missing values for some crosses, the Restricted Estimation of Maximum Likelihood (REML) was used as the standard procedure to estimate the genetic variance components for random effects of sire, dam, and cross and the associated variance-covariance matrix. The missing data were assumed to be random. The Best Linear Unbiased Predictors (BLUP) of individual sires, dams, and cross, and their standard errors were generated with Mixed Procedure of SAS (version 9.4, SAS, Cary, NC) to determine estimates of GCAs of sires, dams, and SCAs of crosses. All analyses were made at $P=0.05$.

The factorial mating design is an experiment that measures the variance of the male and female effects and the male x female interaction effects (Comstock and Robinson 1948). To evaluate the relative importance of the GCA and SCA effects, either of these effects must be significant ($P<0.05$). If both the GCA and SCA effects are not significant, then epistatic gene effects are responsible for the expression of the traits (Fehr 1993). According to Hallauer and Miranda (1988), male and female effects are equivalent to GCA effects for sire and dam, respectively, whereas, the male x female interaction effects are equivalent to SCA effects. For an unbalanced factorial mating design, the significance of these effects can be determined with the mean squares generated in the Type 3 Mixed Procedure of analyses of variance.

The estimate of combining ability using factorial mating design (NC II) determines the additive and non-additive components of genetic variance which are appropriate selection methods for selecting parents for efficient hybridization programs that can improve economically important quantitative characteristics. In this mating design, the GCA variances for sires and dams are equivalent to the sire and dam additive genetic variances, respectively; and the SCA variance is equivalent to the cross' dominant genetic variance (Cotterill et al. 1986). The highest

variance component was considered the most important genetic effect as it determines the type of gene action involved in the control and expression of the traits.

When the values of GCA and SCA variances are relatively close, the method of Longin et al. (2013) can be used to determine the importance of the SCA. Whereas, if $\frac{\sigma^2_{SCA}}{\sigma^2_{GCA_{dam}} + \sigma^2_{GCA_{sire}}} < 0.5$, the impact of SCA can be ignored.

Parents and/or cross from the more important genetic variance component were selected as best combiners based on their GCA and/or SCA estimates. The value of GCA or SCA estimates predicts the phenotypic deviation of the progeny to the overall population mean phenotype, whereas, the highest positive or negative estimates of GCAs or SCAs will most likely give the best or the worst performance traits. The strains of pooled parental sires, dams, or crosses from the more important genetic variance component were subjected to one-way analysis of variance using the GLM Procedure followed by Tukey-Kramer Test to compare their performance means. The Tukey-Kramer procedure has fared extremely well in Monte Carlo studies (Dunnett 1980). It is the modified version of Tukey's "Honestly Significant Difference Test (HSD)" that can be used for unequal sample sizes. Hayter (1989) describe Tukey-Kramer as a more powerful method than the Bonferroni, Sidak or Scheffé for pairwise comparison. The Scheffé Test is more flexible compared to the Tukey's HSD and can be also used for unequal sample size (Scheffé 1999). However, it has a low statistical power. This was only used as 2nd option next to Tukey-Kramer in this study to compare all possible pairs of means. The Scheffé Test was done for mean comparison with no significant difference result after Tukey-Kramer. Parental genotypes with best performance traits would be considered for selection.

RESULTS

Early Growth Performance Traits

The population means and phenotypic standard deviations for the early growth performance traits of the 40 hybrid catfish families in three different intensive rearing systems at two ages are presented in Table 2.1.

Table 2. 1 The population means and phenotypic standard deviations (SD) for final body weight (Wt) and body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing, recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing.

Rearing System	Age (days)	Trait	Population mean	Phenotypic SD
Flow-through system (initial 311-day separate tank rearing)	311	Final Body Wt (g)	9.74 g	3.19
Recirculating system (additional 245-day separate tank rearing)	556	Final Body Wt (g)	91.25 g	36.21
		Body Wt Gain (g)	80.26 g	33.26
Split-pond (additional 245-day communal rearing)	556	Final Body Wt (g)	194.21 g	94.07
		Body Wt Gain (g)	184.21 g	92.12

The early growth performance in terms of final average body weight and body weight gain were analyzed following REML/BLUP joint analyses based on the genetic relationship matrix to calculate the mean squares from the analyses of variance (Table 2.2), the variance components (Table 2.3) and the variance components ratio (Fig. 2.2, 2.5) and estimates for GCAs of sire and dam and/or SCAs of crosses (Fig. 2.3, 2.6, 2.7, 2.9, 2.10, 2.11). The mean comparison of parental strains after analyses of variance through GLM Procedure using Tukey-Kramer Test are presented in Figures 2.4 and 2.8.

Table 2. 2 Mean squares (MS) for the Type 3 Mixed Procedure analyses of variance of the factorial mating design component of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny test and error mean squares for final body weight (Wt) and body weight gain of channel catfish female × blue catfish male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing, recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing.

Rearing System	Age (days)	Trait	Source of variation			
			Dam	Sire	Dam x Sire	Error MS
Flow-through system (initial 311-day separate tank rearing)	311	d.f.	19	11	9	67
		Final Body Wt (g)	14.70 *	5.75 ^{ns}	9.32 ^{ns}	5.16
Recirculating system (additional 245-day separate tank rearing)	556	d.f.	19	11	8	677
		Final Body Wt (g)	5059.56 *	3028.11 *	908.11 ^{ns}	1064.29
		Body Wt Gain (g)	4087.45 *	2463.53 *	760.56 ^{ns}	918.06
Split-pond (additional 245-day communal rearing)	556	d.f.	18	11	7	1480
		Final Body Wt (g)	66867 *	85175 *	7699.88 ^{ns}	7315.98
		Body Wt Gain (g)	62384 *	80256 *	6579.16 ^{ns}	7054.49

After ANOVA *F*-test: * = $p < 0.05$, and ^{ns} = $p > 0.05$
d.f. = degree of freedom.

Table 2. 3 Estimates of general combining ability variance for dam ($\sigma^2\text{GCA}_d$) and sire ($\sigma^2\text{GCA}_s$) and specific combining ability variance ($\sigma^2\text{SCA}$), error variance ($\sigma^2\text{E}$) and corresponding standard errors for final body weight (Wt) and body weight gain of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing, recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing.

Rearing system	Age (days)	Trait	Genetic parameter estimates			
			$\sigma^2\text{GCA}_d (\pm \text{SE})$	$\sigma^2\text{GCA}_s (\pm \text{SE})$	$\sigma^2\text{SCA} (\pm \text{SE})$	$\sigma^2\text{E}$
Flow-through system (initial 311-day separate tank rearing)	311	Final Body Wt	3.25 (2.30)	0.91 (0.92)	0.99 (1.28)	5.13
Recirculating system (additional 245-day separate tank rearing)	556	Final Body Wt	222.83 (124.68)	85.43 (68.21)	20.7 (56.32)	1060.16
		Body Wt Gain	156.44 (99.42)	60.69 (56.34)	25.85 (54.75)	914.56
Split-pond (additional 245-day communal rearing)	556	Final Body Wt	1463.21 (587.61)	1388.25 (663.43)	0	7322.73
		Body Wt Gain	1320.19 (532.95)	1293.47 (619.75)	0	7056.66

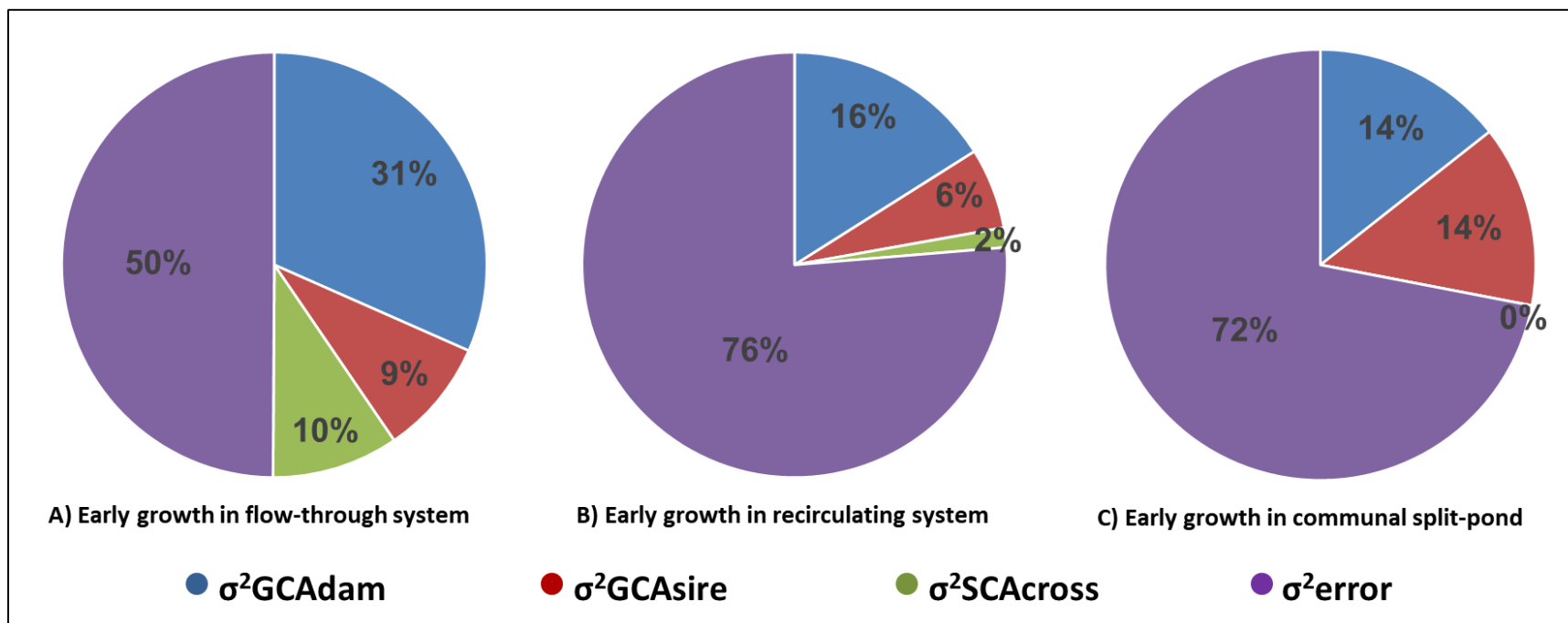


Figure 2. 2 Ratio of estimates of GCA variance components for dam and sire, SCA variance components for cross, and error variance components for early growth in terms of final body weight (Wt) of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing, recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing.

In all the three different intensive rearing systems, the mean squares of hybrid progeny showed significant differences ($P < 0.05$, Table 2.2) for early growth in terms of final body weight and body weight gain in weight, indicating significant family effects, dam effects, sire effects and sometimes interactions. After the initial 311-day separate tank rearing of the hybrids in flow-through system, the mean square of GCA effect of the dam for final body weight was significant ($P < 0.05$) indicating the importance of additive gene effects for this trait. The ratio of the combining ability variance components (Table 2.3, Fig. 2.2) also revealed that the largest component for the final body weight trait was the GCA variance for dam which is indicative of the dam effects having the most influence. The GCA effects of the dam revealed that the female parents 17 and 18 had the highest ($P < 0.05$, Fig. 2.3) positive GCA estimates, 3.52 and 2.53, respectively, for early final average body weight, indicating that their progeny would most likely have a better early growth performance traits in terms of early final body weight when reared in separate tanks in flow-through system. Furthermore, the strains of the dam for the final body weight trait were found to be significantly different ($P < 0.05$). Hybrid progeny of KxTh crossbred dams had the highest ($P < 0.05$, Fig.2.4) mean body weight (17.95 g) compared to all other dam genotypes except Thompson strain that had the second highest (11.73 g) in the flow-through system during the initial 311-day separate tank rearing. The Thompson strain hybrids were not different ($P > 0.05$) to all other dam type hybrids.

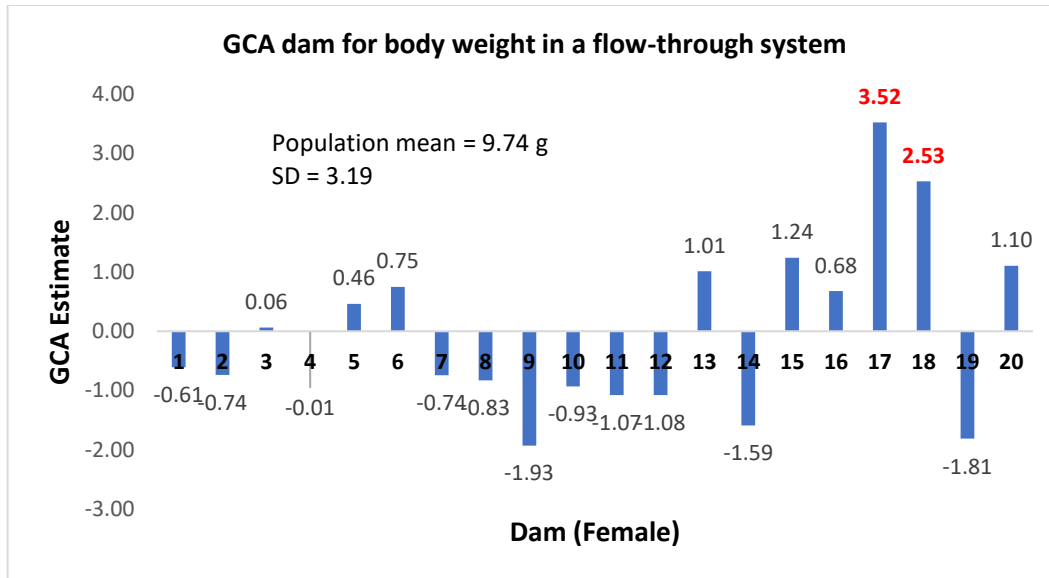


Figure 2. 3 The channel catfish (*Ictalurus punctatus*) female (dam) general combining ability estimates for final average body weight of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, *t*-test).

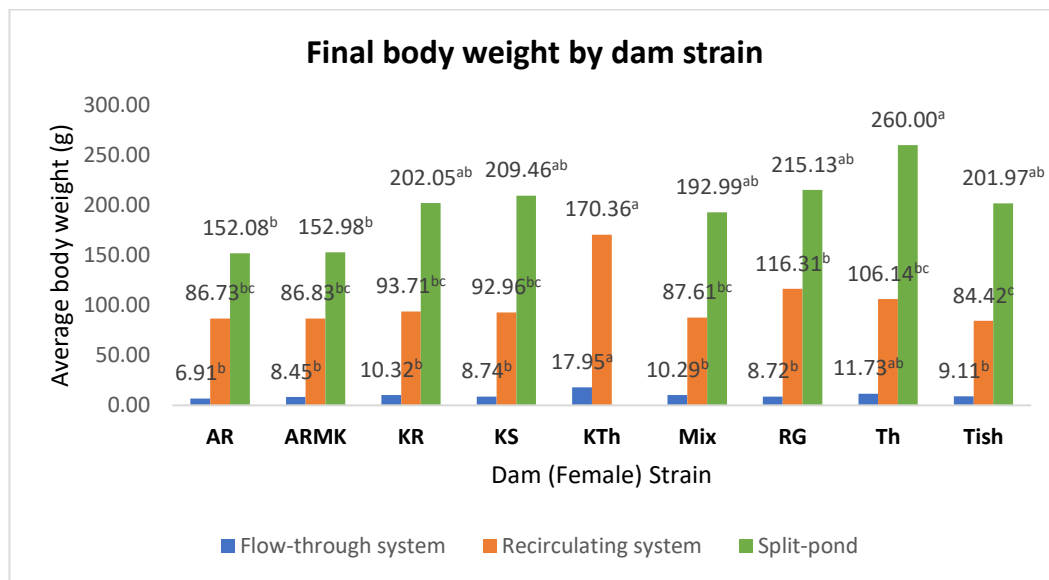


Figure 2. 4 Early growth in terms of final average body weight by parental dam strain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing, recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing. Hybrid genotypes in the same rearing system with the same superscript letter are not

significantly different ($P > 0.05$, Tukey-Kramer Test). For genetic types in the communal split-pond, the mean comparison was done following Scheffe Test.

The mean squares of the final average body weight and body weight gain for the GCA effects of dam and sire parents were significant ($P < 0.05$, Table 2.2) after the additional 245-day separate tank rearing in the recirculating system, indicating genetic variability contributed by the male and female parents. The ratio of the combining ability variance components (Table 2.3) showed that the largest component is the GCA variance for dam indicating that final average body weight (Fig. 2.2) and body weight gain (Fig. 2.5) traits were mostly controlled by the additive gene effects attributed to the dam parents. The GCA effects of the dam revealed that parent 17 gave the best ($P < 0.05$, Fig. 2.6) estimate for final average body weight at 46.51 and body weight gain at 36.04 (Fig. 2.7), which would mean that its hybrid progeny would most likely gain better performance for these two traits compared to other parental dams. The dam parent 17 is a good combiner to produce hybrid catfish with better early growth performance in recirculating system. Hybrid progeny of KxTh crossbred dams strain had the highest ($P < 0.05$, Fig. 2.4) final average body weight, 170.36 g, and highest body weight gain, 146.28 g, ($P < 0.05$, Figure 2.8) followed by the RG hybrid type for these two traits. The RG hybrid type, however, was found not significantly different ($P > 0.05$, Fig 2.4, 2.8) to all other parental dam strains for final average body weight and body weight gain.

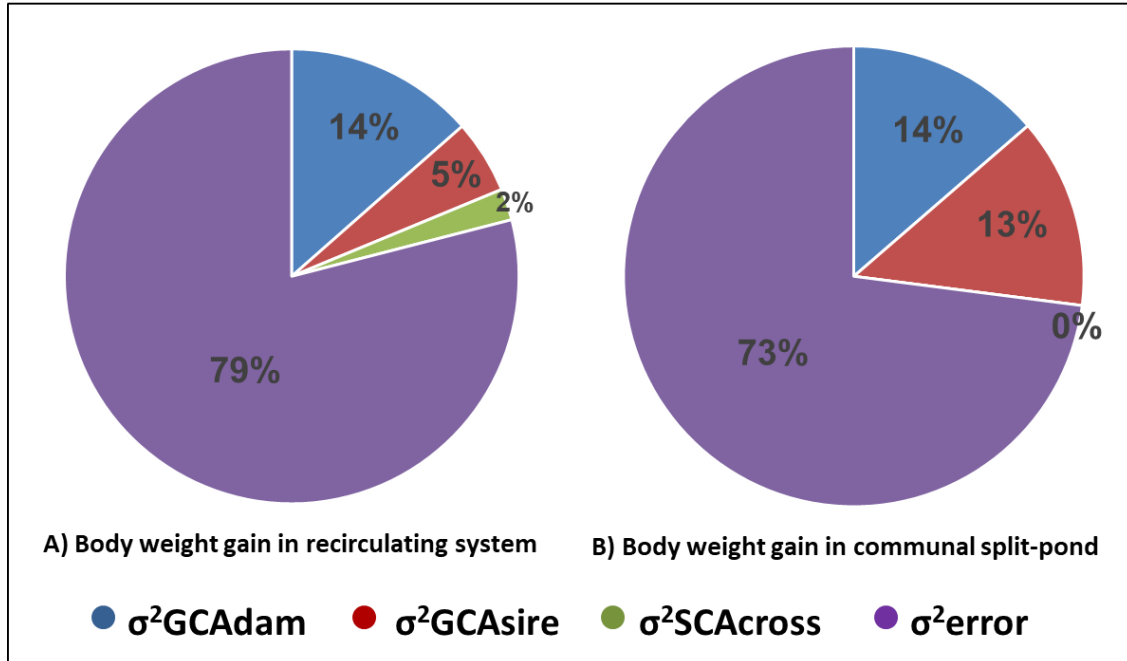


Figure 2. 5 Ratio of estimates of GCA variance components for dam and sire, SCA variance components for cross, and error variance components for body weight gain of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing.

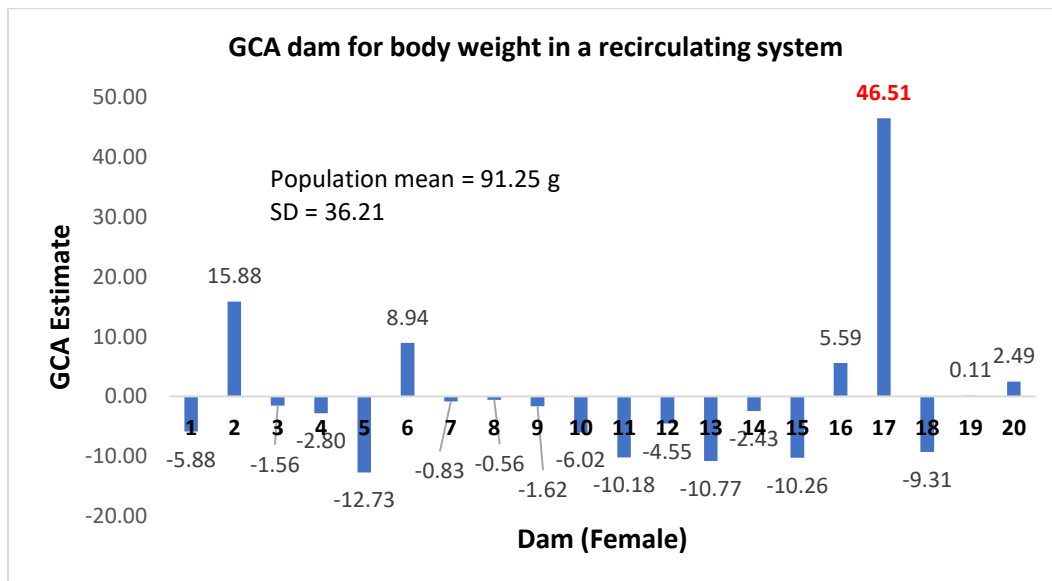


Figure 2. 6 The channel catfish (*Ictalurus punctatus*) female (dam) general combining ability estimates for final average body weight of channel catfish (*I. punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

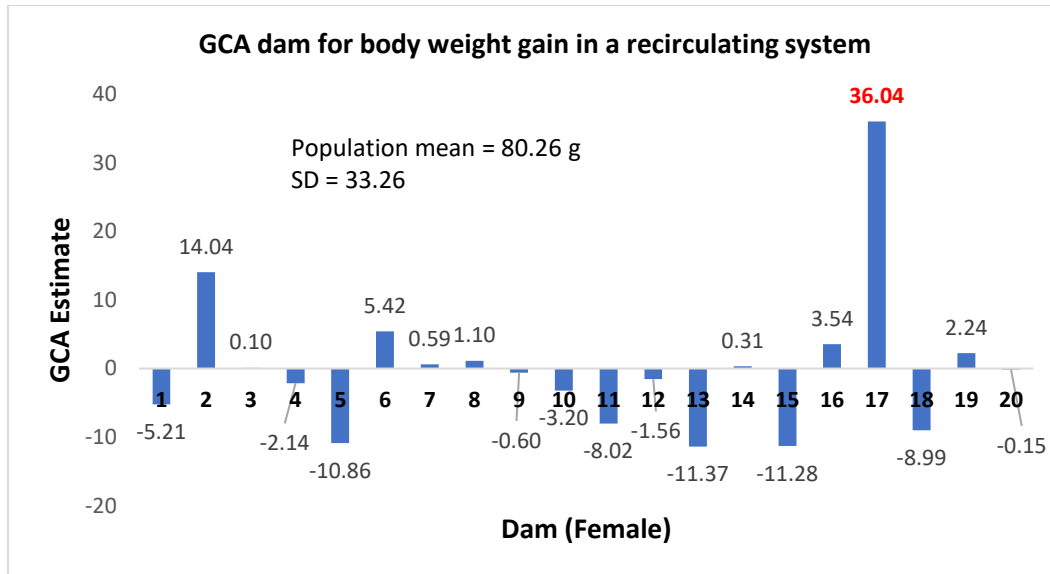


Figure 2. 7 The channel catfish (*Ictalurus punctatus*) female (dam) general combining ability estimates for body weight gain of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

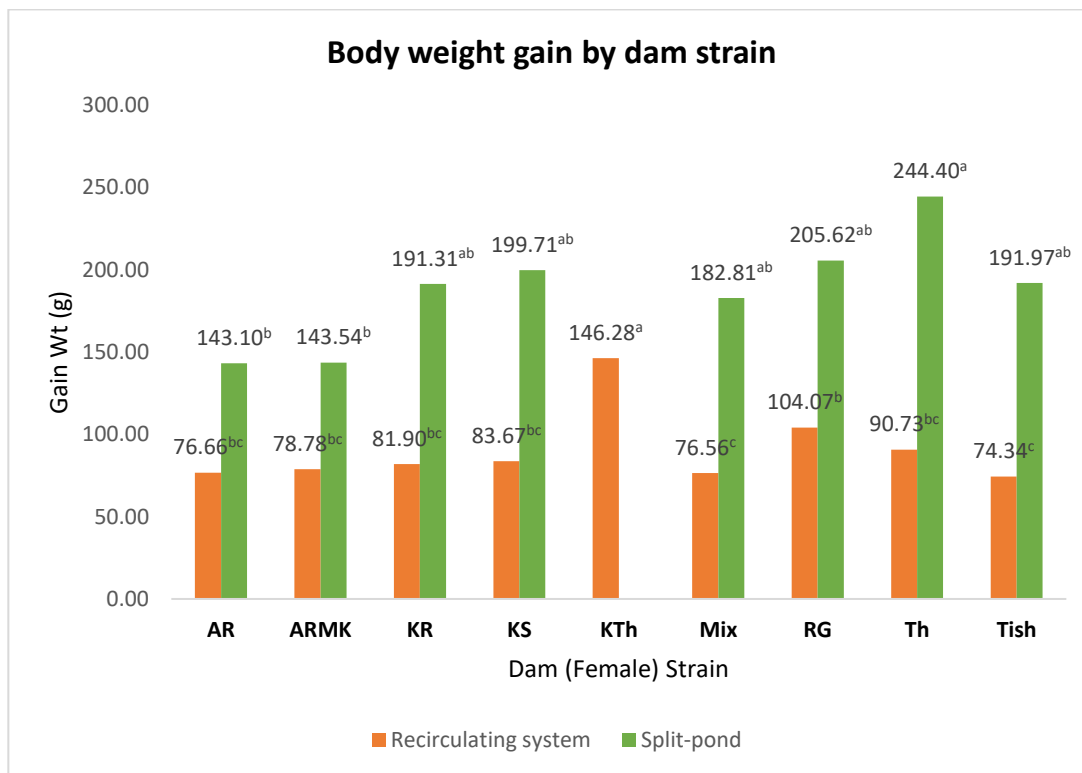


Figure 2. 8 Early growth in terms of body weight gain by parental dam strain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating

system for additional 245 days of separate tank rearing, and split-pond for additional 245 days of communal rearing. Hybrid genotypes in the recirculating system with the same superscript letter are not significantly different ($P>0.05$, Tukey-Kramer Test). For genetic types in the communal split-pond, the mean comparison was done following Scheffe Test.

The mean squares for final average body weight and body weight gain after the additional 245-day rearing of hybrid catfish in the communal split-pond were significant ($P<0.05$, Table 2.2) for the GCA effects of the male and female parents, indicating that the additive gene effects were contributed by the male and female parents. The combining ability variance components ratio (Table 2.3, Fig. 2.2, 2.5) revealed that the largest additive gene effects controlling the two traits were attributed almost equally to both the dam and sire parents. The dam parents 13, 18, and 6 had the best ($P<0.05$) positive GCA estimates for final average body weight at 60.49, 57.88, and 46.35, respectively (Fig. 2.9) and for body weight gain at 57.45, 53.53, and 43.41, respectively (Fig. 2.10). The sire parents 10 and 1 had the best ($P<0.05$) positive GCA estimates for final average body weight at 58.78 and 53.99, respectively (Fig. 2.9) and for body weight gain at 56.52 and 52.65, respectively (Fig. 2.10). The hybrid progeny of these dams and sires should have better early growth traits. Hybrids from Thompson dams had the highest observed early final average body weight (260.00 g, Fig. 2.4) and body weight gain (244.40 g, Fig. 2.8), while AR and ARMK hybrids had the lowest values. Hybrid progeny of KxTh crossbred dams strain was not included in the analyses for final average body weight and body weight gain of F1 hybrid catfish in communal split-pond because this group was not stocked in the pond. Hybrids from DR crossbred sires had the highest observed final average body weight (242.61 g, Fig. 2.11) and body weight gain (244.40 g, Fig. 2.11), followed by the RG hybrids. The TBB and DB hybrids gave the lowest final body weight and body weight gain in communal split-pond.

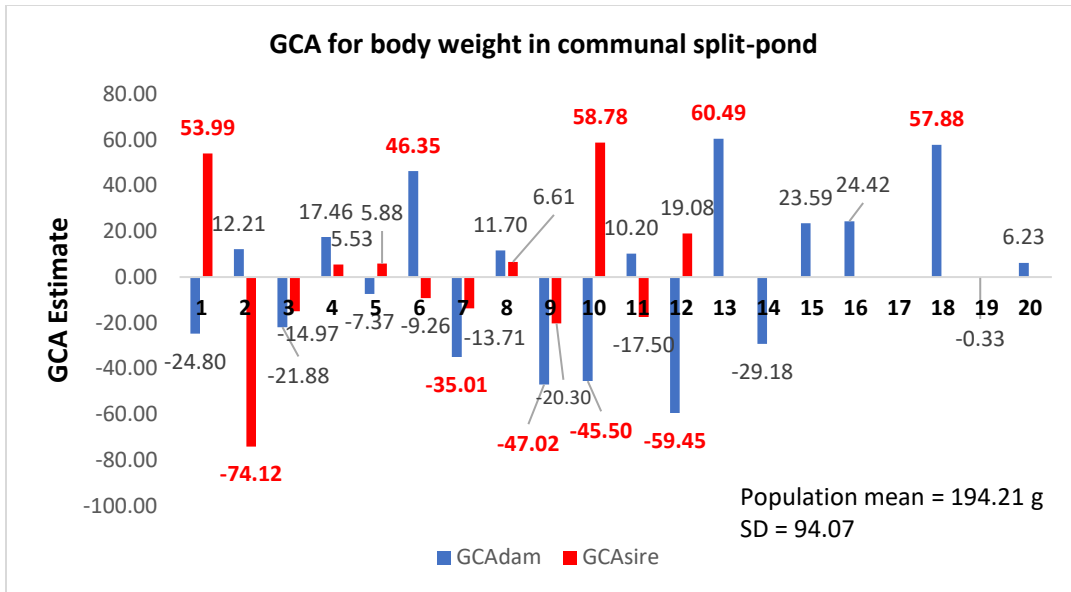


Figure 2. 9 The channel catfish (*Ictalurus punctatus*) female (dam) and blue catfish (*I. furcatus*) male (sire) general combining ability estimates for final mean body weight of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

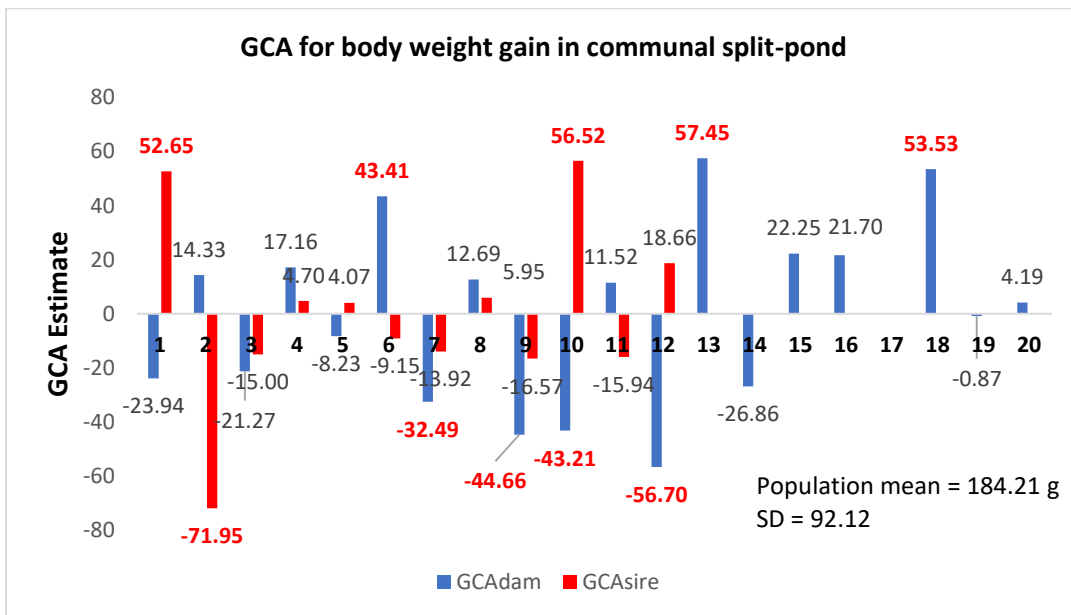


Figure 2. 10 The channel catfish (*Ictalurus punctatus*) female (dam) and blue catfish (*I. furcatus*) male (sire) general combining ability estimates for body weight gain of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

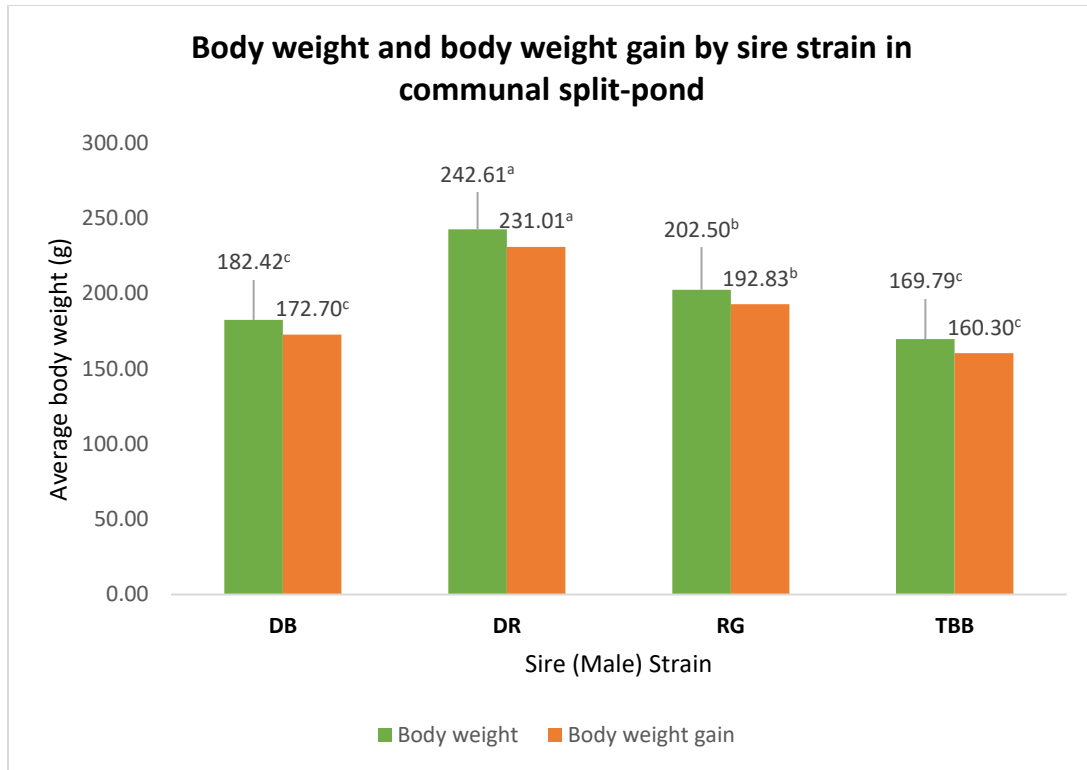


Figure 2. 11 Early growth in terms of body weight and body weight gain by parental sire strain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing. Hybrid genotypes in the same rearing system with the same superscript letter are not significantly different ($P>0.05$, Tukey-Kramer Test). For genetic types in the communal split-pond, the mean comparison was done following Scheffe Test.

Coefficient of Variation in Size

The population means and phenotypic standard deviations for CV in size in terms of body weight of the 40 hybrid catfish families reared in separate tanks in flow-through and recirculating system are shown in Table 2.4.

The coefficients of variation in body weight were analyzed following REML/BLUP joint analyses based on the genetic relationship matrix to calculate for the mean squares from the analyses of variance (Table 2.5), the variance components (Table 2.6), the variance components ratio (Fig. 2.12) and estimates for GCAs of sire and dam and/or SCAs of crosses (Figures 2.13,

2.15). The mean comparison of parental strains after analysis of variance through GLM Procedure using Tukey-Kramer Test are presented in Figures 2.14 and 2.16.

Table 2. 4 The population means and phenotypic standard deviations (SD) for coefficient of variation (CV) in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing and recirculating system for additional 245 days of separate tank rearing.

Rearing System	Age (days)	Population mean	Phenotypic SD
Flow-through system (initial 311-day separate tank rearing)	311	28.24	8.96
Recirculating system (additional 245-day separate tank rearing)	556	30.05	14.69

Table 2. 5 Mean squares (MS) for the Type 3 Mixed Procedure analyses of variance of the factorial mating design component of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny test and error mean squares for coefficient of variation (CV) in body weight of channel catfish female × blue catfish male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing and recirculating system for additional 245 days of separate tank rearing.

Rearing System	Age (days)		Source of variation			
			Dam	Sire	Dam x Sire	Error
Flow-through system (initial 311-day separate tank rearing)	311	d.f.	19	11	8	66
		MS	230.54 *	31.07 ^{ns}	34.5 ^{ns}	22.81
Recirculating system (additional 245-day separate tank rearing)	556	d.f.	19	11	7	41
		MS	401.36 *	365.56 *	380.68 *	126.04

After ANOVA *F*-test: * = $p < 0.05$, and ^{ns} = $p > 0.05$

d.f. = degree of freedom.

Table 2. 6 Estimates of general combining ability variance for dam ($\sigma^2\text{GCA}_d$) and sire ($\sigma^2\text{GCA}_s$) and specific combining ability variance ($\sigma^2\text{SCA}$), error variance (σ^2_E) and corresponding standard errors for coefficient of variation (CV) in body weight of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing and recirculating system for additional 245 days of separate tank rearing.

Rearing system	Age (days)	Genetic parameter estimates			
		$\sigma^2\text{GCA}_d$ (\pm SE)	$\sigma^2\text{GCA}_s$ (\pm SE)	$\sigma^2\text{SCA}$ (\pm SE)	σ^2_E
Flow-through system (initial 311-day separate tank rearing)	311	83.83 (31.08)	1.79 (3.35)	2.65 (4.56)	22.46
Recirculating system (additional 245-day separate tank rearing)	556	21.18 (37.27)	0	46.65 (56.74)	159.10

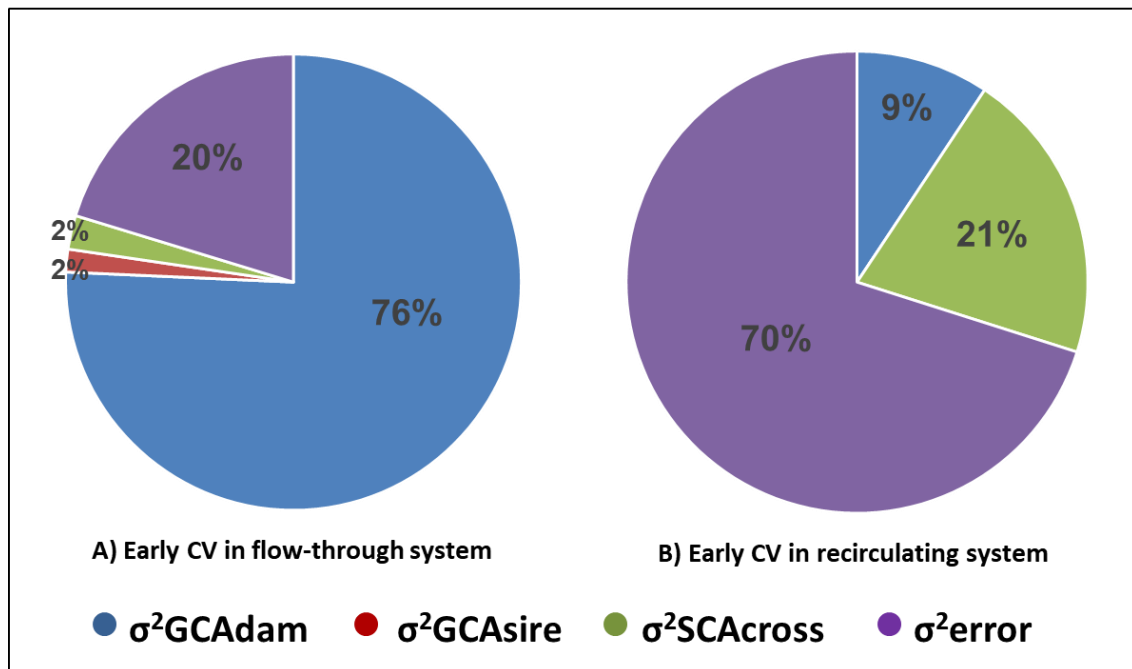


Figure 2. 12 Ratio of estimates of GCA variance components for dam and sire, SCA variance components for cross, and error variance components for coefficient of variance (CV) in body weight of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid

progeny in flow-through system for 311 days of separate tank rearing and recirculating system for additional 245 days of separate tank rearing.

The mean squares of coefficient of variation in body weight was significant ($P < 0.05$) only for the GCA effects of the dam for the hybrid catfish after the initial 311-day separate tank rearing in flow-through system (Table 2.5), indicating importance of additive gene effects of the female parent. The combining ability variance components ratio (Fig. 2.12) revealed that the CV in body weight trait of the hybrid progeny reared in separate tanks in flow-through system was controlled by the additive gene effects attributed to the dam parents. For CV, the best GCA estimate would be the lowest negative value if one were selecting for uniformity. Parental dam 9 had the best or most negative ($P < 0.05$, Fig. 2.13) GCA estimate. The hybrid progeny of this dam would likely have a very low coefficient of variation in body weight. Hybrid progeny of KxTh crossbred dams had the highest ($P < 0.05$) variation in body weight compared to hybrids from other dam types (Fig. 2.14). The parental dam strain with the lowest CV (0.20) was AR strain. However, the AR strain was not significantly different from other dam genotypes except KxTh.

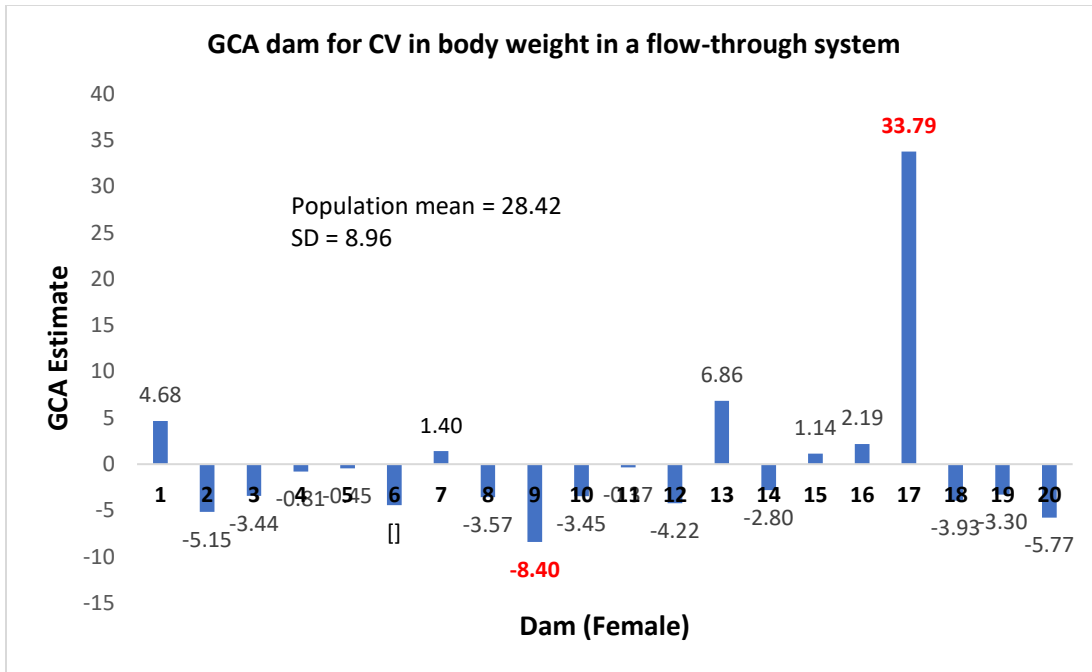


Figure 2. 13 The channel catfish (*Ictalurus punctatus*) female (dam) general combining ability estimates for coefficient of variance (CV) in body weight of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

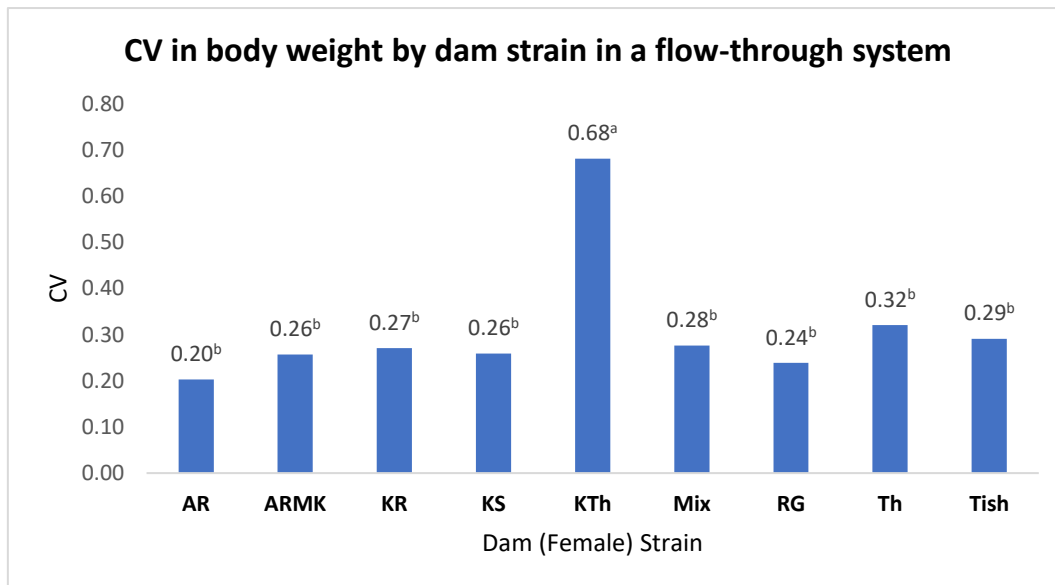


Figure 2. 14 Coefficient of variance (CV) in body weight by parental dam strain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing. Hybrid genotypes in the same rearing

system with the same superscript letter are not significantly different ($P>0.05$, Tukey-Kramer Test).

For CV in body weight of the hybrids reared for an additional 245 days in separate tanks in recirculating system, significant differences ($P<0.05$, Table 2.5) were found on the mean squares of CV in body weight for the GCA effects of the dam, sire, and dam-sire cross suggesting the variability in the genetic materials of this trait. The largest variance component ratio (Fig. 2.12) was found for the SCA which suggests the presence of heterosis and the importance of dominance and epistatic gene effects from the cross in controlling this trait. The SCA effects revealed that the crosses 15x6, 2x3, and 18x1 had the best SCA estimates at -4.72, -4.52, and -4.40, respectively (Fig. 2.15). The hybrid progeny of these crosses will have very low variation in terms of body weight. The cross RGxDB gave the lowest CV of 13.69 which was not different ($P>0.05$) to all other crosses except to ARMKxDB (Fig. 2.16).

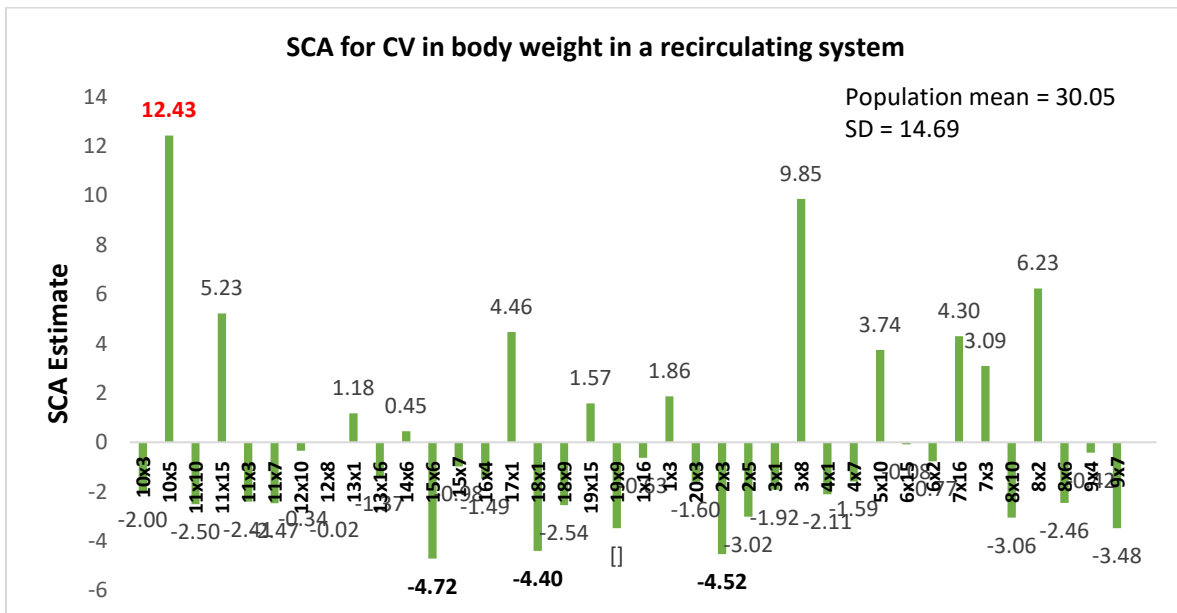


Figure 2. 15 The channel catfish (*Ictalurus punctatus*) female (dam) x blue catfish (*I. furcatus*) male (sire) specific combining ability estimates for coefficient of variance (CV) in body weight of channel catfish female x blue catfish male F1 hybrid progeny in recirculating system for

additional 245 days of separate tank rearing. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

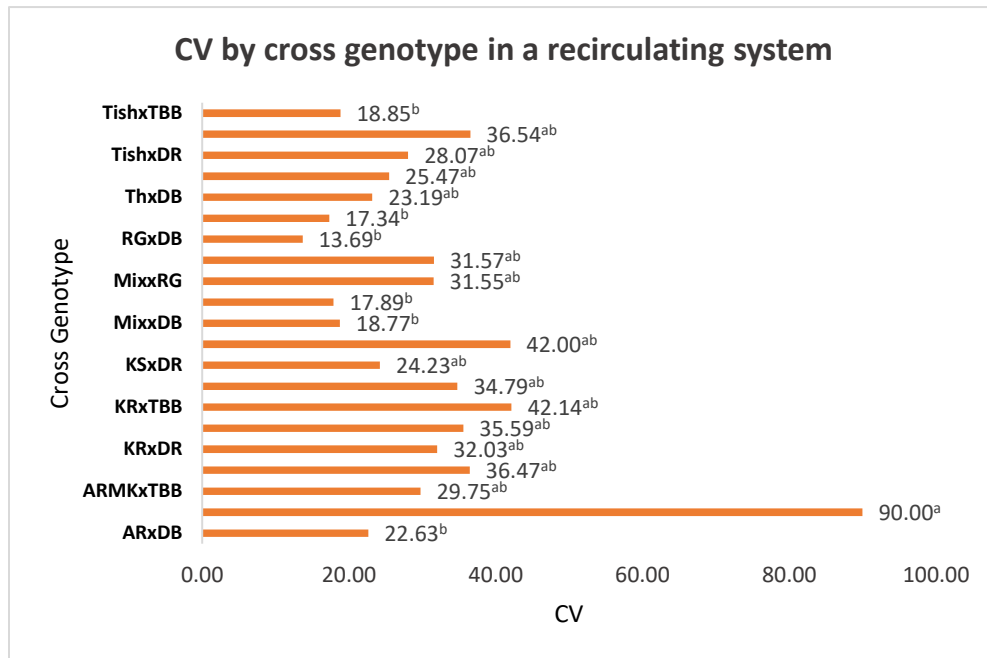


Figure 2. 16 Coefficient of variance (CV) in body weight by parental cross genotype of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing. Hybrid genotypes in the same rearing system with the same superscript letter are not significantly different ($P > 0.05$, Tukey-Kramer Test).

Early Resistance to *Aeromonas hydrophila* Infection

During the initial 311 days of rearing of the 40 hybrid catfish families in separate tanks in the flow-through system, mortality was observed due to natural *Aeromonas hydrophila* infection. The population mean and phenotypic standard deviation for the survival rate of hybrid catfish after *A. hydrophila* infection are presented in Table 2.7. The survival rates of the hybrids were analyzed following REML/BLUP joint analyses based on the genetic relationship matrix to calculate for the mean squares from the analysis of variance (Table 2.7), the variance components (Table 2.8) and the variance components ratio and estimates for GCAs of sire and dam and/or SCAs of crosses

(Fig. 2.17, 2.18, 2.20). The mean comparison of parental strains after analysis of variance through GLM Procedure using Tukey-Kramer Test are presented in Figures (2.19, 2.21).

Table 2. 7 The population mean, phenotypic standard deviation (SD), and mean squares (MS) for the Type 3 Mixed Procedure analysis of variance of the factorial mating design component of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny test and error mean squares for the survival rate of channel catfish female × blue catfish male hybrid catfish after a natural *Aeromonas hydrophila* infection.

Trait	Population mean (%)	Phenotypic SD	Source of Variation				
			dam	sire	dam x sire	Error	
Survival rate from natural <i>Aeromonas hydrophila</i> infection	83.67%	22.76					
			d.f.	19	11	9	67
			MS	670.19 *	915.12 *	527.96 ^{ns}	314.11

After ANOVA *F*-test: * = $p < 0.05$, and ^{ns} = $p > 0.05$
d.f. = degree of freedom.

Table 2. 8 Estimates of general combining ability variance for dam ($\sigma^2\text{GCA}_d$) and sire ($\sigma^2\text{GCA}_s$) and specific combining ability variance ($\sigma^2\text{SCA}$), error variance (σ^2_E) and corresponding standard errors for the survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny after a natural *Aeromonas hydrophila* infection.

Trait	Genetic parameter estimates			
	$\sigma^2\text{GCA}_d$ (± SE)	$\sigma^2\text{GCA}_s$ (± SE)	$\sigma^2\text{SCA}$ (± SE)	σ^2_E
Survival rate from natural <i>Aeromonas hydrophila</i> infection	63.76 (53.55)	109.08 (64.65)	0	335.28

The mean squares of the survival rate of hybrid catfish from natural *A. hydrophila* infection was significant ($P < 0.05$, Table 2.7) for the GCA effects of the dam and sire parents indicating the importance of additive gene effects. The combining ability variance components ratio (Table 2.8, Fig. 2.17) revealed that the early resistance of hybrids to natural *A. hydrophila*

infection is controlled largely (almost double) by the additive gene effects attributed to the sire parent. Parental sire 7 had the best highest positive GCA estimate of 7.29 (Fig. 2.18), which suggests that its hybrid progeny will likely have better early resistance to *A. hydrophila*. The hybrid progeny of TBB, DB, and RG sires had the highest survival rates ($P < 0.05$, Fig. 2.19) after natural *Aeromonas* infection at 90.89, 90.81, and 86.43%, respectively. The hybrid progeny from DxR crossbred sires had the lowest survival rate at 64.08%.

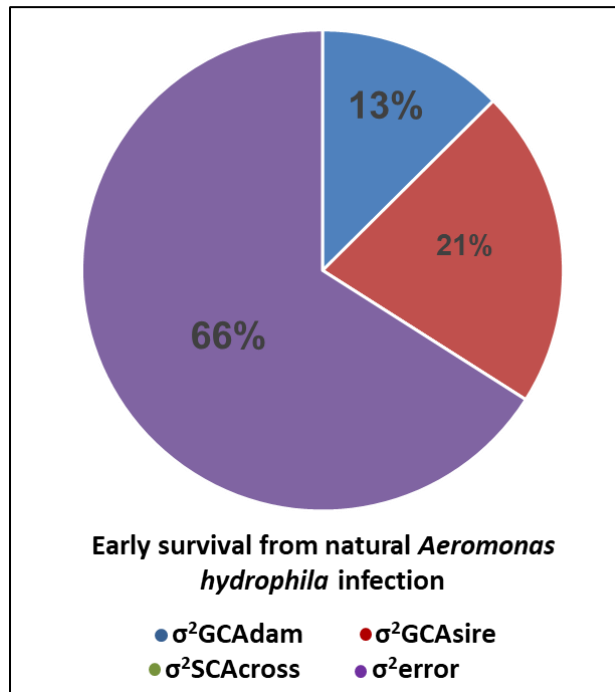


Figure 2. 17 Ratio of estimates of GCA variance components for dam and sire, SCA variance components for cross, and error variance components for the early survival of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

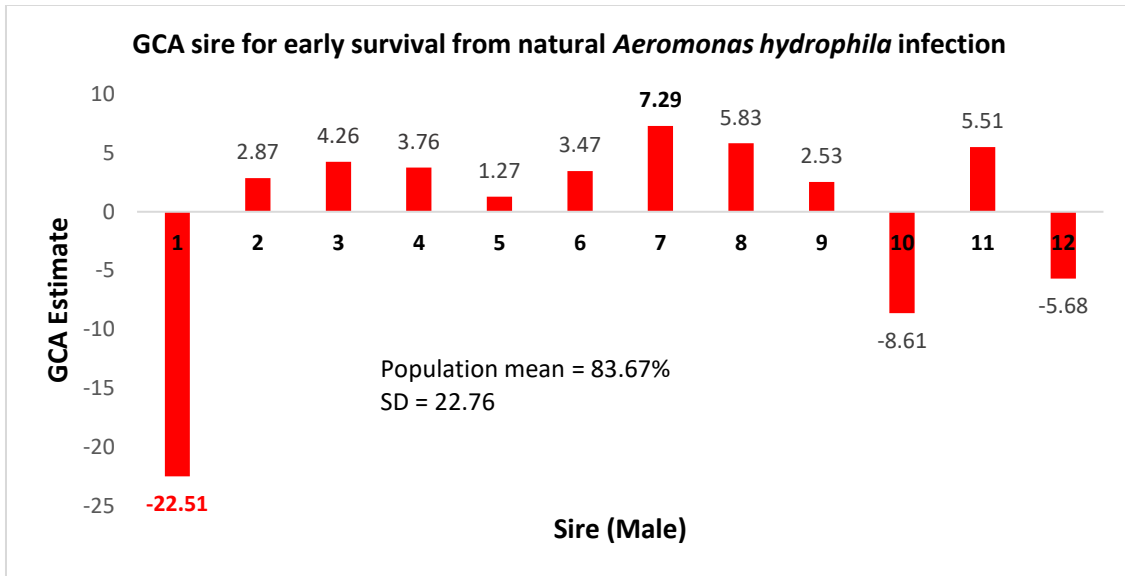


Figure 2. 18 The blue catfish (*Ictalurus furcatus*) male (sire) general combining ability estimates for the early survival of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection. GCA estimates in red font are significantly different among others ($P < 0.05$, *t*-test).

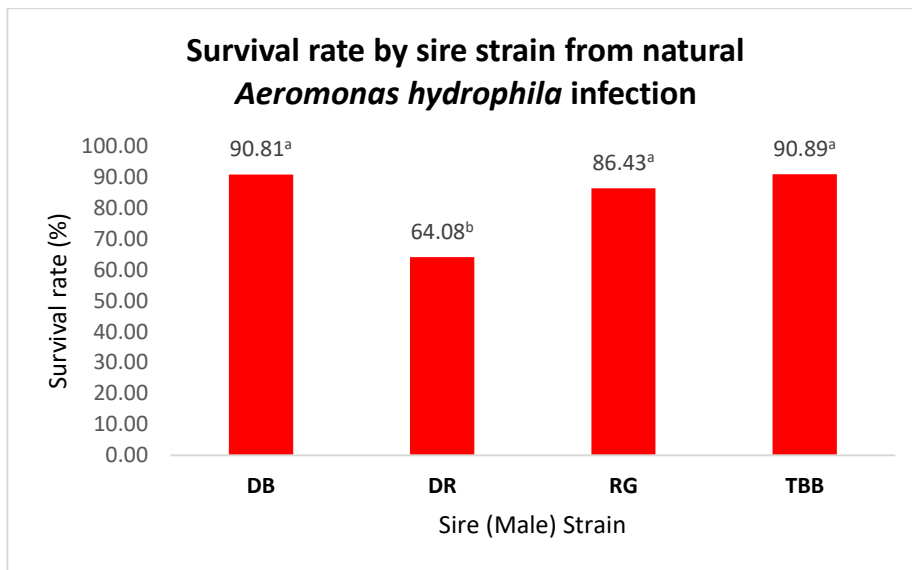


Figure 2. 19 Early resistance of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny to natural *Aeromonas hydrophila* infection in terms of survival rate by parental sire strain of hybrid catfish. Hybrid genotypes in the same rearing system with the same superscript letter are not significantly different ($P > 0.05$, Tukey-Kramer Test).

Since the GCA effects of the dam were also significant ($P < 0.05$, Table 2.7) as revealed by the mean squares for the survival rate of hybrid catfish from natural *A. hydrophila* infection, the additive genetic effects of the dam cannot be ignored. In terms of GCA estimates for this trait, parental dam 3 had the best highest positive GCA estimate of 5.64 (Fig. 2.20), suggesting that its hybrid progeny will have better resistance to *A. hydrophila* infection. The survival rate of hybrid progenies of all nine dam genotypes did not differ significantly for *A. hydrophila* infection except for KxTh crossbred dams.

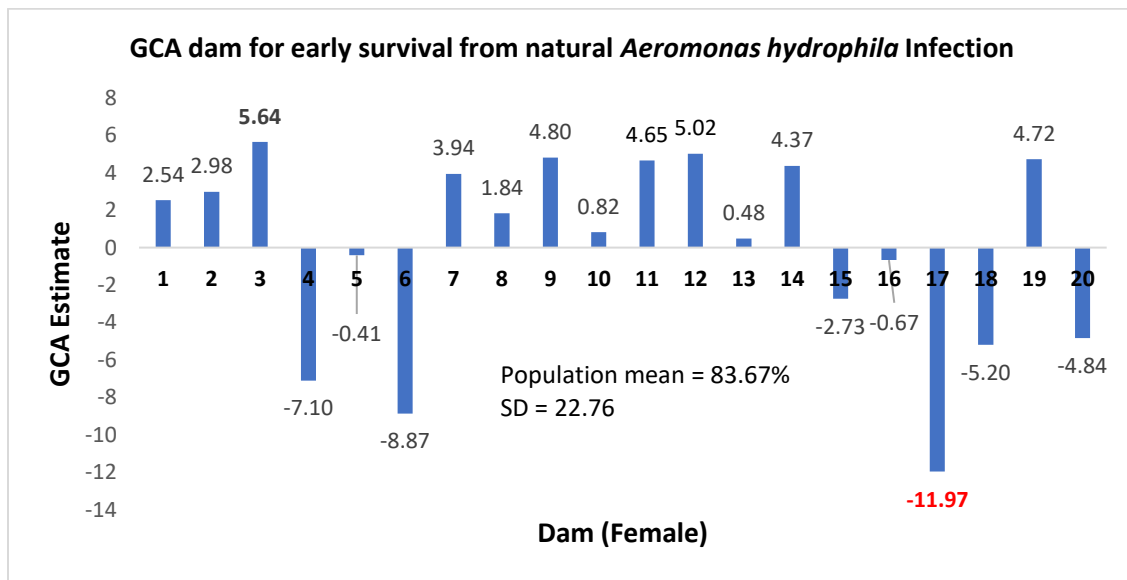


Figure 2. 20 The channel catfish (*Ictalurus punctatus*) female (dam) general combining ability estimates for the early survival of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection. GCA estimates in red font are significantly different among others ($P < 0.05$, *t*-test).

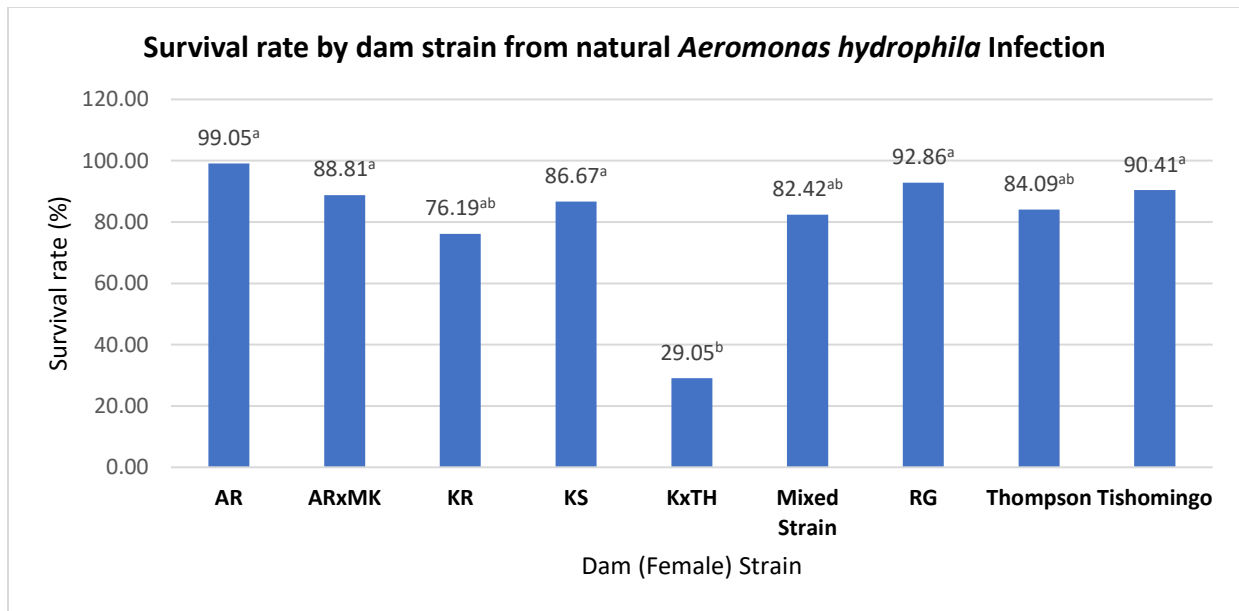


Figure 2. 21 Early resistance of channel catfish (*I. punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny to natural *Aeromonas hydrophila* infection in terms of survival rate by parental dam strain of hybrid catfish. Hybrid genotypes in the same rearing system with the same superscript letter are not significantly different ($P>0.05$, Tukey-Kramer Test).

Dressout Percentage

The dressout percentage of the hybrid catfish was determined after the additional 245-day communal rearing in split-pond. The population mean and phenotypic standard deviation for the dressout percentage of the hybrid catfish are presented in Table 2.9. The mean squares from the analysis of variance (Table 2.9), the variance components (Table 2.10), the variance components ratio and estimates for GCAs of sire and dam and/or SCAs of crosses (Figures 2.22, 2.23). The mean comparison of the cross genotypes after analysis of variance through GLM Procedure using Tukey-Kramer Test is presented in Figures (2.24).

Table 2. 9 The population mean, phenotypic standard deviation (SD), and mean squares (MS) for the Type 3 Mixed Procedure analysis of variance of the factorial mating design component of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny test and error mean squares for the dressout percentage of channel catfish female × blue catfish male hybrid catfish after additional 245-day communal rearing in split-pond.

	Population mean (%)	Phenotypic SD	Source of Variation				
			dam	sire	dam x sire	error	
Dressout Percentage	58.90%	2.73	d.f.	15	10	4	262
			MS	26.09 *	30.51 *	5.72 ^{ns}	5.66

After ANOVA *F*-test: * = $p < 0.05$, and ^{ns} = $p > 0.05$
d.f. = degree of freedom.

Table 2. 10 Estimates of general combining ability variance for dam (σ^2GCA_d) and sire (σ^2GCA_s) and specific combining ability variance (σ^2SCA), error variance (σ^2_E) and corresponding standard errors for the dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny after additional 245-day communal rearing in split-pond.

Trait	Genetic parameter estimates			
	σ^2GCA_d (± SE)	σ^2GCA_s (± SE)	σ^2SCA (± SE)	σ^2_E
Dressout Percentage	0.12 (0.70)	0.41 (0.48)	1.32 (0.92)	5.67

The mean squares of the dressout percentage of the hybrid catfish was found significant ($P < 0.05$, Table 2.9) for the GCA effects of the dam and sire parents. However, the combining ability variance components ratio (Table 2.10, Fig. 2.22) revealed that the most important component that controls this trait is the SCA variance indicating presence of heterosis and dominance and epistatic gene effects of the cross. The cross 11x10 had the best SCA estimate, 1.76 ($P < 0.05$, Fig. 2.23). The other crosses that also had high SCA estimates were 4x7 and 2x5.

These three crosses involved parents that are good combiners (i.e., good GCA x good GCA), indicating the concentration of positive alleles, additive x additive gene action, and interaction of favorable genes from both parents in each cross. The hybrid progeny of these three crosses with their high SCA estimates will likely have better dressout percentage. The cross RGxDB gave the highest mean, 61.57%, which was significantly better ($P < 0.05$, Fig. 2.24) than the 3 crosses with the lowest means. TishxDR, 60.87%, and KSxDR, 60.44%, had the next highest means.

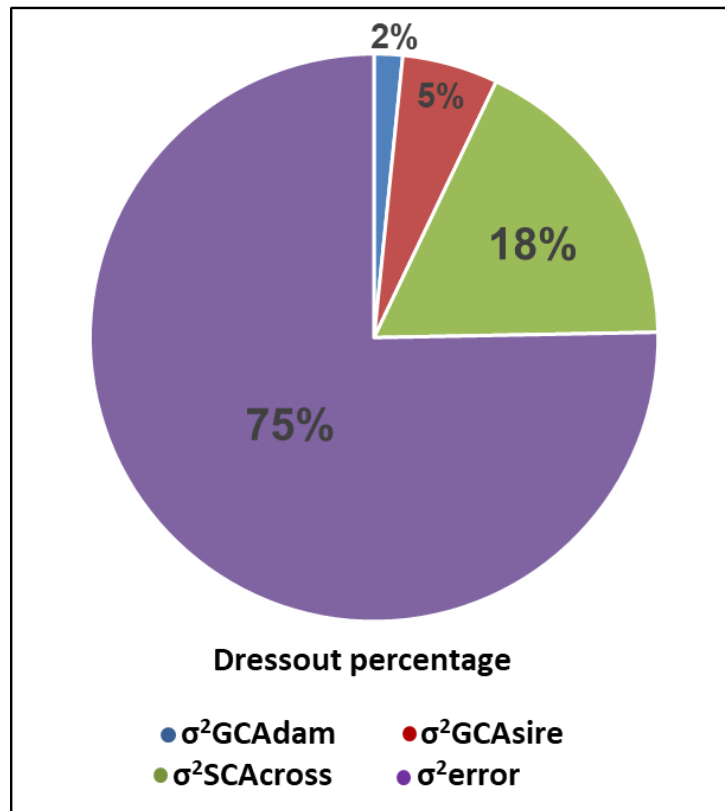


Figure 2. 22 Ratio of estimates of GCA variance components for dam and sire, SCA variance components for cross, and error variance components for the dressout percentage of channel catfish (*Ictalurus punctatus*) female \times blue catfish (*I. furcatus*) male F1 hybrid progeny after additional 245-day communal rearing in split-pond.

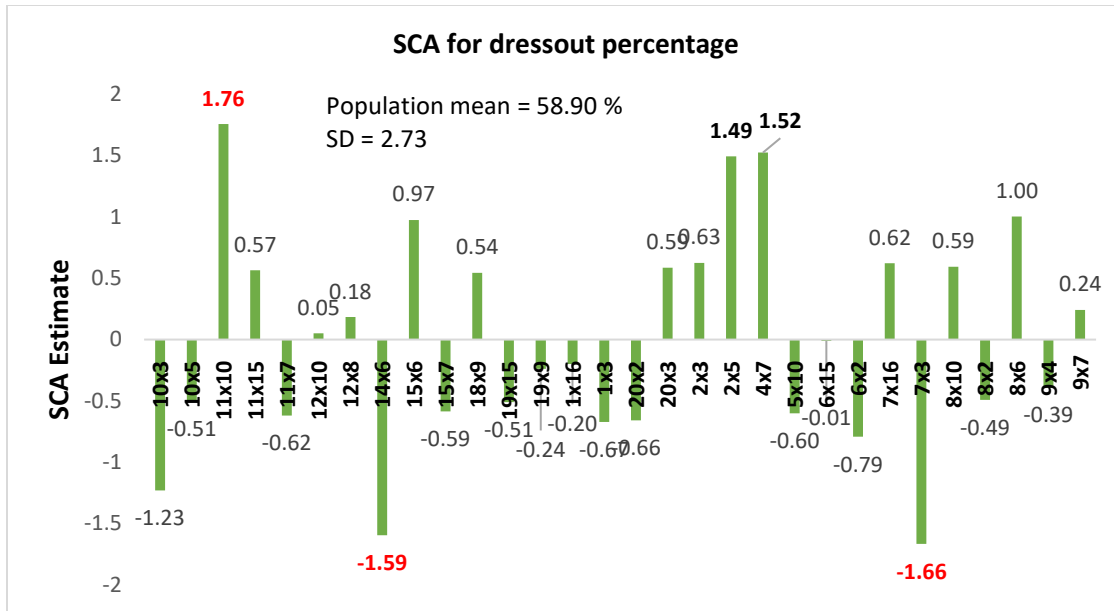


Figure 2. 23 The channel catfish (*Ictalurus punctatus*) female (dam) x blue catfish (*I. furcatus*) male (sire) specific combining ability estimates for the dressout percentage of channel catfish female x blue catfish male F1 hybrid progeny after additional 245-day communal rearing in split-pond. GCA estimates in red font are significantly different among others ($P < 0.05$, t -test).

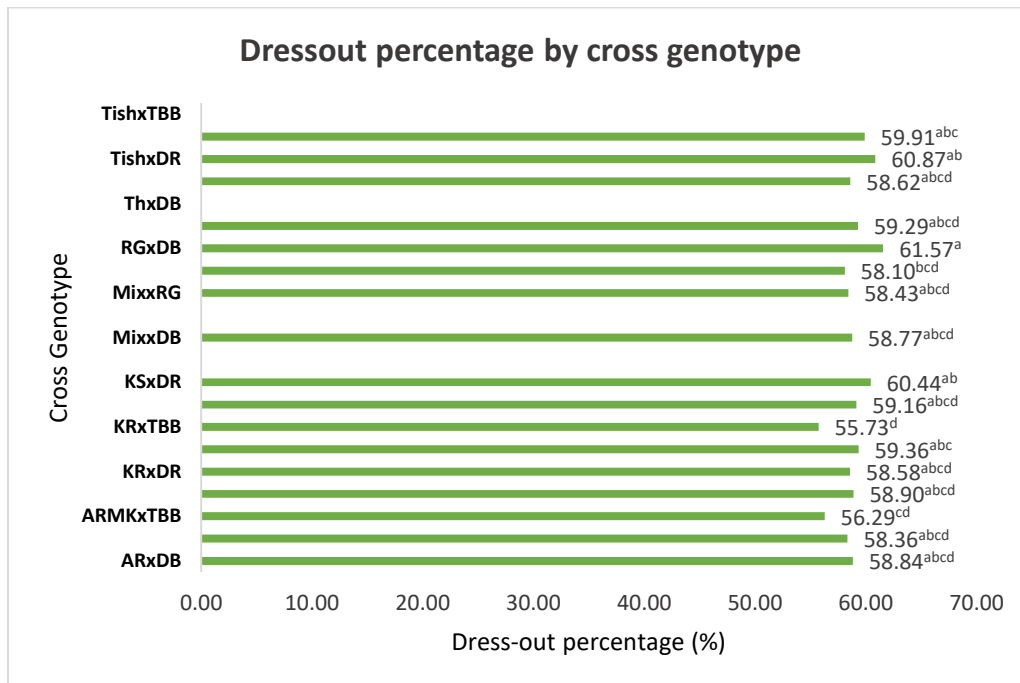


Figure 2. 24 Dressout percentage by parental cross genotype of channel catfish (*Ictalurus punctatus*) female x blue catfish (*I. furcatus*) male F1 hybrid progeny after additional 245-day communal rearing in split-pond. Hybrid genotypes in the same rearing system with the same superscript letter are not significantly different ($P > 0.05$, Tukey-Kramer Test).

Discussion

Application of hybrid catfish is increasingly prevalent due to their faster growth rate, better survival rate, disease resistance, tolerance of low oxygen, carcass yield and seinability. However, hybrid catfish performance could be further improved through reciprocal recurrent selection if GCA and/or SCA are of sufficient magnitude. In the current study, dam GCA had the strongest influence on early growth (body weight) in aquaria. Over time the percentage of variance due to genetics decreased, and after the hybrid progeny were transferred to ponds, the dam and sire GCAs equalized. Similar results were obtained when growth rate was measured as weight gain. Coefficient of variation for body weight was most strongly influenced by dam GCA in the flow-through system, and shifted more to control by SCA as the fish continued to grow in the recirculating system. Sire GCA followed by dam GCA had the strongest genetic influence on hybrid fry resistance to *Aeromonas hydrophila*. SCA was the strongest genetic component for dressout percentage.

Bosworth and Waldbieser (2014) estimated the GCA and SCA variances for growth and carcass yield in hybrid catfish of market-size. The dam GCA for body weight was the strongest factor, however, when maternal effects are accounted for dam and sire GCAs were likely equivalent. In the current study, dam GCA had the strongest influence on early growth (body weight) in aquaria, especially at the initial stage in the flow-through system. SCA was detectable at this time. Over time the percentage of variance due to genetics decreased, and after the hybrid progeny were transferred to ponds, the dam and sire GCAs equalized. The relative influence of dam additive gene effects, sire additive gene effects and dominance shifted in the 3 environments or times evaluated indicative of either genotype-environment interactions or genotype-age interactions. The pond result, the environment used by Bosworth and Waldbieser (2014), with

fish more similar in size to that experiment, resulted in almost identical results, equivalency of sire and dam GCA. However, one difference may be more maternal effects in the study of Bosworth and Waldbieser (2014).

The similarity in the results for body weight between the current study and that of Bosworth and Waldbieser (2014) is significant as they utilized different strains than the current study, suggesting that the genetics of variable hybrid performance are similar across different strains and lines of channel catfish and blue catfish. Thus, a standard breeding program to improve growth rate of hybrid catfish should be applicable industry wide, just as selection for increased body weight of channel catfish was effective in all strains of channel catfish evaluated (Dunham 2011).

Our results and those of Bosworth and Waldbieser (2014) indicate that when hybrid progeny are grown in ponds, selection for channel catfish female and blue catfish male body weight should result in faster growing hybrid progeny. That prediction was not accurate after four generations of selection for body weight in Kansas strain channel catfish (Jeppsen 1995), as hybrids from control females grew at the same rate as hybrids from selected females. However, it was accurate after eight generations of selection for body weight in Kansas strain as hybrid fingerlings from selected females grew faster than hybrids from control females (Makhubu 2014; Alsaqafi 2015). The explanation for the change over a 4-generation period is not clear, however, allele frequency changes would be expected between generations, and this could explain the variable results. The dam GCA suggests that the selection of channel catfish females for body weight should result in faster growing hybrids, and this will need to be verified in multiple populations to determine the generality of this prediction.

The relative importance of the GCAs and SCA were similar when growth rate was measured as body weight or weight gain. Although the type of gene action was changing over time or by environment, this suggests that genetic ranking was staying the same and genotype-environment interactions were minimal. However, this conclusion is not correct. If the dam GCA of individual females is examined, the females with the highest GCA changes for different environments and as the hybrid progeny increase in size. Thus, strong genotype-environment or genotype-age interactions occurred or both.

Size variation of hybrid catfish grown in the catfish industry at high density has become a problem. At low density, the hybrid is a very uniform growing fish (Dunham et al. 1982), however, at high density there is great increase in body weight variability (Ramboux 1990). The coefficient of variation for body weight of hybrid catfish, in regard to combining ability variance differed between the two aquaria rearing systems. The GCA variance for dam was more predominant compared to SCA during the initial 311 days in the flow-through system indicating additive gene effects controlling this trait, whereas the SCA variance became twice as large as dam GCA when hybrids were reared for an additional 245 days in the recirculating system indicating dominance gene effects having greater influence for this trait. Hybrids produced by the KxTh crossbred dams had the largest CV for body weight. This is not surprising as the crossbred females should have a high level of heterozygosity, and should produce a large variety of gametes from a genetic standpoint. Additionally, linkage disequilibrium could contribute to the variability (Christiansen 1989; Slatkin 2008) of hybrid offspring from these crossbred females.

Can channel catfish dams be selected to produce hybrid progeny that grow faster and exhibit more uniform growth. The results from the fry growth in flow through aquaria indicate

that this would be difficult. Dams with the highest GCA for body weight tended to have also have high GCA for CV, and those with low GCA for body weight also had low GCA for CV, indicating selection of fast growing hybrid fingerlings would also increase variability, and selection for uniform growth would also decrease growth.

The top three crosses with desirable negative SCA estimates for CV in body weight were 15x6 (Tishomingo x DB), 2x3 (RG x TBB), and 18x1 (Mix strains x DR). These top 3 crosses all belonged to different strains, thus there were no dramatic strain effects for SCA of CV. However, crosses from dam strains containing the greatest lineage of RG strain tended to have the most uniform growth. The SCA effects of the three desirable crosses, influenced by both additive and dominance genetic variation (Eisen et al. 1983), suggests the potential for improving CV through selection for specific pairs.

In the case of early resistance of F1 hybrid catfish to *Aeromonas hydrophila* natural infection, the sire GCA had more impact than the dam GCA, and the SCA was zero, indicating that additive gene effects were important, but not dominance. Although the GCA values among individual sires were not statistically different, nine sires had positive GCA estimates for this trait, and three sires had relatively low negative GCA estimates. The hybrid progeny from the sire strains DB, TBB, and RG, had the best survival, approximately 90%. The hybrid progeny from the DxR crossbred sires had the poorest survival rate, 64%. Similar to what was observed with F1 KxTh crossbred dams, hybrids from the F1 crossbred males had poor survival related performance. One expectation would be that there might be positive maternal effects from crossbred dams, but the opposite was true. Perhaps, linkage disequilibrium (Christiansen 1989; Slatkin 2008) resulted in lowered overall fitness in the hybrid progeny from these intraspecific F1 parents. It should be beneficial to combine the best alleles from multiple strains or lines, but

the results from the current study suggest that multiple generations may be needed for potential negative effects from linkage disequilibrium dissipate before beneficial effects from selecting in the more diverse genetic background be realized.

Parental sires with best GCA values among the better performing strains can likely be used to improve the early resistance trait of hybrid catfish to *Aeromonas hydrophila* infection through selection. Future studies that would employ controlled disease challenges on the hybrid catfish (at different ages) that are generated from a full factorial mating design would be very informative in exploring the genetic components responsible for the expression of this trait. Combining abilities for measurable parameters in the immune system that are genetically correlated with disease resistance may also be conducted to allow indirect selection for improved disease resistance of hybrid catfish.

The family variability could be attributed to the combination effect of strain differences. The largest genetic variance component for dressout percentage was the SCA variance which indicates the presence of heterosis and dominance gene effects of the specific cross. Bosworth and Waldbieser (2014) found the opposite result with maternal effects and dam GCA being much more influential than SCA. There are many potential explanations as there were several differences in the two studies. Different strains were used, and processing technology was different. In the current study, the fish were much smaller and the dressout percentage much smaller. Thus, many factors, genetic, environmental and genotype-environment interactions are possible explanations of the opposite results of the two studies.

Based on the SCA values, the cross 11x10 had the best significant positive SCA estimate for dressout. The other crosses that also gave relatively high and positive SCA estimates are 4x7 and 2x5. These three crosses involved parents with good x good GCA parental

combinations indicating the concentration of positive alleles and interaction of favorable genes from both parents in each cross. The high SCA effects of these crosses with both parents that are good general combiners also suggest additive x additive gene action (Dey et al. 2014; Verma and Srivastava 2004). The results in this study were consistent with the conclusion of Cotterill et al. (1986), where crossing parents with best GCA estimates would usually produce outstanding progeny, even when dominance variance equals additive variance. Sire strain effects were also evident for dressout percentage. When paired comparisons are made with the same dam strain, but varying sire strain, hybrids from the TBB blue catfish consistently had the lowest dressout percentage and those from RG blue catfish had the highest. Combining parental lines with desirable high GCA values and cross genotypes would likely result in inheritable genetic gains for improving the dressout percentage of hybrid catfish. Additionally, cross genotypes that exhibit heterosis for dressout can also be selected as in common beans, heterosis and SCA are highly correlated (de Fátima Machado et al. 2002). Future research can be conducted on catfish to confirm this correlation. Future research should also determine the relationship of the early dressout percentage of F1 hybrid catfish to the dressout percentage of hybrids at the more typical market-size. If valid, selection and prediction of hybrids with better dressout done at the early age would save time and money. The current data is also relevant from the standpoint that there are a few markets that prefer small fish.

For most traits assessed in this study, the GCA variance of the parental dams were relatively larger compared to the GCA variance of the parental sires and the SCA. Several studies on fish species such as hybrid catfish (Bosworth and Walbieser 2014; Drescher 2017), hybrid striped bass (*Morone chrysops* × *Morone saxatilis*) (Wang et al. 2006), sea bass (*Dicentrarchus labrax* L.) (Saillant et al. 2006), and carp (*Cyprinus carpio* L.) (Vandeputte et al. 2004), after analyses of their

factorial matings also revealed greater degrees of additive variance (GCA) than the dominance variance (SCA). Bosworth and Waldbieser (2014) reported a confounding effect to genetic variance resulting to greater magnitude of additive variance due to greater genetic variation in the channel catfish females, which was supported by microsatellite data that showed high polymorphism in the channel catfish females used and low level of polymorphism in the blue catfish used in their study. The females used in their study were a mixture of fish from different strains from commercial farms with large breeding populations and therefore expected to be more polymorphic. The blue catfish they used in their study were from a single strain of fish obtained from a commercial farm and therefore expected to be of low level of polymorphism. Hence, the magnitude of additive variance in their study was greater in favor of channel catfish females than the blue catfish males. This is assuming that the quantity of additive variation is correlated with the quantity of microsatellite variation. However, alternative explanations exist as the microsatellites do not distinguish between additive and dominance genes and expression. The use of a population made from many strains could also result in a large amount of dominance effects, raising the impact of SCA. Also, significant additive variation can exist even in highly inbred lines (Chan 1971), thus GCA could be of great importance even in the case of limited microsatellite variability.

In the current study, the genetic variance could not be ascribed to such partitioning of the relative importance of the genetic components because of the explanation above, but also because the effects of high polymorphism were expected to be present in both male and female catfish parents used. The female parents used in this study were a mixture of lines and a crossbreed of channel catfish, indicating that the overall female population could be highly polymorphic. On one hand, the male blue catfish were composed of three strains and a

crossbreed, which could also result in high polymorphism. Thus, the polymorphism of the male and female catfish parents in this study could possibly contribute to the magnitude of additive genetic variance.

In the current study, GCA was the strongest genetic component explaining the genetic variation for most of the traits evaluated. According to Griffing (1956), parents with the highest GCA estimates should generate a population with a higher mean yield. GCA estimates close to zero indicate that the progeny's performance does not differ from the general mean of all crosses. On the other hand, positive or negative estimates indicate that the parent is better or worse than the other parents included in the mating design, as compared to the mean yield of the crosses (Griffing 1956). In this study, the GCA estimates obtained correspond to the frequency of desirable or undesirable alleles of the parents with additive effects for the early growth performance traits of the F1 hybrid catfish. Consequently, parents with higher GCA estimates should generate progeny with the highest mean yield, from which elite parental lines can be selected. However, in the process of choosing elite parents, the highest GCA estimate alone is not sufficient enough if the parents are genetically similar because the population will present a restricted variability thereby reducing the chances to select improved lines. On the other hand, SCA measures the degree of allelic complementation. In this study, the magnitude of SCA variance was greater than the GCA variance for the CV in body weight of hybrids reared in the recirculating system and the dressout percentage of hybrids reared in communal split-pond. This result therefore suggests that selecting the cross from those with desirable SCA estimates along with parents with the highest magnitudes of GCA estimates would be feasible and result in the most effective selective breeding program.

For traits where GCA variances are larger than SCA variances, selection of parents that are good combiners is efficient because the value of the parents can be examined at the F1 generation of its hybrid progeny based from the GCA estimates (Melchinger et al. 1998; Smith et al. 2008). Selected parents of hybrids with good GCA estimates can be reproduced to develop parental lines that are good combiners in producing improved hybrids. The GCA performance of these parental lines can be predicted from the GCAs of their parents because the GCA is controlled by the additive gene effects which are heritable from the parents and can be passed onto the progeny. (Lv et al. 2012). Hence, improvement of the hybrid catfish becomes effective and less costly due to the less time taken to release F1 hybrids with low amount of materials needed in the breeding programs. In the case where SCA variance is more important over GCA variance for some traits, selection of parents/cross for hybrids can be done in later generation of the parental lines until the target traits are improved. (Bao et al. 2009; Ertiro et al. 2013).

As this study was conducted on young, small hybrid catfish, future research should confirm that there is a relationship between the genetic mechanisms at this time point, and that of food size hybrid catfish to ensure that the research has practical application not only to fingerling producers, but also food fish producers and processors. Genotype-environment interactions should also be further explored. Future research could also involve integrating molecular aspects of combining ability. Linkage analysis revealed the contribution of several QTLs to GCA effects and heterosis of agronomic traits in rice and maize which provided the information for dissecting the genetic bases of combining ability (Lv et al. 2012; Qi 2013; Qu 2012; Liu et al. 2015; Zhou et al. 2017). Linkage analysis on both the GCA and SCA effects for each trait could also be conducted to explore and unveil the QTLs of combining abilities for important traits and evaluate how they contribute to the overall performance of hybrid catfish.

Conclusion

The early growth traits of the F1 hybrid catfish were found to be controlled by the additive gene effects attributed to the parental channel catfish females when hybrids were reared in aquaria. However, the additive gene effects from both parental channel catfish females and blue catfish males equalized when hybrids were reared in pond. Alternatively, this could be a size effect as the fish were not reared to equal sizes in the two environments. Additive gene effects of the dam controlling coefficient of variation in body weight declined and dominance gene effects of the cross increased as the fish grew. The early resistance of the F1 hybrid catfish to *Aeromonas hydrophila* natural infection was found to be controlled by the additive gene effects attributed to parental blue catfish males, suggesting the importance of selecting blue catfish males with better GCA estimates to generate hybrid catfish with improved resistance to *Aeromonas*. The importance of dominance gene effects of the cross in controlling the dressout percentage of the F1 hybrid catfish was revealed. Cross genotypes exhibiting the highest SCA estimates which involved both parents having high x high GCA estimates would generate F1 hybrid catfish with better dressout percentage.

A breeding plan can be developed to improve the early growth, body weight variation, disease resistance and dressout percentage of F1 channel-blue hybrid catfish utilizing GCA and SCA information from this study. Using the GCA/SCA estimates obtained from the combining ability analyses, elite parental and/or cross genotypes capable of producing superior hybrid catfish were identified and performance of hybrid catfish progeny can be predicted. The genetic mechanisms observed should allow reciprocal recurrent selection of channel catfish and blue catfish to develop high yielding parental lines and hybrids that would be beneficial to the catfish industry.

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APPENDIX

Appendix Table 1 The Type 3 Mixed Procedure of analysis of variance for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
Dam	19	279.28982	14.699464	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	67	2.85	0.0008
Sire	11	63.226235	5.747840	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	67	1.11	0.3643
dam*sire	9	83.893658	9.321518	Var(Residual) + Q(dam*sire)	MS(Residual)	67	1.81	0.0830
Residual	67	345.57193	5.157790	Var(Residual)

Appendix Table 2 REML estimation of variance components for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
Dam	0.6336	3.2529	2.2970	1.42	0.0784
Sire	0.1765	0.9061	0.9232	0.98	0.1632
Cross	0.1928	0.9896	1.2827	0.77	0.2202
Residual	1.0000	5.1337	0.8795	5.84	<.0001

Appendix Table 3 GCA/SCA estimates with corresponding T-test (P=0.05) for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 1	-0.6084	1.0893	67	-0.56	0.5783
DAM 10	-0.9338	1.0948	67	-0.85	0.3967
DAM 11	-1.0748	0.9205	67	-1.17	0.2471
DAM 12	-1.0783	1.0994	67	-0.98	0.3302
DAM 13	1.0104	1.3024	67	0.78	0.4406
DAM 14	-1.5882	1.3041	67	-1.22	0.2275
DAM 15	1.2365	1.0891	67	1.14	0.2603
DAM 16	0.6755	1.4950	67	0.45	0.6528
DAM 17	3.5208	1.2905	67	2.73	0.0081
DAM 18	2.5287	1.0937	67	2.31	0.0239
DAM 19	-1.8133	1.1041	67	-1.64	0.1052
DAM 2	-0.7383	1.0948	67	-0.67	0.5024
DAM 20	1.1038	1.1146	67	0.99	0.3256
DAM 3	0.06081	1.1760	67	0.05	0.9589
DAM 4	-0.01384	1.0794	67	-0.01	0.9898
DAM 5	0.4615	1.2904	67	0.36	0.7217
DAM 6	0.7492	1.0299	67	0.73	0.4695
DAM 7	-0.7404	1.0893	67	-0.68	0.4991
DAM 8	-0.8300	0.9708	67	-0.85	0.3956

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 9	-1.9278	1.1013	67	-1.75	0.0846
SIRE 1	1.6254	0.7222	67	2.25	0.0277
SIRE 10	0.4315	0.6981	67	0.62	0.5386
SIRE 11	-0.3219	0.7448	67	-0.43	0.6669
SIRE 12	0.3077	0.7840	67	0.39	0.6960
SIRE 2	-0.6001	0.7543	67	-0.80	0.4291
SIRE 3	-0.3063	0.6766	67	-0.45	0.6522
SIRE 4	-0.09421	0.8387	67	-0.11	0.9109
SIRE 5	0.08529	0.8094	67	0.11	0.9164
SIRE 6	-0.06679	0.7656	67	-0.09	0.9307
SIRE 7	-0.3870	0.7116	67	-0.54	0.5883
SIRE 8	-0.3471	0.8311	67	-0.42	0.6776
SIRE 9	-0.3265	0.8061	67	-0.40	0.6868
10x3	-0.7634	0.8870	67	-0.86	0.3925
10x5	0.4793	0.8931	67	0.54	0.5932
11x10	0.2686	0.8686	67	0.31	0.7582
11x11	-0.8844	0.8723	67	-1.01	0.3143
11x3	0.4580	0.9259	67	0.49	0.6224
11x7	-0.1692	0.8701	67	-0.19	0.8464
12x10	0.06707	0.8896	67	0.08	0.9401
12x8	-0.3951	0.8958	67	-0.44	0.6606

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
13x1	0.4634	0.9379	67	0.49	0.6229
13x12	-0.1560	0.9389	67	-0.17	0.8686
14x6	-0.4832	0.9198	67	-0.53	0.6011
15x6	0.4739	0.8917	67	0.53	0.5969
15x7	-0.09767	0.8897	67	-0.11	0.9129
16x4	0.2055	0.9463	67	0.22	0.8287
17x1	1.0712	0.9180	67	1.17	0.2474
18x1	0.3648	0.8897	67	0.41	0.6831
18x9	0.4046	0.8947	67	0.45	0.6526
19x11	0.2094	0.8920	67	0.23	0.8151
19x9	-0.7611	0.8945	67	-0.85	0.3978
1x12	0.005037	0.8914	67	0.01	0.9955
1x3	-0.1901	0.8868	67	-0.21	0.8309
20x2	-0.3758	0.9069	67	-0.41	0.6799
20x3	0.7116	0.8919	67	0.80	0.4277
2x3	0.1616	0.8870	67	0.18	0.8560
2x5	-0.3862	0.8931	67	-0.43	0.6668
3x1	0.002459	0.9011	67	0.00	0.9978
3x8	0.01604	0.9358	67	0.02	0.9864
4x1	-0.1265	0.8888	67	-0.14	0.8872
4x7	0.1223	0.8895	67	0.14	0.8910

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
5x10	0.1404	0.9180	67	0.15	0.8789
6x10	-0.3326	0.9286	67	-0.36	0.7214
6x11	0.3233	0.8833	67	0.37	0.7155
6x2	0.2372	0.8837	67	0.27	0.7892
7x12	0.4870	0.8914	67	0.55	0.5867
7x3	-0.7122	0.8868	67	-0.80	0.4248
8x10	0.3278	0.8738	67	0.38	0.7087
8x2	-0.5167	0.8776	67	-0.59	0.5580
8x6	-0.06361	0.8782	67	-0.07	0.9425
9x4	-0.3084	0.8960	67	-0.34	0.7318
9x7	-0.2781	0.8904	67	-0.31	0.7558

Appendix Table 4 ANOVA for mean performance by parental strains following GLM Procedure for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	305.583505	38.197938	4.98	<.0001
Error	98	751.570970	7.669092		
Corrected Total	106	1057.154475			

Appendix Table 5 Mean comparison of performance by parental strains using Tukey-Kramer Test for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Tukey-Kramer Comparison Lines for Least Squares Means of dam				
LS-means with the same letter are not significantly different.				
		wt LSMEAN	dam	LSMEAN Number
	A	17.946667	5	5
	A			
B	A	11.730000	8	8
B				
B		10.318462	3	3
B				
B		10.285217	6	6
B				
B		9.110741	9	9
B				
B		8.738889	4	4
B				
B		8.721667	7	7
B				
B		8.445000	2	2
B				
B		6.908333	1	1

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 6 The Type 3 Mixed Procedure of analysis of variance for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	19	96132	5059.55948 6	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	677	4.75	<.0001
sire	11	33309	3028.11342 3	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	677	2.85	0.0012
dam*sire	8	7264.878620	908.109828	Var(Residual) + Q(dam*sire)	MS(Residual)	677	0.85	0.5560
Residual	677	720521	1064.28561 8	Var(Residual)

Appendix Table 7 REML estimation of variance components for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	0.2102	222.83	124.68	1.79	0.0370
sire	0.0805	85.4252	68.2055	1.25	0.1052
cross	0.0195	20.6986	56.3180	0.37	0.3566
Residual	1.0000	1060.16	57.3733	18.48	<.0001

Appendix Table 8 GCA/SCA estimates with corresponding T-test (P=0.05) for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 1	-5.8803	7.5527	677	-0.78	0.4365
DAM 10	-6.0247	8.2881	677	-0.73	0.4675
DAM 11	-10.1791	5.5604	677	-1.83	0.0676
DAM 12	-4.5508	6.5838	677	-0.69	0.4897
DAM 13	-10.7686	7.7604	677	-1.39	0.1657
DAM 14	-2.4328	9.9062	677	-0.25	0.8061
DAM 15	-10.2612	7.3960	677	-1.39	0.1658
DAM 16	5.5880	10.3220	677	0.54	0.5884
DAM 17	46.5104	8.7521	677	5.31	<.0001
DAM 18	-9.3132	7.1152	677	-1.31	0.1910
DAM 19	0.1124	7.6187	677	0.01	0.9882
DAM 2	15.8794	8.2216	677	1.93	0.0538
DAM 20	2.4863	8.3499	677	0.30	0.7660
DAM 3	-1.5614	7.4637	677	-0.21	0.8344
DAM 4	-2.7999	7.3786	677	-0.38	0.7045
DAM 5	-12.7271	7.9134	677	-1.61	0.1082
DAM 6	8.9377	7.6978	677	1.16	0.2460
DAM 7	-0.8289	7.5527	677	-0.11	0.9126
DAM 8	-0.5627	6.4654	677	-0.09	0.9307

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 9	-1.6237	8.1159	677	-0.20	0.8415
SIRE 1	13.9749	5.4988	677	2.54	0.0113
SIRE 10	5.0489	5.1000	677	0.99	0.3225
SIRE 11	-11.1101	5.5812	677	-1.99	0.0469
SIRE 12	-2.9743	6.3798	677	-0.47	0.6412
SIRE 2	-3.1889	6.1763	677	-0.52	0.6058
SIRE 3	2.1881	5.3719	677	0.41	0.6839
SIRE 4	4.3505	7.6694	677	0.57	0.5707
SIRE 5	0.4893	7.9336	677	0.06	0.9508
SIRE 6	-2.7782	6.4419	677	-0.43	0.6664
SIRE 7	-5.9728	5.3763	677	-1.11	0.2670
SIRE 8	7.8346	6.4767	677	1.21	0.2268
SIRE 9	-7.8621	6.4893	677	-1.21	0.2261
10x3	-1.1834	4.3637	677	-0.27	0.7863
10x5	0.6238	4.4582	677	0.14	0.8888
11x10	0.6036	4.1365	677	0.15	0.8840
11x11	-4.1875	4.1574	677	-1.01	0.3142
11x3	1.1967	4.3002	677	0.28	0.7809
11x7	1.4418	4.1407	677	0.35	0.7278
12x10	-1.0314	4.2062	677	-0.25	0.8064
12x8	0.6087	4.2714	677	0.14	0.8867

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
13x1	-0.3765	4.3349	677	-0.09	0.9308
13x12	-0.6238	4.3621	677	-0.14	0.8863
14x6	-0.2260	4.4297	677	-0.05	0.9593
15x6	0.5316	4.4076	677	0.12	0.9040
15x7	-1.4848	4.3141	677	-0.34	0.7308
16x4	0.5191	4.4379	677	0.12	0.9069
17x1	4.3204	4.4087	677	0.98	0.3275
18x1	0.4187	4.2762	677	0.10	0.9220
18x9	-1.2838	4.3098	677	-0.30	0.7659
19x11	0.6317	4.3281	677	0.15	0.8840
19x9	-0.6212	4.3240	677	-0.14	0.8858
1x12	-0.2247	4.3405	677	-0.05	0.9587
1x3	-0.3215	4.3027	677	-0.07	0.9405
20x2	1.1679	4.4530	677	0.26	0.7932
20x3	-0.9370	4.3688	677	-0.21	0.8302
2x3	1.9803	4.3612	677	0.45	0.6499
2x5	-0.5052	4.4580	677	-0.11	0.9098
3x1	-1.4346	4.3143	677	-0.33	0.7396
3x8	1.2896	4.3953	677	0.29	0.7693
4x1	0.4582	4.3169	677	0.11	0.9155
4x7	-0.7183	4.3173	677	-0.17	0.8679

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
5x10	-1.1822	4.3950	677	-0.27	0.7880
6x11	0.8639	4.3217	677	0.20	0.8416
6x2	-0.03365	4.3423	677	-0.01	0.9938
7x12	0.1279	4.3405	677	0.03	0.9765
7x3	-0.2048	4.3027	677	-0.05	0.9620
8x10	2.8334	4.2132	677	0.67	0.5015
8x2	-1.9069	4.2623	677	-0.45	0.6547
8x6	-0.9788	4.2949	677	-0.23	0.8198
9x4	0.5351	4.4387	677	0.12	0.9041
9x7	-0.6859	4.3554	677	-0.16	0.8749

Appendix Table 9 ANOVA for mean performance by parental strains following GLM Procedure for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	145211.943	18151.4928	16.20	<.0001
Error	707	792052.295	1120.3003		
Corrected Total	715	937264.237			

Appendix Table 10 Mean comparison of performance by parental strains using Tukey-Kramer Test for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Tukey-Kramer Comparison Lines for Least Squares Means of dam				
LS-means with the same letter are not significantly different.				
		wt LSMEAN	dam	LSMEAN Number
	A	170.3611	5	5
	B	116.3095	7	7
	B			
C	B	106.1364	8	8
C	B			
C	B	93.7065	3	3
C	B			
C	B	92.9576	4	4
C	B			
C	B	87.6129	6	6
C	B			
C	B	86.8250	2	2
C	B			
C	B	86.7273	1	1
C				
C		84.4196	9	9
The LINES display does not reflect all significant comparisons. The following additional pairs are significantly different: (7,6)				

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 11 The Type 3 Mixed Procedure of analysis of variance for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	19	77662	4087.453408	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	677	4.45	<.0001
sire	11	27099	2463.530809	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	677	2.68	0.0022
dam*sire	8	6084.486762	760.560845	Var(Residual) + Q(dam*sire)	MS(Residual)	677	0.83	0.5776
Residual	677	621526	918.059091	Var(Residual)

Appendix Table 12 REML estimation of variance components for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	0.1711	156.44	99.4165	1.57	0.0578
sire	0.0664	60.6901	56.3441	1.08	0.1407
cross	0.0283	25.8533	54.7523	0.47	0.3184
Residual	1.0000	914.56	49.5005	18.48	<.0001

Appendix Table 13 GCA/SCA estimates with corresponding T-test (P=0.05) for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 1	-5.2105	6.8687	677	-0.76	0.4484
DAM 10	-3.2010	7.5143	677	-0.43	0.6702
DAM 11	-8.0232	5.1024	677	-1.57	0.1163
DAM 12	-1.5576	6.0759	677	-0.26	0.7977
DAM 13	-11.3735	7.0551	677	-1.61	0.1074
DAM 14	0.3124	8.8226	677	0.04	0.9718
DAM 15	-11.2753	6.8081	677	-1.66	0.0982
DAM 16	3.5377	9.0714	677	0.39	0.6967
DAM 17	36.0375*	7.9547	677	4.53	<.0001
DAM 18	-8.9922	6.5014	677	-1.38	0.1671
DAM 19	2.2359	6.9241	677	0.32	0.7469
DAM 2	14.0387	7.4621	677	1.88	0.0604
DAM 20	-0.1454	7.5726	677	-0.02	0.9847
DAM 3	0.1025	6.8400	677	0.01	0.9880
DAM 4	-2.1393	6.7517	677	-0.32	0.7515
DAM 5	-10.8634	7.3213	677	-1.48	0.1383
DAM 6	5.4239	7.0063	677	0.77	0.4391
DAM 7	0.5919	6.8687	677	0.09	0.9313
DAM 8	1.0981	5.8969	677	0.19	0.8523

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 9	-0.5973	7.3830	677	-0.08	0.9355
SIRE 1	10.6884	4.9066	677	2.18	0.0297
SIRE 10	3.7095	4.6289	677	0.80	0.4232
SIRE 11	-8.7648	5.0658	677	-1.73	0.0841
SIRE 12	-2.6356	5.6573	677	-0.47	0.6414
SIRE 2	-1.7333	5.5326	677	-0.31	0.7542
SIRE 3	2.1749	4.7785	677	0.46	0.6491
SIRE 4	2.8325	6.6075	677	0.43	0.6683
SIRE 5	0.9457	6.8522	677	0.14	0.8903
SIRE 6	-2.1950	5.7094	677	-0.38	0.7008
SIRE 7	-5.5191	4.8563	677	-1.14	0.2562
SIRE 8	7.1018	5.8130	677	1.22	0.2222
SIRE 9	-6.6050	5.7753	677	-1.14	0.2532
10x3	-1.2740	4.7665	677	-0.27	0.7893
10x5	0.7450	4.9355	677	0.15	0.8801
11x10	1.1408	4.4483	677	0.26	0.7977
11x11	-5.2384	4.4702	677	-1.17	0.2417
11x3	1.2756	4.6915	677	0.27	0.7858
11x7	1.4961	4.4474	677	0.34	0.7367
12x10	-1.3269	4.5290	677	-0.29	0.7696
12x8	1.0695	4.6359	677	0.23	0.8176

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
13x1	-1.4866	4.7328	677	-0.31	0.7535
13x12	-0.3930	4.7799	677	-0.08	0.9345
14x6	0.05162	4.8689	677	0.01	0.9915
15x6	0.1335	4.8575	677	0.03	0.9781
15x7	-1.9968	4.6899	677	-0.43	0.6704
16x4	0.5846	4.8814	677	0.12	0.9047
17x1	5.9555	4.8279	677	1.23	0.2178
18x1	1.2470	4.6396	677	0.27	0.7882
18x9	-2.7330	4.6956	677	-0.58	0.5607
19x11	0.4501	4.7281	677	0.10	0.9242
19x9	-0.08063	4.7155	677	-0.02	0.9864
1x12	-0.6471	4.7510	677	-0.14	0.8917
1x3	-0.2140	4.6854	677	-0.05	0.9636
20x2	1.6797	4.9289	677	0.34	0.7334
20x3	-1.7038	4.7767	677	-0.36	0.7214
2x3	2.6622	4.7619	677	0.56	0.5763
2x5	-0.3422	4.9351	677	-0.07	0.9447
3x1	-1.9388	4.6912	677	-0.41	0.6795
3x8	1.9558	4.8377	677	0.40	0.6861
4x1	0.7761	4.7108	677	0.16	0.8692
4x7	-1.1296	4.7126	677	-0.24	0.8106

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
5x10	-1.7953	4.8005	677	-0.37	0.7085
6x11	1.0546	4.7170	677	0.22	0.8232
6x2	-0.1582	4.7514	677	-0.03	0.9734
7x12	-0.08269	4.7510	677	-0.02	0.9861
7x3	0.1805	4.6854	677	0.04	0.9693
8x10	3.5615	4.5568	677	0.78	0.4347
8x2	-2.2599	4.6243	677	-0.49	0.6252
8x6	-1.1202	4.6725	677	-0.24	0.8106
9x4	0.6220	4.9027	677	0.13	0.8991
9x7	-0.7207	4.7553	677	-0.15	0.8796

Appendix Table 14 ANOVA for mean performance by parental strains following GLM Procedure for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	104729.284	13091.1604	13.49	<.0001
Error	707	686109.444	970.4518		
Corrected Total	715	790838.728			

Appendix Table 15 Mean comparison of performance by parental strains using Tukey-Kramer Test for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Tukey-Kramer Comparison Lines for Least Squares Means of dam				
LS-means with the same letter are not significantly different.				
		gw LSMEAN	dam	LSMEAN Number
	A	146.2778	5	5
	B	104.0714	7	7
	B			
C	B	90.7273	8	8
C	B			
C	B	83.6695	4	4
C	B			
C	B	81.9000	3	3
C	B			
C	B	78.7750	2	2
C	B			
C	B	76.6591	1	1
C				
C		76.5605	6	6
C				
C		74.3357	9	9

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 16 The Type 3 Mixed Procedure of analysis of variance for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	18	1203607	66867	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	1480	9.14	<.0001
sire	11	936922	85175	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	1480	11.64	<.0001
dam*sire	7	53899	7699.882732	Var(Residual) + Q(dam*sire)	MS(Residual)	1480	1.05	0.3922
Residual	1480	10827647	7315.977758	Var(Residual)

Appendix Table 17 REML estimation of variance components for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
Dam	0.1998	1463.21	587.61	2.49	0.0064
Sire	0.1896	1388.25	663.43	2.09	0.0182
Cross	0	0	.	.	.
Residual	1.0000	7322.73	268.69	27.25	<.0001

Appendix Table 18 GCA/SCA estimates with corresponding T-test (P=0.05) for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 1	- 24.7995	15.2140	1480	-1.63	0.1033
DAM 10	- 45.4955	15.2412	1480	-2.99	0.0029
DAM 11	10.2043	12.1881	1480	0.84	0.4026
DAM 12	- 59.4547	14.5064	1480	-4.10	<.0001
DAM 13	60.4941	21.2309	1480	2.85	0.0044
DAM 14	- 29.1778	17.1418	1480	-1.70	0.0889
DAM 15	23.5872	14.4909	1480	1.63	0.1038
DAM 16	24.4196	28.3809	1480	0.86	0.3897
DAM 18	57.8824	17.7588	1480	3.26	0.0011
DAM 19	-0.3281	14.5993	1480	-0.02	0.9821
DAM 2	12.2091	15.9535	1480	0.77	0.4442
DAM 20	6.2279	15.2221	1480	0.41	0.6825
DAM 3	- 21.8796	25.8394	1480	-0.85	0.3973
DAM 4	17.4613	16.8679	1480	1.04	0.3008
DAM 5	-7.3654	18.6712	1480	-0.39	0.6933
DAM 6	46.3458	14.6558	1480	3.16	0.0016
DAM 7	- 35.0115	15.0933	1480	-2.32	0.0205
DAM 8	11.6990	12.9791	1480	0.90	0.3675
DAM 9	- 47.0187	14.8313	1480	-3.17	0.0016

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
SIRE 1	53.9887	19.4715	1480	2.77	0.0056
SIRE 10	58.7832	14.2127	1480	4.14	<.0001
SIRE 11	-17.5024	14.0829	1480	-1.24	0.2141
SIRE 12	19.0782	16.7352	1480	1.14	0.2545
SIRE 2	-74.1187	14.7094	1480	-5.04	<.0001
SIRE 3	-14.9721	14.5224	1480	-1.03	0.3027
SIRE 4	5.5255	17.8006	1480	0.31	0.7563
SIRE 5	5.8792	17.1939	1480	0.34	0.7324
SIRE 6	-9.2582	15.1569	1480	-0.61	0.5414
SIRE 7	-13.7118	13.9885	1480	-0.98	0.3271
SIRE 8	6.6053	17.4065	1480	0.38	0.7044
SIRE 9	-20.2970	16.6829	1480	-1.22	0.2239
10x3	0
10x5	0
11x10	0
11x11	0
11x3	0
11x7	0
12x10	0
12x8	0
13x1	0
13x12	0
14x6	0
15x6	0
15x7	0
16x4	0
18x1	0
18x9	0
19x11	0

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
19x9	0
1x12	0
1x3	0
20x2	0
20x3	0
2x3	0
2x5	0
3x1	0
4x1	0
4x7	0
5x10	0
6x11	0
6x2	0
7x12	0
7x3	0
8x10	0
8x2	0
8x6	0
9x4	0
9x7	0

Appendix Table 19 ANOVA for mean performance by parental strains following GLM Procedure for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	7	533951.04	76278.72	8.94	<.0001
Error	150 9	12880632.6 1	8535.87		
Corrected Total	151 6	13414583.6 5			

Appendix Table 20 Mean comparison of performance by parental strains using Scheffe Test for final body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Means with the same letter are not significantly different.				
Scheffe Grouping	Mean	N	dam	
	A	260.00	5	8
	A			
B	A	215.13	78	7
B	A			
B	A	209.46	148	4
B	A			
B	A	202.05	239	3
B	A			
B	A	201.97	497	9
B	A			
B	A	192.99	321	6
B				
B		152.98	104	2
B				
B		152.08	125	1

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 21 The Type 3 Mixed Procedure of analysis of variance for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	18	1122919	62384	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	1480	8.84	<.0001
sire	11	882814	80256	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	1480	11.38	<.0001
dam*sire	7	46054	6579.159764	Var(Residual) + Q(dam*sire)	MS(Residual)	1480	0.93	0.4800
Residual	1480	10440639	7054.486114	Var(Residual)

Appendix Table 22 REML estimation of variance components for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
Dam	0.1871	1320.19	532.95	2.48	0.0066
Sire	0.1833	1293.47	619.75	2.09	0.0184
Cross	0	0	.	.	.
Residual	1.0000	7056.66	258.91	27.26	<.0001

Appendix Table 23 GCA/SCA estimates with corresponding T-test (P=0.05) for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
DAM 1	- 23.9430	14.6870	1480	-1.63	0.1033
DAM 10	- 43.2113	14.7060	1480	-2.94	0.0034
DAM 11	11.5210	11.7401	1480	0.98	0.3266
DAM 12	- 56.7031	14.0044	1480	-4.05	<.0001
DAM 13	57.4523 *	20.5523	1480	2.80	0.0053
DAM 14	- 26.8623	16.5961	1480	-1.62	0.1057
DAM 15	22.2547	14.0060	1480	1.59	0.1123
DAM 16	21.7013	27.3263	1480	0.79	0.4272
DAM 18	53.5325	17.1902	1480	3.11	0.0019
DAM 19	-0.8690	14.1011	1480	-0.06	0.9509
DAM 2	14.3252	15.4061	1480	0.93	0.3526
DAM 20	4.1863	14.7245	1480	0.28	0.7762
DAM 3	- 21.2656	24.9317	1480	-0.85	0.3938
DAM 4	17.1634	16.3409	1480	1.05	0.2937
DAM 5	-8.2298	18.0817	1480	-0.46	0.6491
DAM 6	43.4050	14.1753	1480	3.06	0.0022
DAM 7	- 32.4871	14.5680	1480	-2.23	0.0259
DAM 8	12.6917	12.5112	1480	1.01	0.3105
DAM 9	- 44.6623	14.3326	1480	-3.12	0.0019

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
SIRE 1	52.6480	18.9098	1480	2.78	0.0054
SIRE 10	56.5157	13.7779	1480	4.10	<.0001
SIRE 11	- 15.9389	13.6651	1480	-1.17	0.2436
SIRE 12	18.6552	16.2407	1480	1.15	0.2509
SIRE 2	- 71.9454	14.2898	1480	-5.03	<.0001
SIRE 3	- 14.9984	14.0598	1480	-1.07	0.2863
SIRE 4	4.6961	17.2947	1480	0.27	0.7860
SIRE 5	4.0668	16.6793	1480	0.24	0.8074
SIRE 6	-9.1548	14.7101	1480	-0.62	0.5338
SIRE 7	- 13.9157	13.5653	1480	-1.03	0.3051
SIRE 8	5.9452	16.9186	1480	0.35	0.7253
SIRE 9	- 16.5737	16.1963	1480	-1.02	0.3063
10x3	0
10x5	0
11x10	0
11x11	0
11x3	0
11x7	0
12x10	0
12x8	0
13x1	0
13x12	0
14x6	0
15x6	0
15x7	0
16x4	0
18x1	0
18x9	0
19x11	0

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
19x9	0
1x12	0
1x3	0
20x2	0
20x3	0
2x3	0
2x5	0
3x1	0
4x1	0
4x7	0
5x10	0
6x11	0
6x2	0
7x12	0
7x3	0
8x10	0
8x2	0
8x6	0
9x4	0
9x7	0

Appendix Table 24 ANOVA for mean performance by parental strains following GLM Procedure for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	7	515345.82	73620.83	9.00	<.0001
Error	150 9	12350203.0 1	8184.36		
Corrected Total	151 6	12865548.8 3			

Appendix Table 25 Mean comparison of performance by parental strains using Scheffe Test for body weight gain of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in split-pond for additional 245 days of communal rearing.

Means with the same letter are not significantly different.				
Scheffe Grouping	Mean	N	dam	
A	244.40	5	8	
A				
B	205.62	78	7	
B				
B	199.71	148	4	
B				
B	191.97	497	9	
B				
B	191.31	239	3	
B				
B	182.81	321	6	
B				
B	143.54	104	2	
B				
B	143.10	125	1	

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 26 The Type 3 Mixed Procedure of analysis of variance for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	19	4380.200908	230.536890	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	66	10.11	<.0001
sire	11	341.735121	31.066829	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	66	1.36	0.2121
dam*sire	8	276.019249	34.502406	Var(Residual) + Q(dam*sire)	MS(Residual)	66	1.51	0.1699
Residual	66	1505.60	22.812053	Var(Residual)

Appendix Table 27 REML estimation of variance components for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	3.7327	83.8272	31.0813	2.70	0.0035
sire	0.07975	1.7910	3.3471	0.54	0.2963
cross	0.1178	2.6454	4.5594	0.58	0.2809
Residual	1.0000	22.4578	3.8466	5.84	<.0001

Appendix Table 28 GCA/SCA estimates with corresponding T-test (P=0.05) for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 1	4.6814	3.0538	66	1.53	0.1301
DAM 10	-3.4484	3.0614	66	-1.13	0.2641
DAM 11	-0.3669	2.7089	66	-0.14	0.8927
DAM 12	-4.2204	3.0698	66	-1.37	0.1738
DAM 13	6.8620	3.8395	66	1.79	0.0785
DAM 14	-2.7981	3.7015	66	-0.76	0.4524
DAM 15	1.1446	3.0548	66	0.37	0.7091
DAM 16	2.1887	4.7876	66	0.46	0.6491
DAM 17	33.7885	3.6748	66	9.19	<.0001
DAM 18	-3.9315	3.0570	66	-1.29	0.2029
DAM 19	-3.2957	3.0744	66	-1.07	0.2876
DAM 2	-5.1492	3.0614	66	-1.68	0.0973
DAM 20	-5.7670	3.3130	66	-1.74	0.0864
DAM 3	-3.4358	3.3209	66	-1.03	0.3046
DAM 4	-0.8147	3.0391	66	-0.27	0.7895
DAM 5	-0.4491	3.6843	66	-0.12	0.9034
DAM 6	-4.4154	3.0695	66	-1.44	0.1550
DAM 7	1.3993	3.0538	66	0.46	0.6483
DAM 8	-3.5701	2.7928	66	-1.28	0.2056

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 9	-8.4022	3.0661	66	-2.74	0.0079
SIRE 1	0.6935	1.1823	66	0.59	0.5595
SIRE 10	1.4358	1.1577	66	1.24	0.2193
SIRE 11	0.2093	1.1763	66	0.18	0.8594
SIRE 12	0.5552	1.2198	66	0.46	0.6505
SIRE 2	-0.7100	1.1965	66	-0.59	0.5550
SIRE 3	-0.2080	1.1164	66	-0.19	0.8528
SIRE 4	-0.2640	1.2745	66	-0.21	0.8366
SIRE 5	-0.1649	1.2394	66	-0.13	0.8946
SIRE 6	-0.3717	1.2129	66	-0.31	0.7602
SIRE 7	-0.2955	1.1398	66	-0.26	0.7962
SIRE 8	-0.3317	1.2546	66	-0.26	0.7923
SIRE 9	-0.5481	1.2350	66	-0.44	0.6587
10x3	-0.3494	1.5238	66	-0.23	0.8193
10x5	0.2406	1.5244	66	0.16	0.8751
11x10	0.7460	1.4869	66	0.50	0.6175
11x11	0.03531	1.4874	66	0.02	0.9811
11x3	-0.2893	1.5533	66	-0.19	0.8528
11x7	-0.5036	1.4866	66	-0.34	0.7359
12x10	0.3011	1.5254	66	0.20	0.8442
12x8	-0.4343	1.5260	66	-0.28	0.7769

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
13x1	-0.2300	1.5800	66	-0.15	0.8847
13x12	0.4465	1.5801	66	0.28	0.7784
14x6	-0.08830	1.6049	66	-0.06	0.9563
15x6	0.6002	1.5251	66	0.39	0.6952
15x7	-0.5640	1.5248	66	-0.37	0.7126
16x4	0.06907	1.6077	66	0.04	0.9659
17x1	1.0663	1.6048	66	0.66	0.5087
18x1	0.7037	1.5255	66	0.46	0.6461
18x9	-0.8278	1.5260	66	-0.54	0.5893
19x11	-0.1223	1.5256	66	-0.08	0.9364
19x9	0.01826	1.5258	66	0.01	0.9905
1x12	-0.5820	1.5241	66	-0.38	0.7038
1x3	0.7297	1.5236	66	0.48	0.6336
20x2	-0.3736	1.5668	66	-0.24	0.8123
20x3	0.1916	1.5574	66	0.12	0.9025
2x3	0.3217	1.5238	66	0.21	0.8335
2x5	-0.4842	1.5244	66	-0.32	0.7518
3x1	-0.05267	1.5579	66	-0.03	0.9731
3x8	-0.05576	1.5673	66	-0.04	0.9717
4x1	-0.4630	1.5245	66	-0.30	0.7623
4x7	0.4373	1.5246	66	0.29	0.7752

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
5x10	- 0.01417	1.6048	66	-0.01	0.993 0
6x11	0.3960	1.5251	66	0.26	0.795 9
6x2	-0.5354	1.5252	66	-0.35	0.726 7
7x12	0.9556	1.5241	66	0.63	0.532 8
7x3	-0.9114	1.5236	66	-0.60	0.551 8
8x10	1.0879	1.4952	66	0.73	0.469 4
8x2	-0.1398	1.4960	66	-0.09	0.925 8
8x6	-1.0608	1.4962	66	-0.71	0.480 8
9x4	-0.4590	1.5260	66	-0.30	0.764 5
9x7	0.1938	1.5255	66	0.13	0.899 3

Appendix Table 29 ANOVA for mean performance by parental strains following GLM Procedure for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.53794931	0.06724366	21.72	<.0001
Error	96	0.29726650	0.00309653		
Corrected Total	104	0.83521581			

Appendix Table 30 Mean comparison of performance by parental strains using Tukey-Kramer Test for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in flow-through system for 311 days of separate tank rearing.

Tukey- Kramer Comparison Lines for Least Squares Means of dam LS-means with the same letter are not significantly different.			
	cv LSMEAN	dam	LSMEAN Number
A	0.68062432	5	5
B	0.32076927	8	8
B			
B	0.29084218	9	9
B			
B	0.28137894	3	3
B			
B	0.27611228	6	6
B			
B	0.25900928	4	4
B			
B	0.25653502	2	2
B			
B	0.23849914	7	7
B			
B	0.20307101	1	1
The LINES display does not reflect all significant comparisons. The following additional pairs are significantly different: (9,1)			

Note: Dam strain 1 – AR; 2 – ARMK; 3 – KR; 4 – KS; 5 – KTh; 6 – Mix; 7 RG; 8 – Thompson; 9 - Tishomingo

Appendix Table 31 The Type 3 Mixed Procedure of analysis of variance for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	19	7625.773812	401.356516	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	41	3.18	0.0009
sire	11	4021.114628	365.555875	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	41	2.90	0.0065
dam*sire	7	2664.769003	380.681286	Var(Residual) + Q(dam*sire)	MS(Residual)	41	3.02	0.0118
Residual	41	5167.79	126.043691	Var(Residual)

Appendix Table 32 REML estimation of variance components for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	0.1331	21.1784	37.2660	0.57	0.2849
sire	0	0	.	.	.
cross	0.2932	46.6488	56.7361	0.82	0.2055
Residual	1.0000	159.10	44.1313	3.61	0.0002

Appendix Table 33 GCA/SCA estimates with corresponding T-test (P=0.05) for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 1	0.5588	4.0186	41	0.14	0.8901
DAM 10	4.7344	4.1081	41	1.15	0.2558
DAM 11	-0.9771	3.6067	41	-0.27	0.7878
DAM 12	-0.1630	3.9083	41	-0.04	0.9669
DAM 13	-0.08875	4.2069	41	-0.02	0.9833
DAM 14	0.2030	4.3866	41	0.05	0.9633
DAM 15	-2.5861	4.0456	41	-0.64	0.5262
DAM 16	-0.6762	4.3866	41	-0.15	0.8782
DAM 17	2.0262	4.1964	41	0.48	0.6318
DAM 18	-3.1508	4.0456	41	-0.78	0.4405
DAM 19	-0.8703	4.0186	41	-0.22	0.8296
DAM 2	-3.4252	4.0456	41	-0.85	0.4021
DAM 20	-0.7279	4.3866	41	-0.17	0.8690
DAM 3	3.6011	4.0456	41	0.89	0.3786
DAM 4	-1.6795	4.0186	41	-0.42	0.6782
DAM 5	1.6985	4.1964	41	0.40	0.6878
DAM 6	-0.3871	3.9617	41	-0.10	0.9226
DAM 7	3.3553	4.1081	41	0.82	0.4188
DAM 8	0.3246	3.6928	41	0.09	0.9304

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 9	-1.7700	4.0456	41	-0.44	0.6640
SIRE 1	0
SIRE 10	0
SIRE 11	0
SIRE 12	0
SIRE 2	0
SIRE 3	0
SIRE 4	0
SIRE 5	0
SIRE 6	0
SIRE 7	0
SIRE 8	0
SIRE 9	0
10x3	-2.0029	5.6634	41	-0.35	0.7254
10x5	12.4312	6.0890	41	2.04	0.0477
11x10	-2.5028	5.2743	41	-0.47	0.6376
11x11	5.2250	5.2743	41	0.99	0.3277
11x3	-2.4054	6.0643	41	-0.40	0.6937
11x7	-2.4691	5.2743	41	-0.47	0.6422
12x10	-0.3384	5.3454	41	-0.06	0.9498
12x8	-0.02065	5.3454	41	-0.00	0.9969
13x1	1.1776	6.0942	41	0.19	0.8477
13x12	-1.3731	6.0942	41	-0.23	0.8229
14x6	0.4471	6.1037	41	0.07	0.9420
15x6	-4.7154	6.0858	41	-0.77	0.4429
15x7	-0.9808	5.3787	41	-0.18	0.8562
16x4	-1.4894	6.1037	41	-0.24	0.8084

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
17x1	4.4630	5.4161	41	0.82	0.4147
18x1	-4.3958	5.3787	41	-0.82	0.4185
18x9	-2.5444	6.0858	41	-0.42	0.6781
19x11	1.5697	5.6504	41	0.28	0.7826
19x9	-3.4866	5.6504	41	-0.62	0.5406
1x12	-0.6326	5.6504	41	-0.11	0.9114
1x3	1.8635	5.6504	41	0.33	0.7432
20x2	-1.6033	6.1037	41	-0.26	0.7941
20x3	-4.5245	5.3787	41	-0.84	0.4051
2x3	-3.0200	6.0858	41	-0.50	0.6224
2x5	-1.9224	5.3787	41	-0.36	0.7226
3x1	9.8543	6.0858	41	1.62	0.1131
3x8	-2.1103	5.6504	41	-0.37	0.7107
4x1	-1.5890	5.6504	41	-0.28	0.7799
4x7	3.7413	5.4161	41	0.69	0.4936
5x10	-0.08137	5.3583	41	-0.02	0.9880
6x11	-0.7713	5.6422	41	-0.14	0.8919
6x2	4.3020	6.0890	41	0.71	0.4839
7x12	3.0886	5.6634	41	0.55	0.5885
7x3	-3.0572	5.2943	41	-0.58	0.5668
8x10	6.2275	5.2943	41	1.18	0.2463

Estimates					
Parents/ Cross	Estimate	Standard Error	DF	t Value	Pr > t
8x2	-2.4553	5.2943	41	-0.46	0.6453
8x6	-0.4198	6.0858	41	-0.07	0.9453
9x4	-3.4790	5.3787	41	-0.65	0.5214

Appendix Table 34 ANOVA for mean performance by parental cross following GLM Procedure for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	20	7324.18037	366.20902	2.23	0.0092
Error	58	9512.73205	164.01262		
Corrected Total	78	16836.91242			

Appendix Table 35 Mean comparison of performance by parental cross using Tukey-Kramer Test for coefficient of variation in body weight of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny in recirculating system for additional 245 days of separate tank rearing.

Tukey-Kramer Comparison Lines for Least Squares Means of Parental Cross				
LS-means with the same letter are not significantly different.				
		cv LSMEAN	Cross	LSMEAN Number
	A	89.99541	ARMKxDB	12
	A			
B	A	42.14426	KRxTBB	19
B	A			
B	A	41.99625	KThxDR	2
B	A			
B	A	36.53805	TishxRG	13
B	A			

Tukey- Kramer Comparison Lines for Least Squares Means of Parental Cross				
LS-means with the same letter are not significantly different.				
		cv LSMEAN	Cross	LSMEAN Number
B	A	36.46542	KRxDB	16
B	A			
B	A	35.59495	KRxRG	18
B	A			
B	A	34.78819	KSxDB	20
B	A			
B	A	32.03125	KRxDR	17
B	A			
B	A	31.56692	MixxTBB	6
B	A			
B	A	31.54520	MixxRG	5
B	A			
B	A	29.74938	ARMKxTB B	15
B	A			
B	A	28.07211	TishxDR	11
B	A			
B	A	25.46654	TishxDB	10
B	A			
B	A	24.22536	KSxDR	21
B	A			
B	A	23.18816	ThxDB	9
B				
B		22.62508	ARxDB	1
B				
B		18.84733	TishxTBB	14
B				
B		18.77399	MixxDB	3
B				
B		17.88942	MixxDR	4
B				
B		17.34018	RGxTBB	8
B				
B		13.68837	RGxDB	7
The LINES display does not reflect all significant comparisons. The following additional pairs are significantly different: (12,16) (12,18) (12,20) (12,17) (12,6) (12,5) (12,15) (12,11) (12,10) (12,21)				

Appendix Table 36 The Type 3 Mixed Procedure of analysis of variance for survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	19	12734	670.185319	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	67	2.13	0.0122
sire	11	10066	915.116399	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	67	2.91	0.0034
dam*sire	9	4751.611118	527.956791	Var(Residual) + Q(dam*sire)	MS(Residual)	67	1.68	0.1110
Residual	67	21045	314.106132	Var(Residual)

Appendix Table 37 REML estimation of variance components for survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	0.1902	63.7632	53.5457	1.19	0.1169
sire	0.3253	109.08	64.6532	1.69	0.0458
cross	0	0	.	.	.
Residual	1.0000	335.28	53.0717	6.32	<.0001

Appendix Table 38 GCA/SCA estimates with corresponding T-test (P=0.05) for survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 1	2.5436	5.9755	67	0.43	0.6717
DAM 10	0.8185	6.0172	67	0.14	0.8922
DAM 11	4.6496	5.2101	67	0.89	0.3754
DAM 12	5.0202	6.0903	67	0.82	0.4127
DAM 13	0.4764	6.9063	67	0.07	0.9452
DAM 14	4.3685	6.7570	67	0.65	0.5202
DAM 15	-2.7308	5.9508	67	-0.46	0.6478
DAM 16	-0.6678	7.4238	67	-0.09	0.9286
DAM 17	-11.9721	6.6694	67	-1.80	0.0772
DAM 18	-5.2013	6.0152	67	-0.86	0.3903
DAM 19	4.7178	6.0835	67	0.78	0.4408
DAM 2	2.9751	6.0172	67	0.49	0.6226
DAM 20	-4.8381	6.0697	67	-0.80	0.4282
DAM 3	5.6405	6.3495	67	0.89	0.3775
DAM 4	-7.1048	5.8837	67	-1.21	0.2315
DAM 5	-0.4136	6.6661	67	-0.06	0.9507
DAM 6	-8.8653	5.7783	67	-1.53	0.1297
DAM 7	3.9399	5.9755	67	0.66	0.5119
DAM 8	1.8398	5.4473	67	0.34	0.7366

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
DAM 9	4.8039	6.1049	67	0.79	0.4341
SIRE 1	-22.5061	5.9158	67	-3.80	0.0003
SIRE 10	-8.6100	5.7534	67	-1.50	0.1392
SIRE 11	5.5067	6.2921	67	0.88	0.3846
SIRE 12	-5.6789	6.7959	67	-0.84	0.4063
SIRE 2	2.8739	6.4566	67	0.45	0.6577
SIRE 3	4.2565	5.5364	67	0.77	0.4447
SIRE 4	3.7607	7.6520	67	0.49	0.6247
SIRE 5	1.2749	7.0887	67	0.18	0.8578
SIRE 6	3.4663	6.4253	67	0.54	0.5914
SIRE 7	7.2911	5.8804	67	1.24	0.2193
SIRE 8	5.8336	7.6141	67	0.77	0.4463
SIRE 9	2.5314	7.0516	67	0.36	0.7207
10x3	0
10x5	0
11x10	0
11x11	0
11x3	0
11x7	0
12x10	0
12x8	0
13x1	0
13x12	0
14x6	0
15x6	0
15x7	0
16x4	0
17x1	0

Estimates					
Parents/ Cross	Estimate	Standard Error	D F	t Value	Pr > t
18x1	0
18x9	0
19x11	0
19x9	0
1x12	0
1x3	0
20x2	0
20x3	0
2x3	0
2x5	0
3x1	0
3x8	0
4x1	0
4x7	0
5x10	0
6x10	0
6x11	0
6x2	0
7x12	0
7x3	0
8x10	0
8x2	0
8x6	0
9x4	0
9x7	0

Appendix Table 39 ANOVA for mean performance by parental strains following GLM Procedure for survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	3	13434.96016	4478.32005	11.12	<.0001
Error	103	41468.88548	402.61054		
Corrected Total	106	54903.84564			

Appendix Table 40 Mean comparison of performance by parental strains using Tukey-Kramer Test for survival rate of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny from natural *Aeromonas hydrophila* infection.

Tukey-Kramer Comparison Lines for Least Squares Means of Sire			
LS-means with the same letter are not significantly different.			
	aer LSMEAN	Sire	LSMEAN Number
A	90.89312	4	4
A			
A	90.81245	1	1
A			
A	86.42813	3	3
B	64.07923	2	2

Note: Sire strain 1 – DB; 2 – DR; 3 – RG; 4 – TBB

Appendix Table 41 The Type 3 Mixed Procedure of analysis of variance for dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny.

Type 3 Analysis of Variance								
Source	DF	Sum of Squares	Mean Square	Expected Mean Square	Error Term	Error DF	F Value	Pr > F
dam	15	391.322448	26.088163	Var(Residual) + Q(dam,dam*sire)	MS(Residual)	262	4.61	<.0001
sire	10	305.088231	30.508823	Var(Residual) + Q(sire,dam*sire)	MS(Residual)	262	5.39	<.0001
dam*sire	4	22.861745	5.715436	Var(Residual) + Q(dam*sire)	MS(Residual)	262	1.01	0.4028
Residual	262	1482.90	5.659907	Var(Residual)

Appendix Table 42 REML estimation of variance components for dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny.

Covariance Parameter Estimates					
Cov Parm	Ratio	Estimate	Standard Error	Z Value	Pr > Z
dam	0.02144	0.1215	0.6955	0.17	0.4307
sire	0.07248	0.4108	0.4763	0.86	0.1942
cross	0.2337	1.3244	0.9241	1.43	0.0759
Residual	1.0000	5.6669	0.4956	11.43	<.0001

Appendix Table 43 GCA/SCA estimates with corresponding T-test (P=0.05) for dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny.

Estimates					
Label	Estimate	Standard Error	DF	t Value	Pr > t
DAM 1	-0.07989	0.3315	262	-0.24	0.8097
DAM 10	-0.1592	0.3315	262	-0.48	0.6315
DAM 11	0.1562	0.3241	262	0.48	0.6302
DAM 12	0.02149	0.3321	262	0.06	0.9484
DAM 14	-0.1463	0.3395	262	-0.43	0.6670
DAM 15	0.03570	0.3314	262	0.11	0.9143
DAM 18	0.04995	0.3398	262	0.15	0.8832
DAM 19	-0.06872	0.3319	262	-0.21	0.8361
DAM 2	0.1943	0.3315	262	0.59	0.5582
DAM 20	-0.00668	0.3323	262	-0.02	0.9840
DAM 4	0.1398	0.3406	262	0.41	0.6819
DAM 5	-0.05502	0.3393	262	-0.16	0.8713
DAM 6	-0.07372	0.3316	262	-0.22	0.8242
DAM 7	-0.09561	0.3315	262	-0.29	0.7732
DAM 8	0.1013	0.3243	262	0.31	0.7551
DAM 9	-0.01368	0.3321	262	-0.04	0.9672
SIRE 10	0.5586	0.4968	262	1.12	0.2619
SIRE 11	0.01382	0.5190	262	0.03	0.9788
SIRE 12	0.1308	0.5482	262	0.24	0.8116

Estimates					
Label	Estimate	Standard Error	DF	t Value	Pr > t
SIRE 2	-0.6028	0.5231	262	-1.15	0.2502
SIRE 3	-0.7293	0.4795	262	-1.52	0.1295
SIRE 4	-0.1214	0.5865	262	-0.21	0.8362
SIRE 5	0.3059	0.5482	262	0.56	0.5773
SIRE 6	0.1187	0.5195	262	0.23	0.8194
SIRE 7	0.1739	0.5003	262	0.35	0.7284
SIRE 8	0.05690	0.5865	262	0.10	0.9228
SIRE 9	0.09479	0.5485	262	0.17	0.8629
10x3	-1.2289	0.7414	262	-1.66	0.0986
10x5	-0.5059	0.7749	262	-0.65	0.5144
11x10	1.7558	0.7478	262	2.35	0.0196
11x11	0.5659	0.7586	262	0.75	0.4564
11x7	-0.6189	0.7492	262	-0.83	0.4095
12x10	0.05080	0.7497	262	0.07	0.9460
12x8	0.1835	0.7942	262	0.23	0.8175
14x6	-1.5941	0.7635	262	-2.09	0.0378
15x6	0.9749	0.7608	262	1.28	0.2012
15x7	-0.5858	0.7515	262	-0.78	0.4364
18x9	0.5444	0.7775	262	0.70	0.4844
19x11	-0.5102	0.7607	262	-0.67	0.5030
19x9	-0.2388	0.7746	262	-0.31	0.7581

Estimates					
Label	Estimate	Standard Error	DF	t Value	Pr > t
1x12	-0.2003	0.7749	262	-0.26	0.7962
1x3	-0.6704	0.7414	262	-0.90	0.3667
20x2	-0.6591	0.8260	262	-0.80	0.4256
20x3	0.5862	0.7419	262	0.79	0.4302
2x3	0.6259	0.7414	262	0.84	0.3993
2x5	1.4922	0.7749	262	1.93	0.0552
4x7	1.5233	0.8203	262	1.86	0.0644
5x10	-0.5997	0.7529	262	-0.80	0.4265
6x11	-0.01109	0.7608	262	-0.01	0.9884
6x2	-0.7924	0.7628	262	-1.04	0.2998
7x12	0.6221	0.7749	262	0.80	0.4229
7x3	-1.6642	0.7414	262	-2.24	0.0256
8x10	0.5941	0.7477	262	0.79	0.4275
8x2	-0.4922	0.7604	262	-0.65	0.5180
8x6	1.0021	0.7583	262	1.32	0.1875
9x4	-0.3913	0.7941	262	-0.49	0.6226
9x7	0.2422	0.7512	262	0.32	0.7474

Appendix Table 44 ANOVA for mean performance by parental cross following GLM Procedure for dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny.

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	16	384.033369	24.002086	3.71	<.0001
Error	275	1778.674549	6.467907		
Corrected Total	291	2162.707917			

Appendix Table 45 Mean comparison of performance by parental cross using Tukey-Kramer Test for dressout percentage of channel catfish (*Ictalurus punctatus*) female × blue catfish (*I. furcatus*) male F1 hybrid progeny.

Tukey-Kramer Comparison Lines for Least Squares Means of Parental Cross						
LS-means with the same letter are not significantly different.						
				dress LSMEA N	Cross	LSMEA N Number
		A		61.56575	RGxDB	5
		A				
B		A		60.87204	TishxDR	8
B		A				
B		A		60.44303	KSxDR	17
B		A				
B		A	C	59.91281	TishxRG	10
B		A	C			
B		A	C	59.35864	KRxRG	14
B		A	C			
B	D	A	C	59.29353	RGxTBB	6
B	D	A	C			
B	D	A	C	59.15804	KSxDB	16
B	D	A	C			
B	D	A	C	58.90101	KRxDB	12
B	D	A	C			
B	D	A	C	58.84092	ARxDB	1
B	D	A	C			
B	D	A	C	58.76714	MixxDB	2
B	D	A	C			
B	D	A	C	58.61534	TishxDB	7
B	D	A	C			
B	D	A	C	58.58214	KRxDR	13

Tukey-Kramer Comparison Lines for Least Squares Means of Parental Cross						
LS-means with the same letter are not significantly different.						
				dress LSMEA N	Cross	LSMEA N Number
B	D	A	C			
B	D	A	C	58.42555	MixxRG	3
B	D	A	C			
B	D	A	C	58.35914	ARMKxD B	9
B	D		C			
B	D		C	58.10218	MixxTBB	4
	D		C			
	D		C	56.29161	ARMKxT BB	11
	D					
	D			55.73371	KRxTBB	15