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Pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture

Qingchao Xie[a,b], Hao Li[a], Yinhui Li[a], Jiaying Xie[a], Yong Zhao[a,b,c,*], Hongmin Zhang[a,b,*]

[a]*College of Food Science and Technology, Shanghai Ocean University, Shanghai 201306, China, email: y_zhao1975@163.com (Y. Zhao)*
[b]*Laboratory of Quality and Safety Risk Assessment for Aquatic Product on Storage and Preservation (Shanghai), Ministry of Agriculture and Rural Affairs, Shanghai 201306, China*
[c]*Shanghai Engineering Research Center of Aquatic Product Processing and Preservation, Shanghai 201306, China*

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ABSTRACT

Antibiotic resistance genes in aquaculture have different breeding effects on different kinds of aquatic animals. Therefore, the pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture were studied. Based on the whole genome selection model, the growth parameters were calculated, the genomic breeding values of different traits of animals were estimated, and the overall relationship matrix of pedigree structure was obtained; The noise variable is introduced to reduce breeding algebra, the influence of external environmental variables on genes and systems is comprehensively considered, and the noise statistical standard deviation is calculated; Trace the genetic breeding pedigree of aquaculture animals, construct the genetic breeding pedigree structure of aquaculture animals, and study the pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture. The experimental results show that the research content can better optimize and improve the genetic breeding of aquaculture animals and improve the yield of aquaculture.

Keywords: Aquaculture; Antibiotic; Drug resistance gene; Pollution characteristics; Diffusion mechanism

1. Introduction

Antibiotics are secondary metabolites that can interfere with cell growth and development, mainly from microorganisms. Penicillin was first discovered in the 1920s, and this chemical substance was the first antibiotic found [1,2]. Penicillin played a great role in World War II. It was very effective in controlling bacterial infection. As a new environmental pollutant, antibiotic resistance gene poses a potential threat to human health all over the world, especially the multi drug resistant pathogens caused by excessive use or abuse of antibiotics pose a severe challenge to clinical treatment. In aquaculture, a large number of antibiotics are often used to treat diseases and promote growth. Bacteria develop drug resistance under the pressure of antibiotic selection, antibiotic resistance genes (ARGs) are the internal cause of drug resistance. Previous studies found that drug-resistant bacteria can transfer the drug-resistant genes contained in them to other bacteria through animal excreta, and finally lead to the large-scale existence of drug-resistant bacteria [3,4]. Drug resistant bacteria (ARB) are some originally sensitive bacteria that become drug-resistant [5,6]. However, in the environment of low concentration of antibiotics, some bacteria that originally showed drug resistance are easy to lose drug resistance. This is because sensitive bacteria require less nutrients than drug-resistant bacteria and have more advantages in competition with drug-resistant bacteria. Therefore, the growth of drug-resistant bacteria

* Corresponding authors.

is inhibited. Therefore, reducing the abuse of antibiotics can reduce the risk of drug resistance. Generally speaking, long-term use of antibiotics is easy to lead to bacterial drug resistance.

Anupama and Wood [7] proposed the spatial separation and synergy of radially expanding microbial colonies under antibiotic stress. The antibiotic resistance in microbial communities reflects the combination of processes running on different scales. The spatiotemporal dynamics of bacterial colonies composed of drug-resistant and drug-sensitive cells under antibiotic stress were studied. Using plasmid encoded β- the conditional pathogenic bacterium Enterococcus faecalis with lactamase tracked the colony expansion kinetics and visualized the spatial pattern of fluorescent labeled populations exposed to antibiotics. Stennett et al. [8] proposed the effect of prolonging the duration of preventive antibiotics in the treatment of open fracture wounds due to differences in the degree of pollution, and determined the relationship between the duration of preventive antibiotics after the final wound closure of open fractures and deep surgical site infection. The different effects of prolonging the duration of antibiotics after closure on the probability of infection at the deep surgical site depend on the pollution degree of open fracture wound. Although the prolonged duration of antibiotics reduced the probability of deep surgical site infection in patients with seriously polluted wounds, the trend of increasing the probability of deep surgical site infection in slightly polluted wounds was observed. Although the above research has made some progress, it is not applicable to antibiotics in aquaculture. There is insufficient research on the drug resistance of pathogenic bacteria such as Aeromonas, Vibrio and Listeria monocytogenes isolated from aquatic products. The pollution of antibiotic resistance genes in aquatic products is serious, which brings very serious environmental and health problems to mankind. It is urgent to study the antibiotic resistance gene pollution of aquatic products to ensure food safety. Therefore, the characteristics and diffusion mechanism of antibiotic resistance gene pollution in aquaculture are put forward.

2. Whole genome selection model design and aquaculture genetic breeding method

2.1. Calculation of aquaculture growth parameters by genome-wide selection model

The whole genome selection model, also known as GS model, calculates the growth parameters in aquaculture genetics and breeding through high-density molecular markers [9]. Assuming that the number of individuals in aquaculture is i, the variant effect of gene is expressed in X, and the number of haplotype markers in the whole genome selection model is z, the general expression of the model is:

$$F(z) = \alpha X_i + \beta X_z + \lambda \tag{1}$$

In Eq. (1), $F(z)$ represents the vector of aquaculture traits, X_i represents the expression form of the characterization value of the vector in the fixed marker effect, X_z represents the vector composed of the genetic effect of molecules in the process of genome-wide selection, α and β represent the standard matrix under the genetic effect respectively, and λ represents the random error. Under this multivariate normal distribution, the genetic environmental error can be calculated, and the breeding value estimation of aquaculture unit trait genome can be obtained [10,11]. The formula is:

$$Y_{zz} = \sum_{i=1}^{n} B_i C_i \tag{2}$$

In Eq. (2), Y_{zz} represents the zz-th coordinate vector of the genetic breeding association matrix, B_i represents the i calculated value of the transposed vector of aquaculture genetic breeding, and C_i represents the predicted value of the i-th marker marked. The model estimated by linear deviation can adjust the normal distribution to a homogeneous vector and approximate the genetic variance to a mixed vector model [12,13]. By designing the frequency error parameters of the genome in the covariance matrix, the estimated values of genetic and breeding parameters can be obtained as follows:

$$R_m = \frac{W_{ab}}{Q_{cd}} \times Y_{zz} \tag{3}$$

In Eq. (3), R_m represents the estimation of genetic and breeding parameters based on environmental effects; W_{ab} represents the homogeneity normal distribution parameter representing genetic variance under fixed markers; Q_{cd} represents the normal distribution parameter under random marking. By introducing the dimension model into the kinship matrix, the overall parameters of the pedigree structure can be obtained:

$$E_{ab} = \frac{U \times U^T}{\sum_{i=1}^{n} N_i} \tag{4}$$

In Eq. (4), H_y represents the parameters of all gene samples in the $a \times b$ matrix structure, U and U^T represent the number of markers and marker matrix of gene samples respectively, and N_i represents the operation frequency of i allele in genetic breeding calculation. The linear estimation model of genome-wide selection can be obtained through the above equation, and then the growth parameters of aquaculture alleles can be calculated based on the model, which provides a theoretical basis for allelic effects.

2.2. Introducing noise variable to reduce breeding algebra

When considering the variables of the external environment, the selective influence of the gene itself on the system can be appropriately reduced. The noise limit related to additivity can be expressed as:

$$\begin{cases} P(x) = W_n \sin\left(\sqrt{\dfrac{2}{\delta_x}}\omega_x(t_a)\right) \\ P(y) = W_n \cos\left(\sqrt{\dfrac{2}{\delta_y}}\omega_y(t_b)\right) \end{cases} \tag{5}$$

In Eq. (5), $P(x)$ and $P(y)$ respectively represent the upper and lower bounds of noise under additive conditions [14], W_n represents the standard intensity of noise within the boundary, δ_x and δ_y represent that the standard correlation time within the noise boundary usually has a positive correlation with the noise intensity, ω_x and ω_y respectively represent the normal distribution curves of the upper and lower bounds of noise under standard conditions, and t_a and t_b respectively represent the mechanical time of normal distribution.

Generally, by converting the random equivalent noise into two mutually independent units, the independent standard of noise can be obtained, and then the property statistics of priority noise can be carried out through time delay [15,16]. When the delay time t_h is greater than the original time t_d, the two noises can be equivalent and Eq. (6) can be obtained:

$$D_j = \frac{\rho(t_h)}{\rho(t_d)} = 1 \tag{6}$$

In Eq. (6), ρ ( ) represents the two noises described above, and the ratio of the statistical results of the two noises is 1. Therefore, the noise fluctuation parameters of random genes can be obtained and introduced into the process of aquaculture genetics and breeding as variables, so as to reduce the breeding algebra.

2.3. Pedigree tracing of aquaculture genetics and breeding

By establishing the batch structure of aquaculture genetic breeding, the binary tree of aquaculture animal and plant lineage can be established [17]. The definition of this binary tree comes from the data structure, and is soon applied to various academic fields as an important tool to explore the source of a definition. In aquaculture genetics and breeding, neither parent node nor parent node can be changed. Through the genome-wide selection linear model designed above, a matrix solution that can reduce the number of iterations can be obtained:

$$H_{abpq} = N_n + F_r + G_{abc} \tag{7}$$

In Eq. (7), H_{abc} represents the a aquaculture animal, the number of breeding iterations of the b, and the number of days of the c individual; N_n represents the total number of descendants of aquaculture animals after several iterations; F_r represents the data after the individual effect is iteratively read by the indirect inverse matrix; G_{abc} represents the overall effect of the a aquaculture animal, the b breeding iteration, and the c individual. Through this formula, the effect of whole genome selection model on aquaculture genetics and breeding can be solved, and the pedigree of aquaculture genetics and breeding can be tracked. Based on the above, we can get a method to apply the whole genome selection model to aquaculture genetics and breeding.

3. Pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture

3.1. Characteristics of antibiotic resistance gene contamination in aquaculture

3.1.1. Treatment and resource utilization of aquaculture waste

Aquaculture wastewater contains high concentrations of organic pollutants, ammonia nitrogen and suspended solids. If it is not effectively treated, it will pose a threat to the urban environment, drinking water sources and agricultural ecological environment [18]. In recent years, intensive aquaculture has developed rapidly. More and more large and medium-sized aquaculture plants have gradually replaced the traditional small and scattered aquaculture methods. This intensive culture is conducive to standardized management, unified feeding technology, improve production efficiency and increase economic benefits. However, due to the greatly increased breeding density, the feces produced every day are highly concentrated, and the scouring water of aquaculture plant site is also greatly increased, which not only brings great challenges to the treatment of fecal sewage, but also brings great pressure to the surrounding receiving environment. Intensive livestock and poultry breeding started late, but developed rapidly. The fecal pollution discharged by aquaculture plants has become a new pollution source in many cities and rural areas. Many large and medium-sized aquaculture plants have built on-site fecal sewage treatment facilities, but the operation and treatment effect are not good. Generally speaking, the fecal sewage treatment of large-scale aquaculture plants mainly includes three modes: returning to the field mode, no power natural treatment mode and industrialized treatment mode.

3.1.1.1. Returning field mode

That is, fecal sewage is returned to the field for agriculture as fertilizer, which is the treatment method adopted by traditional decentralized aquaculture. The process flow is shown in Fig. 1.

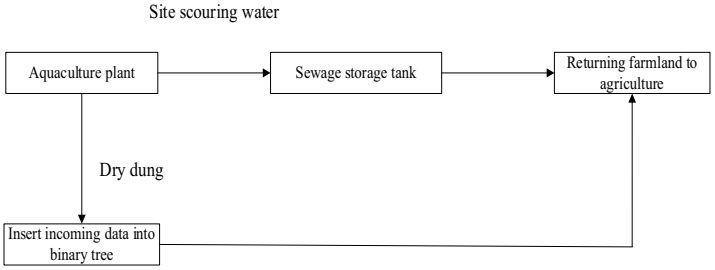

Fig. 1. Process flow of field returning mode.

Most of the feces will be cleaned out of the aquaculture plant site by manual fecal cleaning. The feces will be packaged for export or used to produce organic fertilizer, and finally returned to the field for agriculture. A small amount of residual feces is washed with water, fecal and urine wastewater enters the sewage storage tank, and the fecal water is used as fertilizer for the surrounding farmland. This treatment model uses the ecosystem composed of soil microorganism plant to realize the ecological treatment of harmless and stable fecal pollution and resource recovery and utilization. It is applicable to remote areas with enough farmland to receive fecal pollution, and the scale of aquaculture plant is within the specified range. The utility model has the advantages of less investment and low energy consumption. But the disadvantages are obvious: large floor area, small scope of use and great environmental harm.

3.1.1.2. Unpowered natural treatment mode

On the basis of returning farmland model, anaerobic digestion is the main body, combined with natural treatment units such as oxidation pond or land management system and constructed wetland, which is widely used in biogas research and promotion. The process flow is shown in Fig. 2.

After manual fecal cleaning, the wastewater from the aquaculture plant is washed. The feces and feed residues are intercepted through the grid solid-liquid separation. The dry feces and the residues intercepted by the grid are packaged and sold or used for the production of organic fertilizer. The wastewater after solid-liquid separation enters the anaerobic digestion tank. Under the action of anaerobic microorganisms, some organic matter is degraded and some pathogenic bacteria are killed or inhibited. The addition of fillers in the anaerobic biofilter is conducive to the attachment of microorganisms and further remove organic pollutants. Microorganisms in facultative anaerobic filter can further remove organic pollutants. The effluent enters oxidation pond, land treatment system or constructed wetland, etc. The utility model has the advantages of less investment, less energy consumption, simple equipment, low environmental pressure, and can recover energy such as biogas. The disadvantages are occupation of land resources, low load and potential threat to the ecological environment.

3.1.1.3. Factory processing mode

The main processes are pretreatment, anaerobic treatment, aerobic treatment, post-treatment, sludge treatment and utilization of biogas purifier. The design parameters and structure are more complex. Compared with the field return mode and non-power natural treatment mode, it has high technical content, complex process, wide application range and large treatment load. However, the investment is relatively large, the energy consumption is high and the operation cost is high, which requires special technical personnel for management. The process flow is shown in Fig. 3.

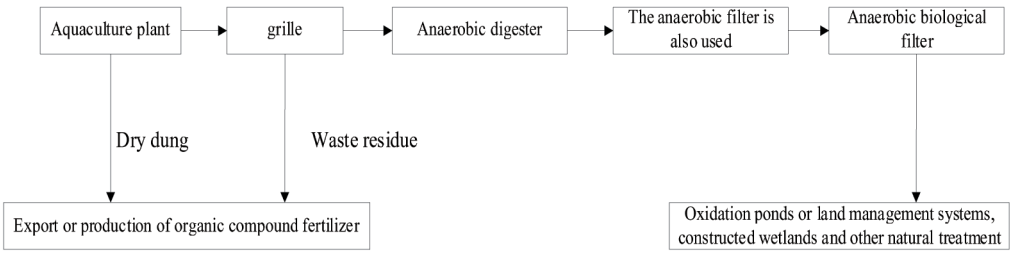

Fig. 2. Process flow of unpowered natural treatment mode.

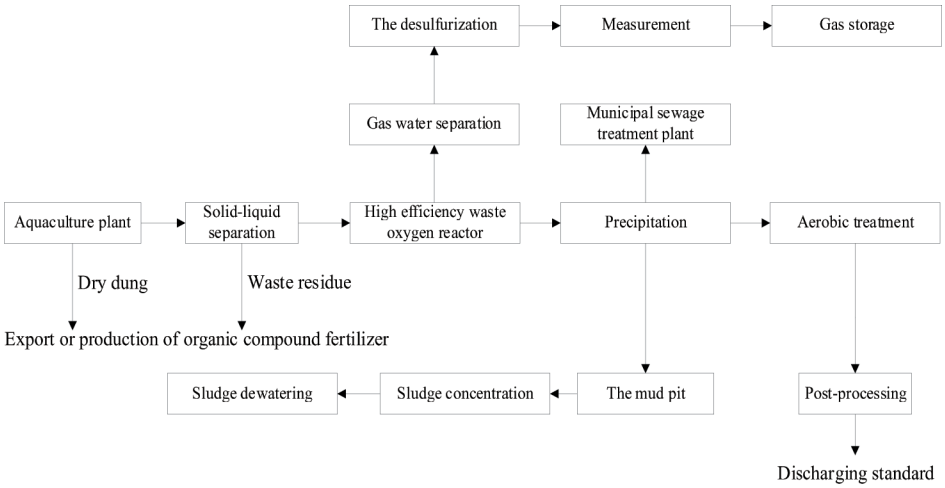

Fig. 3. Process flow of industrialized treatment mode.

At present, the application of these three treatment modes in intensive large-scale pig farms is not invariable. The three modes are combined according to local conditions to gradually form the sewage treatment and comprehensive utilization of aquaculture plants, such as biogas (anaerobic) – returning to the field, biogas (anaerobic) – natural treatment and biogas (anaerobic) – aerobic treatment. The core of these three comprehensive treatment modes is biogas fermentation. To sum up, anaerobic + aerobic biological treatment is the main method to control the wastewater pollution of aquaculture plant site, supplemented by physicochemical method, natural treatment and other methods. At present, the purpose of wastewater treatment in aquaculture plants has shifted from the traditional removal of high concentration organic pollutants and suspended solids to the removal of nutrients such as nitrogen and phosphorus, so as to meet the requirements of controlling the eutrophication of receiving water. The new biological denitrification process has been applied to the treatment of pig wastewater with high ammonia nitrogen.

3.1.2. Pollution level of antibiotic resistance genes in aquaculture environment

From the perspective of environmental pollution, the existing sewage treatment process design does not aim at the removal of new organic pollutants such as antibiotics, so antibiotics are largely released into the environment from agricultural and urban sewage channels. After entering the environment, the selection pressure produced by antibiotics makes the drug-resistant bacteria gradually screened out, and the drug-resistant genes are also screened; In addition, after removing the pressure of antibiotics, the drug resistance genes still spread and spread with the proliferation of bacteria; From the gene environment of the resistant genes, integrons, gene cassettes, plasmids and other mobile elements integrate various genotypes to form simultaneous interpreting and multidrug resistance, and when a class of antibiotics is selected, many genes will be screened and expanded together. At the same time, after the cell dies, the released genes can also be dissociated in various environmental media, and finally transferred to the cell through transformation. Therefore, drug resistance gene is regarded as a new environmental pollutant. The research methods of this new type of environmental pollutants have also changed from micro traditional bacterial isolation and culture method to macro non culture method.

Antibiotics commonly used in aquaculture are mainly sulfonamides, penicillins, macrolides, quinolones, florfenicol and tetracyclines. The corresponding research on the pollution of antibiotic resistance genes in aquaculture environment also focuses on the above drug resistance types. The research angles mainly include molecular mechanism, genome and gene epidemic investigation. At present, the research on drug resistance of aquaculture bacteria mainly focuses on the isolated strains related to aquatic pathogens.

Salmonella has 90% resistance to bacitracin, penicillin and neomycin, and has different resistance to antibiotics such as chloramphenicol, oxytetracycline, amoxicillin, gentamicin, polymyxin B and naphthyridic acid. The drug resistance genotypes were *gyrA* gene mutation (naphthyridic acid), acetyltransferase (chloramphenicol) and ampicillin.

Vibrio showed resistance to ampicillin, carboxybenzylpenicillin, kanamycin and cephalothin, but most of the existing research reports were limited to the isolation and identification of Vibrio and drug resistance phenotype, and almost no research reported the drug resistance gene carried by Vibrio. Vibrio isolated from mariculture fish carry a variety of integron like mobile elements, which mediate the tolerance of Vibrio to tetracycline, rifampicin antibiotics, mercury and quaternary ammonium compounds. Some elements contain *tetA* and *tetR* genes, indicating that Vibrio also has a large number of antibiotic resistance genes.

Enterobacteriaceae in aquaculture environment has a resistance rate of up to 50% to ampicillin, tetracycline and trimethoprim, carrying a variety of tetracycline resistance genes and a class of integron elements. *E. coli* also carries a variety of tetracycline resistance genes, sulfonamide resistance genes, ESBLs genes and PMQR genes. Enterococci were mainly found to carry tetracycline and erythromycin resistance genes.

A new tetracycline resistance gene *tet47* and multidrug resistance plasmids carrying tetracycline + kanamycin + streptomycin or macrolides + tetracycline + aminoglycosides + chloramphenicols were also found in aquaculture. There are many strains resistant to sulfamethoxazole/trimethoprim, tetracycline, erythromycin or cefotaxime in feed, fish and aquaculture water environment, which carry drug resistance genes.

In conclusion, the drug resistance genes in aquaculture environment mainly include: (1) quinolone resistance genes: DNA gyrase gene and topoisomerase gene; (2) tetracycline *tet* gene; (3) florfenicol resistance gene; (4) sulfonamides *sul* gene; (4) ESBLs gene family; (5) genes related to mobile elements, integrons and gene boxes; (6) macrolide *erm* gene, etc.

3.2. Diffusion mechanism of antibiotic resistance genes in aquaculture

In view of the wide detection of drug resistance genes and their impact on public health, this paper discusses the origin of drug resistance genes and how they migrate and spread in various environments from different angles. The discussion on the origin of drug resistance genes initially focused on gene mutations, such as β- the random mutation of lactamase gene is now TEM, CTX-M, SHV and so on β-lactamase is one of the important reasons for its prevalence in the world. β-antibiotic resistance genes such as lactams, tetracyclines and glycopeptides have existed naturally in the environment long before human clinical use of antibiotics. The current popular genotypes only have corresponding mutations in sequence because β- It is not surprising that antibiotics such as lactams come from natural biosynthesis, and their drug resistance genes are also popular. However, drugs with chemical synthesis and action sites different from natural synthetic antibiotics quickly appear drug resistance in a short time. Fluoroquinolones are a kind of synthetic antibiotics used in recent years. They take DNA topoisomerase as the target to form quinolone topoisomerase DNA complex and induce the configuration

changes of DNA gyrase and topoisomerase. Due to the natural existence of antibiotics, the corresponding drug resistance genes are also associated.

At present, it is generally believed that the screening of drug resistance genes by antibiotic use is one of the important driving forces leading to its wide spread in clinic. The screening pressure of antibiotics initially comes from bacteria 'own metabolism and synthesis for self-defense. After the discovery of antibiotics, a large number of biosynthetic, semi synthetic and synthetic antibiotics have been widely used in production practice and medical health, becoming the main source of screening pressure. On the other hand, heavy metals play a very important role in maintaining antibiotic resistance. The level of metal in the environment caused by human activities is much higher than that of antibiotics, and metal ions can persist in the environment and form long-term selection pressure under the background of lack of biodegradation. The resistance mechanism of bacteria to heavy metals is similar to that of antibiotics. Therefore, metal contamination may maintain and promote the gene pool of drug-resistant bacteria in clinic and environment. In addition, other substances in the environment also participate in the joint screening of antibiotic resistance, such as quaternary amines, antiseptic disinfectants, detergents and so on.

Human activities play an important role in the migration and diffusion of drug resistance genes, mainly focusing on medical and health care and animal husbandry and aquaculture. Livestock and poultry aquaculture is one of the production practices with frequent activities, large use of antibiotics and the largest output of drug resistance genes. A large number of antibiotics, drug-resistant bacteria and drug-resistant genes enter the water and soil environment with breeding waste. Through the food chain or direct or indirect contact, bacterial drug resistance is exchanged between human and animal sources. Drug resistance genes can migrate and transform in soil, water, groundwater and other environmental media, integrate into mobile gene elements, enter environmental microorganisms or pathogenic microorganisms, and spread among bacteria through gene horizontal transfer. The specific steps are:

- Sequence information related to drug resistance genes, including drug resistance genes and heavy metal resistance genes: this analysis content is the focus of macro gene sequencing analysis. The main comparison database is Antibiotic Resistance Genes Database;
- Mobile elements related to horizontal transfer of drug resistance genes, such as plasmids, transposons and phages, help to explain the transmission and diffusion of drug resistance genes. The optimized effective sequences were compared to NCBI reference sequence database with BLASTN, that is, annotated to plasmid information; The transposon database needs to download the transposon related sequences from GenBank and establish them as a database, and then compare and annotate them; Phage alignment and annotation in BLASTP;
- Microbial communities and virulence factors related to pathogenic microorganisms: First compare the data to the Ribosomal Database Project database to obtain species level sequences, and then annotate them to the pathogenic bacteria database Microbial Rosetta Stone Database. You can also consult the literature, establish a database about pathogenic bacteria, compare it with it and annotate it.
- Traceability based on microbial community composition: it is helpful to trace the source of environmental pollution and further elaborate the environmental impact, but at present, this analysis has not been calculated completely.
- Microbial communities carrying drug resistance genes: it is helpful to analyze the evolution of bacterial drug resistance, but there is no reliable analysis method for this content at present.
- Risk assessment: At present, there is no scientific model for the risk assessment of bacterial drug resistance. The drug resistance genome and its movable elements based on macrogenomic analysis, the host microbial community of drug resistance gene, pathogenic microbial community and Pollution Tracing Analysis Based on microbial community, Combined with quantitative microbial risk assessment, it may be helpful to establish the risk assessment of bacterial drug resistance.

4. Experimental analysis

An aquaculture base was selected as the experimental site, and the whole gene selection model was used as the theoretical basis for the practice of aquaculture genetic breeding. Four common species in aquaculture, *Pseudosciaena crocea*, crucian carp, herring and loach, were taken as the main research objects to judge the impact of whole genome selection model on aquaculture genetics and breeding. Initially, the number of large yellow croaker, crucian carp, herring and crayfish was 5, 50, 100 and 100 respectively. The pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture designed above are used as the experimental process to carry out breeding research on the above aquaculture animals, so as to test the acceptance and adaptability of the four types of animals to the pollution characteristics and diffusion mechanism.

In the experiment of aquaculture genetic breeding, the breeding value usually represents the seed value of breeding animals. Generally speaking, it is the individual genetic advantage of an aquaculture animal. In the experiment, the calculation of breeding value is mainly divided into several steps as shown in Fig. 4.

As shown in Fig. 4, during the calculation of breeding value, it is necessary to initialize all the binary tree parameter indexes of aquaculture animals of all offspring by querying the respective gene characterization information of different aquaculture animals. At this time, the animal gene information is a relatively perfect pedigree structure. By coding all animals, we can intuitively see the role of the whole genome selection model in aquaculture genetics and breeding. By comparing the incoming node with the parent node, we can get the opportunity to insert the binary tree, and obtain the minimum value of population breeding in the calculation of effect value and minimum value. The formula for calculating breeding value is:

$$S_{zy} = \frac{A_a \times B_b}{A_a \times B_b \times C_c} \tag{8}$$

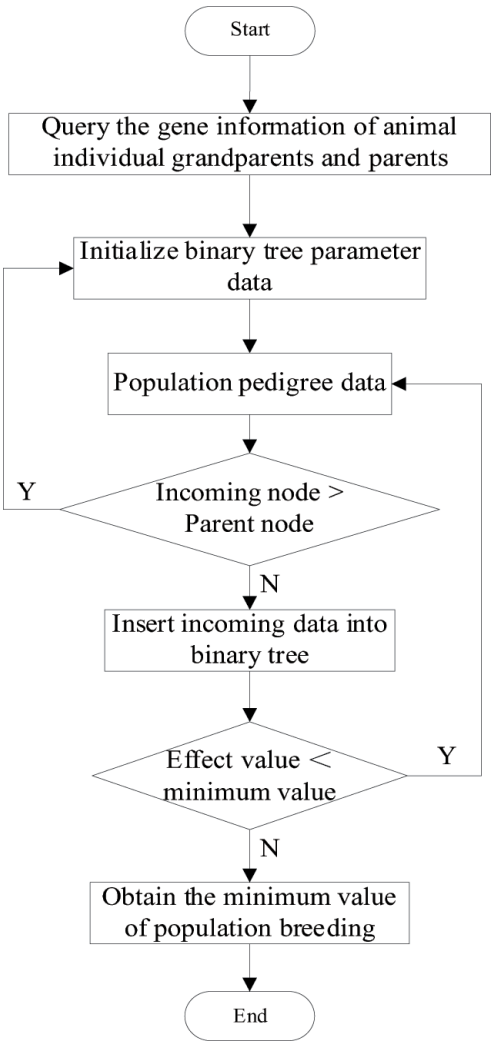

Fig. 4. Calculation flow of breeding value.

In Eq. (8), S_{zy} represents the breeding value that four aquaculture animals can achieve under continuous breeding iteration; A_a represents the number of reference samples of the animal population, that is, the initial number of samples; B_b indicates the genetic ability of an animal in weight gain; C_c represents the marker site of an aquaculture animal. Through this formula, the breeding values of the four aquaculture animals in the third generation can be obtained as shown in Fig. 5.

As shown in Fig. 5, when the breeding value of four aquaculture animals, namely, large yellow croaker, crucian carp, herring and crayfish, is in the parent generation, the breeding value of large yellow croaker in weight traits is the highest, followed by crayfish and crucian carp, and finally herring. Under the whole genome selection model, the breeding value of four aquaculture animals is declining. The decline of breeding value can usually represent the enhancement of genetic ability of this kind of organisms in some traits. Up to the third generation, the breeding value of large yellow croaker is still the highest, followed by herring and crayfish, and finally crucian carp. Through the expression of these three generations of genetic samples, we can

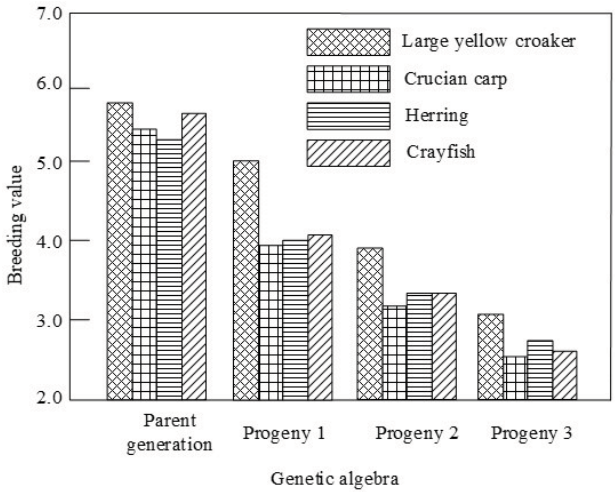

Fig. 5. Calculation of breeding value of different genetic algebra.

know that the whole genome selection model has an obvious effect on crucian carp, has a poor effect on large yellow croaker, and has a stronger effect on herring than crayfish.

After the comparison of the above genetic and breeding values, it is also necessary to further verify the weight changes of the four aquaculture animals in different breeding stages. The weight of aquaculture animals directly represents the economic value of the species. In the measurement indicators of animal weight, it is necessary to measure the average weight of all contemporary aquaculture animals. Because the maturity time of each animal is different, each aquaculture animal is divided into 0%–100% maturity from birth to the end of maturity. In this experiment, the weight change of each aquaculture animal in different maturity stages was recorded in detail, and the image was drawn, as shown in Fig. 6.

As shown in Fig. 6, with the change of genetic algebra, the average weight of the four aquaculture animals increased in varying degrees. From the average birth weight of the parent sample and the weight at maturity to the average weight at birth of the third offspring to the average weight at maturity, the crucian carp has the largest growth rate, followed by crayfish and herring, and the *Pseudosciaena crocea* has the smallest growth rate.

5. Conclusion and prospect

5.1. Conclusion

Pollution characteristics and diffusion mechanism of antibiotic resistance genes in aquaculture through efficient and convenient breeding methods, higher edible yield of aquaculture can be obtained. However, the overall effect of a genetic breeding method will always be affected by the genes of aquaculture animals. Therefore, this paper designs an experiment at the end, takes the four most common aquaculture animals as the experimental objects, studies them, and obtains the aquaculture animals with the most obvious effect of this genetic breeding method, Aquaculture animal species with relatively poor effect. Through methods and experiments, we can better optimize and improve the genetic

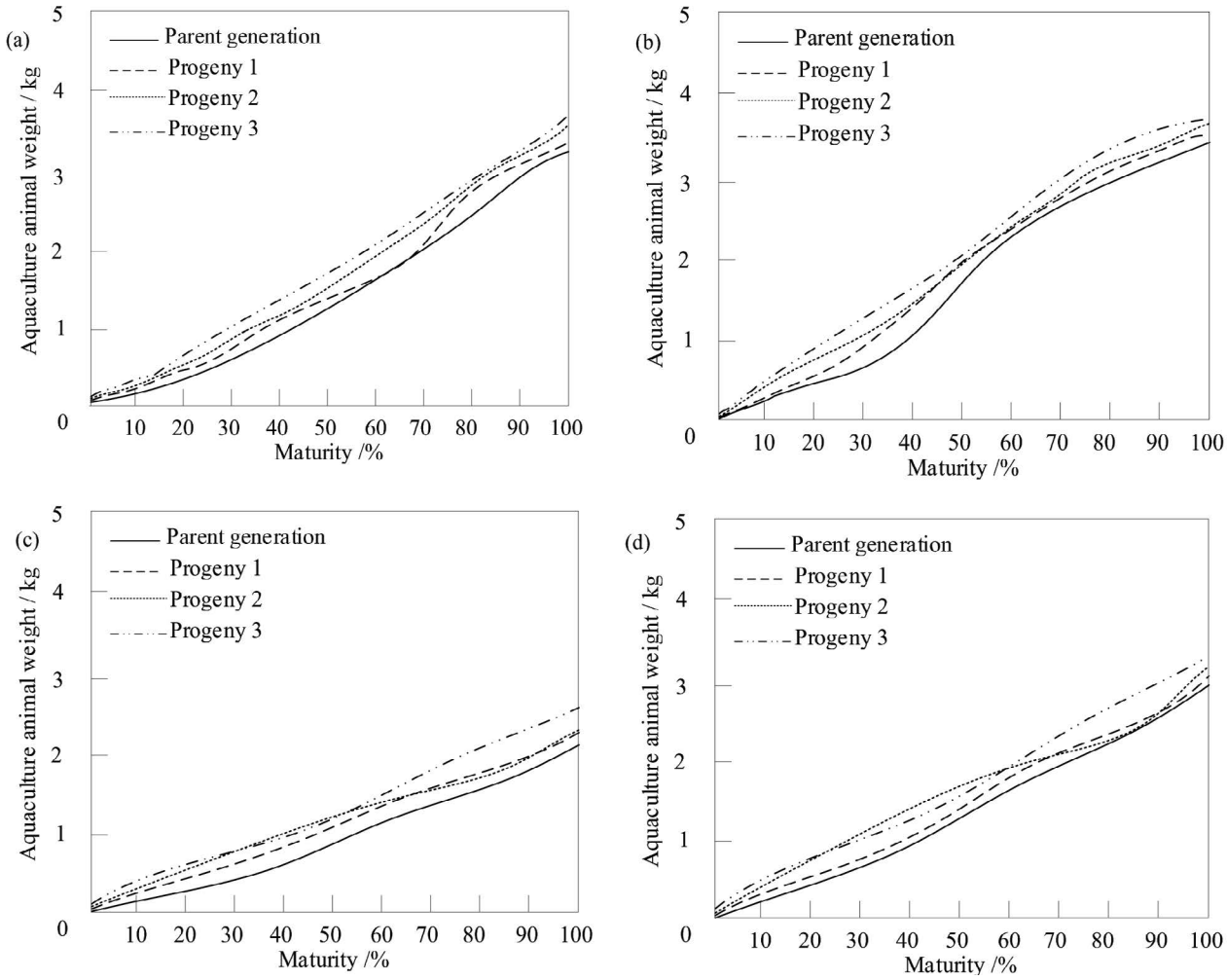

Fig. 6. Genetic breeding effect test. (a) Large yellow croaker, (b) crucian carp, (c) herring, and (d) crayfish.

breeding of aquaculture animals and improve the yield of aquaculture to a certain extent.

5.2. Prospect

- Due to the closed management of the aquaculture plant, only a single sample was taken from the aquaculture plant, resulting in the weak representativeness of some samples, which is difficult to calculate and compare the removal rates of drug-resistant genes and antibiotics in the wastewater treatment unit.
- At present, the diffusion mechanism of drug-resistant genes in aquaculture environment is only based on correlation analysis and ecological multi factor analysis, lacking the test and verification of actual experiments. In the future, the traceability research of drug-resistant genes from pollution source to receiving environment can be carried out.
- In the future, environmental bacterial drug resistance risk assessment can be carried out to further clarify the adaptability, viability and persistence of drug-resistant genes and drug-resistant bacteria in the receiving environment in combination with soil microbial ecology.

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