

BioResource Now!

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Resource Center
No. 49

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(Avian Bioscience Research Center, Nagoya University)

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Introduction to Resource Center (NO. 49)

Introduction to the National BioResource Project "Chicken/Quail"

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About Chicken and Quail Bioresources

Chicken (*Gallus gallus domesticus*) was domesticated from red jungle fowl (*G. gallus*) in the southern part of China at around 6000 BC. It is not known whether the existing domestic fowls are descendants of the red jungle fowl. Hundreds of chicken breeds have been established at present. These chicken breeds are used for various purposes such as egg and meat production, religious ceremonies, and cockfighting. Some of these breeds are used as pets.

Currently, four original breeds or allied wild breeds live in Asia. The red jungle fowl is considered as their main ancestral breed. The Avian Bioscience Research Center conserves a closed colony of a subspecies of the red jungle fowl (*G. gallus gallus*) living in Sumatra (Fig. 1).



Fig. 1: Red jungle fowl (subspecies living in Sumatra) Adult male (left) and female (right)

Although this line can be used as a chicken control line, the chickens are timid and their fertility is low. Therefore, a breeding method must be urgently established for this chicken line. In addition to this line, the NBRP Chicken/Quail provides 20 chicken strains and lines, including inbred strains and long-term closed colonies with high genetic homogeneity (refer to its homepage for the details of each strain or line). Because many of these strains and lines have originated from European and American breeds, the NBRP Chicken/Quail has newly introduced Japanese chicken breeds possessing specific mutable traits with different genetic backgrounds and foreign pet chicken breeds, as well as addressed the establishment of new lines originating from these chicken breeds (Fig. 2).



Fig. 2: New lines originating from Japanese chicken breeds and foreign pet chicken breeds Dwarf chicken with a short-leg trait, male (left); dwarf chicken with a feather mutation, female (center); and male Polish bantam with feather combs on the head and a cerebral hernia (right)

The NBRP Chicken/Quail has also isolated new mutants, which incidentally appeared in maintained lines, and established new lines originating from these new mutants (Fig.3).



Fig. 3: New mutants that incidentally developed during the breeding processes of chicken lines Imperfect albino mutant that appeared in an inbred strain (GSP) (left) and a new mutant (right) with white spots and abnormal eyeball formation, derived from a dwarf chicken hybrid line

The quail was domesticated as a pet during the Muromachi Period (AD 1333–1573) in Japan by the samurai to enjoy its call. From the Edo Period (AD 1600–1868) to about the end of the Meiji Period (AD 1868–1912), the quail was reared throughout the country. At present, approximately 6 million quail are reared for egg production throughout the country, particularly in the Toyohashi area of Aichi Prefecture.

Similar to chicken, quail belongs to the family Phasianidae. The body weights of male and female quails are as low as 100–120 g and 120–150 g, respectively. Because the time required for sexual maturation is around 50 days after hatching, 3–4 generations of quail can be produced in a year. The quail also has excellent fecundity as well as disease resistance. Therefore, it has been used as an avian model animal and a pilot animal for chicken breeding in life science studies.

At present, the NBRP Chicken/Quail maintains 11 long-term closed colonies. This resource includes standard lines with high genetic homogeneity, eggshell/plumage color mutant lines, and models for diseases such as glycogen storage disease and muscular dystrophy (Fig. 4) (refer to the homepage for details).

The Avian Bioscience Research Center has performed genetic monitoring using microsatellite markers originally developed by the Center and published information obtained by monitoring. In the future, quail bioresources are expected to be used to a greater extent.



Fig. 4: Long-term closed colonies of quail WE line, male (left); AMRP line, male (center); eggshell color mutant (right) [normal type (left) and white eggshell type (right)]

Breeding of Mutant Lines and Evaluation of their Genetic Characteristics

At least 190 mutable traits have been reported for the chicken. The NBRP Chicken/Quail has begun to rear new lines based on Japanese and foreign chickens possessing these mutable traits and identified the hereditary modes and causative genes of these mutable traits in genetic thremmatology analyses. In these analyses, when an inbred strain with high genetic homogeneity is used as a mating partner, there can be reduction of phenotypic variation caused by different genetic backgrounds. Consequently, genetic analysis using polymorphic genetic markers can be performed efficiently and quickly.

As examples of mutable traits, fibromelanosis (*Fm*) expressed in the silky fowl and the new recessive white plumage color mutation (*mo^w*) found in Japanese chicken are discussed below.

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Fm is a mutable trait that causes excessive melanization in tissues of the skin, internal organs, and periosteum. Silky fowl means crow bone fowl in Chinese, because the color of the skin and bones of this fowl is as dark as that of a crow. Silky fowl is an important part of the Chinese medicated diet (Fig. 5).



Fig. 5: Fibromelanosis (*Fm*) expressed in the silky fowl
SIL line of a closed colony, male (left); *Fm* strain obtained by hybridization with an inbred strain (right) [wild-type individual (left) and mutant individual (right)]

The recessive white plumage color mutation (*mo^W*) has been newly identified in the chicken, which differs from the two white plumage color mutations (dominant white: *I*; recessive white: *c*) that are already known in the chicken. This mutant is almost covered with white plumage, and pigmented feathers only grow on the small dorsal parts of the head, shoulder, and waist. At present, this mutation has been observed only in Japanese long-tailed chicken breeds (Fig. 6).



Fig. 6: New recessive white plumage color mutation (*mo^W*) found in Japanese chicken
White mutant of the Minohiki chicken, male

To identify causative genes of these mutable traits, the NBRP Chicken/Quail reared a reference line obtained by hybridization with an inbred strain and then performed linkage analysis using genetic markers. Consequently, *Fm* was confirmed to be linked to a marker on chromosome 20. Detailed genetic analysis detected duplication in the genomic region containing the endothelin-3 gene (*END 3*) (Shinomiya *et al.*, 2013). Similar to *Fm*, *mo^W* was also confirmed to be linked to a marker on chromosome 4. Detailed genetic analysis showed that *mo^W* was caused by a single nucleotide substitution along with an amino acid substitution in the coding region of the endothelin receptor B2 gene (*EDNRB2*) (Kinoshita *et al.*, 2013). Although both traits are controlled by different genes, the two traits are caused by mutations in genes that are associated with ligand-receptor interactions. Therefore, a hybridization experiment was performed for these two traits. Consequently, the phenotype of *Fm*, a dominant trait, was found to be controlled by *mo^W*. Thus, by analyzing mutants with abnormal melanin synthesis, new information was obtained on the functions and roles of *END 3* and *EDNRB2* in the melanin synthesis pathway as well as a correlation between these two genes.



Fig. 7: Homepage of the NBRP Chicken/Quail
<http://www.agr.nagoya-u.ac.jp/~nbrp/en/index.html>

In the future, a large amount of information can be obtained on gene functions specific to avians by performing genetic analysis of many mutants of the chicken and quail, whose causative genes have not been identified. Aves and Mammalia have evolutionary backgrounds of 310 million years after diverging from a common ancestor in the Amniota. During this evolutionary time, the Aves originally acquired and lost many traits. Bioresources of the chicken and quail play a very important role in elucidating the biological functions and molecular mechanism underlying morphogenesis specific to Aves, which differ from those of Mammalia and other animal species.

The NBRP Chicken/Quail will continuously collect and conserve chicken and quail bioresources that are scattered all over Japan and possess various genetic characteristics. We will also rear new lines, improve the quality of resources based on strict genetic control, and provide chicken and quail bioresources for researchers, the quality and quantity of which are of the highest standards. Through these activities, the NBRP Chicken/Quail aims to contribute to the development of life science research in Japan.

References

Shinomiya A, Kayashima Y, Kinoshita K, Mizutani M, Namikawa T, Matsuda Y, Akiyama T.
Gene duplication of *endothelin 3* is closely correlated with the hyperpigmentation of the internal organs (*Fibromelanosis*) in Silky chickens. *Genetics* 190:627–638, 2012.
Kinoshita K, Akiyama T, Mizutani M, Shinomiya A, Ishikawa A, Younis HH, Tsudzuki M, Namikawa T, Matsuda Y.
Endothelin receptor B2 (*EDNRB2*) is responsible for the tyrosinase-independent recessive white (*mo^W*) and mottled (*mo*) plumage phenotypes in chicken. *PLoS ONE* (in press).

Database of This Month

National BioResource Project "TOMATO"



DB name :
Tomatoma (URL: <http://tomatoma.nbrp.jp/index.jsp>)
NBRP-TOMATO (URL: <http://tomato.nbrp.jp/indexEn.html>)
Language : Japanese, English
Original contents :
In the TOMATOMA database, strain resources for research (EMS mutagenesis lines of Micro-Tom, gamma irradiation-induced mutant lines, and wild-type cultivars, as well as EMS and gamma irradiation-induced mutant lines), an image gallery, phenotypes, and plant ontology (PO) data are available to the public. In the NBRP-TOMATO database, a conspectus by researchers of plants of the family Solanaceae in Japan, a mailing list, and FAQs are available to the public.
Features :
You can order resources from these databases as well as search resources by the traits of mutants or images that have been classified according to the growth stage.
Cooperative DB : KafTom, MiBASE
DB construction group : NBRP-TOMATO, NBRP Information Management organization : Genetic Resource Center, NIG
Year of DB publication : 2009 Year of last DB update: 2013

Number of strains: 1,602
(as of November 2013)

Comment from a practicing developer :TOMATOMA (database), KafTom (cDNA database), and MiBASE (cDNA database) can be accessed from the NBRP-TOMATO (portal site). In particular, the TOMATOMA contains a registration system of tomato mutants. Therefore, the TOMATOMA can provide the latest information. The NBRP-TOMATO also contains a system through which organizations can update their information. More than 3000 photographs of mutants are available; therefore, please visit our photo gallery. We will continuously improve the usability of our database. Please feel free to use our database and do not hesitate to send us your comments, questions, or opinions using the Contact Us* on the top menu.

About Ongoing Column

The Ongoing Column "Easy and Free Mapping of NGS Data to Genomic Data, Part II", which was announced last month, will appear in next month's issue.

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Editor's Note

In 2012, Chicken/Quail was added to the National Bioresource Project (NBRP). However, chicken and quail resources have a very long history and are expected to display Japan's advantages. Chicken genome sequencing was completed in 2004. This month, the director and researcher of the organization representing chicken and quail resources kindly introduced the activities of the NBRP Chicken/Quail and its informative resources (Y. Y.).

BioResource Information

(NBRP) www.nbrp.jp/
(SHIGEN) www.shigen.nig.ac.jp/
(WGR) www.shigen.nig.ac.jp/wgr/
(JGR) www.shigen.nig.ac.jp/wgr/jgr/jgrUrlList.jsp

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