Genet. Res., Camb. (1981), **37**, *pp.* 161–171
With 2 text-figures
Printed in Great Britain

Gonosome–autosome translocations in fowl: the development of chromosomally unbalanced embryos sired by singly and doubly heterozygous cockerels

W. F. BLAZAK[1] AND N. S. FECHHEIMER

Department of Dairy Science, The Ohio State University, Columbus, Ohio 43210, U.S.A.

(*Received* 1 *April* 1980, *and in revised form* 29 *September* 1980)

SUMMARY

Cockerels singly or doubly heterozygous (t1/+, t2/+ and t1/t2, respectively; collectively heterokaryotypic, HTK) for two different Z-autosome translocations (t1, t2) produce an array of chromosomally balanced and unbalanced spermatozoa owing to adjacent segregation and nondisjunction at the first meiotic division. This study addresses the developmental capacity of embryos derived from matings of control (+/+) and HTK (t1/+, t2/+, t1/t2) cockerels with hens bearing normal chromosome complements (+/W).

Estimates of the hatchability of fertile eggs sired by +/+, t1/+, t2/+ and t1/t2 cockerels were 82·8 %, 43·0 %, 41·3 % and 10·9 %, respectively. Approximately 75 % of the mortality observed in embryos sired by HTK cockerels occurred by four days of incubation. Developmental arrest generally occurred earlier in embryos sired by t2/+ and t1/t2 cockerels than in those by t1/+ cockerels. These differences reflect variation in the degree of embryonic chromosome unbalance expected among embryos of the different sire groups. The pattern of mortality after three days was similar in embryos sired by HTK cockerels. In control embryos, mortality was highest on days 20–21 of incubation.

Chromosome analysis of 16–18 h embryos, day 1–5 embryos and hatched chicks sired by HTK cockerels revealed that most, if not all, chromosomally unbalanced embryos died during development; the majority before three days of incubation. Partial monosomy for chromosome one was found to be more deleterious to embryonic development than partial trisomy.

1. INTRODUCTION

A proportion of embryos derived from matings involving a translocation heterozygote often exhibit reduced developmental capacity. This departure from normal development is causally related to chromosome unbalance in the embryo resulting from adjacent segregations and non-disjunction, at the first meiotic division, of the chromosomes comprising the translocation multivalent in the

[1] Present address: Department of Human Anatomy, University of California–Davis 95616, U.S.A.

0016-6723/81/2828-8450 $01.00

heterozygous parent. The proportion of affected embryos is directly related to the frequency of production of chromosomally unbalanced gametes by the heterozygote, as well as the effects of different unbalanced chromosome complements on embryo development (see Ford, 1975 for review).

Chromosomally unbalanced embryos derived from matings involving a translocation heterozygote permit the experimental investigation of the effects of chromosome unbalance on embryological development. White *et al.* (1974*a*, *b*), Gropp, Giers & Kolbus (1974) and Gropp, Kolbus & Giers (1975) used mice doubly heterozygous for Robertsonian fusions with monobrachial homology to produce embryos trisomic for specific autosomes. Trisomy is generally less deleterious to mammalian development than monosomy (see Ford, 1975), and although the development of trisomic (White *et al.* 1974*a*, *b*; Gropp *et al.* 1974, 1975) and otherwise chromosomally unbalanced (Oshimura & Takagi, 1975) mouse embryos is often characterized only by severe growth retardation (and subsequent death *in utero*), a number of specific developmental abnormalities have been attributed to specific chromosome disorders (White *et al.* 1974*a*, *b*; Gropp *et al.* 1974, 1975). The association between abnormal karyotype and developmental anomalies is well documented in many human chromosomal syndromes (Hamerton, 1971).

In domestic fowl, *Gallus domesticus* L., translocation heterozygosity is associated with an approximate 50 % reduction in hatchability of fertile eggs (Telloni, Jaap & Fechheimer, 1977; Wooster, Fecheimer & Jaap, 1977). The reduction in hatchability is attributable to decreased embryonic viability, which is manifested by a high rate of embryonic death prior to the fifth day of development (Telloni *et al.* 1977). Although approximately 50 % of 16–18 h chick embryos derived from a translocation heterozygote bear an unbalanced chromosome complement (Dinkel *et al.* 1979; Blazak & Fechheimer, 1979*b*), karyotypic investigations of hatched chicks from karyologically identical parents have failed to reveal a single individual with an unbalanced karyotype (Telloni *et al.* 1977; Wooster *et al.* 1977). These observations suggest that the majority, if not all, of chromosomally unbalanced chick embryos die prior to hatching, but the relative viability of embryos possessing different unbalanced chromosome complements and the possible relationship between such chromosome complements and specific developmental errors remain unexplored.

The present investigation was undertaken to study the development of embryos sired by cockerels singly or doubly heterozygous for two different *Z*-autosome translocations. Approximately 50 % of embryos sired by singly heterozygous cockerels are chromosomally unbalanced whereas about 85 % of those sired by the double heterozygotes bear an unbalanced chromosome complement (Blazak & Fechheimer, 1979*b*). A small, but significant, proportion of spermatozoa produced by these cockerels bear a deletion/duplication or nullisomy/disomy of the *Z* chromosome (Blazak & Fechheimer, 1979*b*). An attempt was made, therefore, to study the effects of *Z* chromosome unbalance on gonadal sex differentiation.

2. MATERIALS AND METHODS

Cockerels singly or doubly heterozygous for the two different *Z*-autosome translocations have been described elsewhere (Blazak & Fechheimer, 1979*a*, *b*) and previously adopted nomenclature will be used. Single heterozygotes are designated t1/+ and t2/+, double heterozygotes t1/t2, and controls with normal chromosome complements +/+. Cockerels bearing these translocations are collectively referred to as heterokaryotypic (HTK).

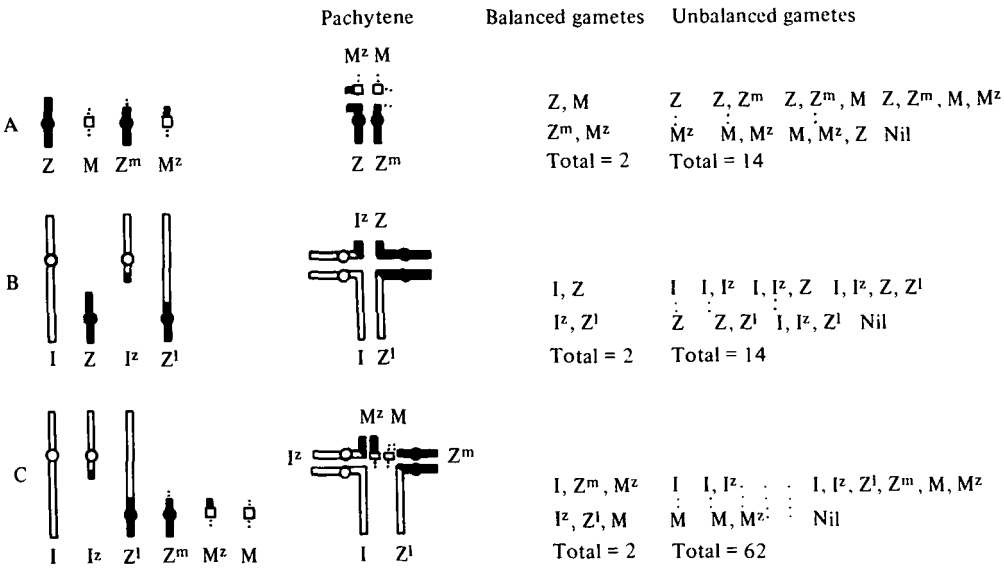

Fig. 1. Diagrams of chromosome translocations and resultant chromosome complements of spermatozoa from t1/+ (A), t2/+ (B) and t1/t2 (C) cockerels.

The different *Z*-autosome translocations, expected pachytene configurations and types of chromosomally balanced and unbalanced spermatozoa produced by heterozygous cockerels are presented in Fig. 1. Briefly, t1/+ cockerels (Fig. 1A) produce spermatozoa bearing duplications/deficiencies or disomy/nullisomy for a microchromosome and/or *Z* chromosome. A spermatozoon designated as *Z* (Fig. 1A), for example, results in an embryo monosomic for a microchromosome. Segregation in t2/+ cockerels (Fig. 1B) results in spermatozoa bearing unbalance for chromosome one and/or *Z*. A spermatozoon designated as 1, 1^z, Z^1 (Fig. 1B), for example, results in an embryo trisomic for chromosome one. Cockerels bearing both translocations (t1/t2, Fig. 1C) produce spermatozoa bearing unbalance for a microchromosome, chromosome one and/or *Z* chromosome. The sire, therefore, is the source of the abnormal chromosome complement in embryos under investigation. Blazak & Fechheimer (1979*b*) describe the frequency with which spermatozoa bearing different chromosome complements are produced.

The experimental design is outlined in Fig. 2. Four cockerels per karyotypic

https://doi.org/10.1017/S0016672300020139 Published online by Cambridge University Press

group (+/+, t1/+, t2/+, t1/t2) were used weekly for artificial insemination of White Leghorn hens bearing the normal chromosome complement (+/W). Approximately 3–5 hens were inseminated with semen collected from each cockerel. Specifically identified (by sire, dam, and date of lay) eggs were collected daily and

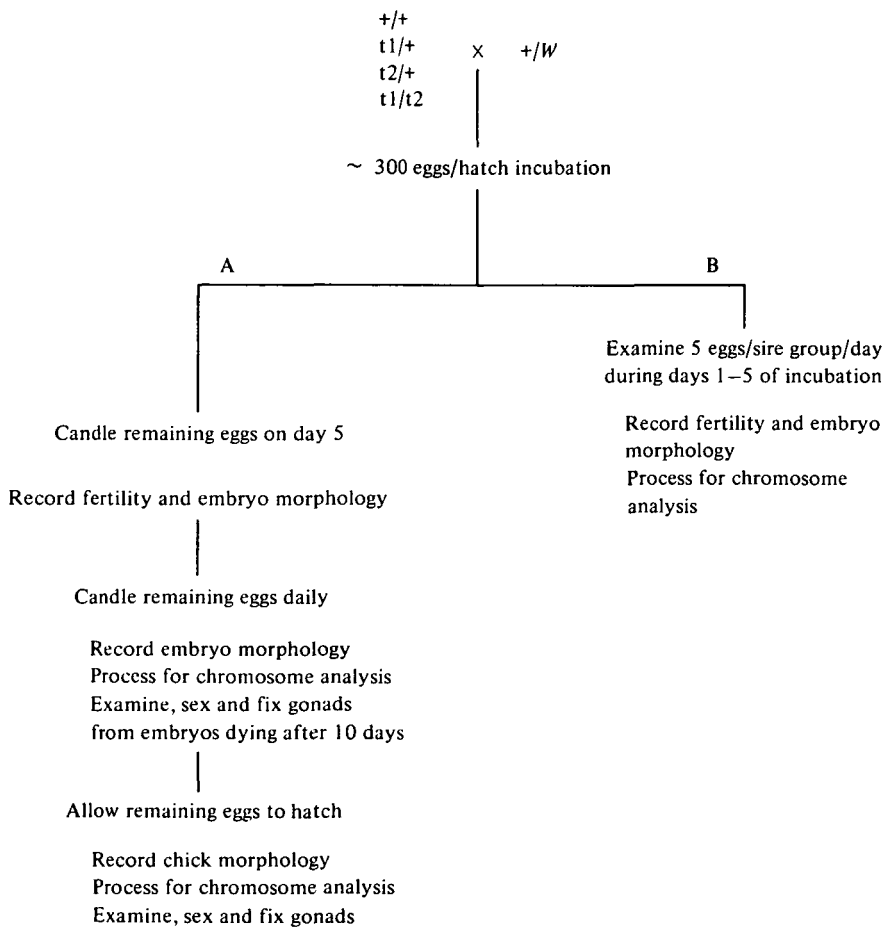

Fig. 2. Experimental design for the investigation of the developmental capacity of embryos sired by HTK cockerels.

stored at 10–12 °C. The total number of eggs collected during a two-week interval constituted a hatch and were set in a commercial incubator at 37·8 °C. Three hatches were set; two different experiments (A and B, Fig. 2) were conducted per hatch.

Experiment A was undertaken to study embryo development throughout incubation and the karyotypes of hatching chicks. Experiment B was conducted to determine the phenotype and karyotype of embryos during the first five days of incubation.

Metaphase chromosome preparations from embryos in both experiments were

made according to an established air-dry procedure (Fechheimer, Lodge & Miller, 1970; Dinkel *et al.* 1979). Yolks were injected with 0·1 ml 1·0 mg/ml solution of colchicine 3–4 h prior to the extirpation of embryonic tissues. The choice of tissue used for chromosome analysis depended upon the age of the embryo (see Bloom & Buss, 1967). Chromosome analyses of hatched chicks were made within one week after hatching. Chicks were injected intraperitoneally with 0·1 ml 2·0 mg/ml colchicine 3–4 h prior to sacrifice by cervical dislocation. Cell suspensions were prepared from minced liver and spleen and processed according to Fechheimer *et al.* (1970). A minimum of three cells was carefully examined under oil immersion (970 ×) to determine the karyotype.

The morphology of embryos was examined under a dissecting microscope and compared to the normal stages of chick embryo development of Hamburger & Hamilton (1951). Embryonic developmental stages are reported in days of incubation. The gonads from all embryos dying after 10 days of incubation and those from hatched chicks were carefully dissected out, sexed, and preserved in Bouin's fixative. Chi-square was used in the testing of significance of differences.

3. RESULTS

Experiment A

(i) *Hatchability and karyotypes of hatched chicks*

Similar proportions of eggs were fertilized among the different karyotypic groups (Table 1, $P > 0{\cdot}05$). Hatchability of fertile eggs sired by single translocation heterozygotes, t1/+ and t2/+, was reduced approximately 50 % as compared to control hatchability. Hatchability was further reduced in matings of the double heterozygotes, t1/t2, and amounted to only 13 % of hatchability of controls. *A priori*, hatchability from t1/t2 cockerels is expected to be equivalent to the product of the hatchabilities of the single heterozygotes (expressed in terms of control hatchability, $0{\cdot}5189(t/1+) \times 0{\cdot}4988(t2/+) \times 100 = 25{\cdot}88\,\%(t1/t2)$). The difference between observed (13·13 %) and expected (25·88 %) hatchability from t1/t2 cockerels is significant ($P < 0{\cdot}001$).

The karyotypes of all hatched chicks sired by HTK cockerels are summarized in Table 2. Unbalanced chromosome complements were not observed and the translocation chromosomes were recovered independently of sex and in the expected ratio of 1 balanced translocation heterozygote : 1 normal in chicks sired by t1/+ or t2/+ cockerels. Only balanced translocation heterozygotes were observed in the progeny of t1/t2 cockerels. The overall sex proportion, 54·05 % males, did not differ significantly from that expected.

Gonadal sex of each chick was concordant with sex chromosome analysis of liver and spleen cells, and no gross morphological abnormality of the gonads was observed. These findings, and the complete absence of chromosomally unbalanced karyotypes (especially sex chromosome aneuploidy of the types *ZZZ*, *ZO*, etc.) among hatched chicks, prevented the study of the effects of chromosome unbalance on gonadal sex differentiation.

(ii) *Embryonic mortality, karyotype and phenotype*

The proportions of embryos reaching a specific developmental stage before death differed significantly between karyotypic groups (Table 3). In control matings, approximately 40 % of all embryo deaths occurred by a developmental age of 4 days; the majority of the remaining deaths occurred immediately prior to, or

Table 1. *Hatchability of fertile eggs sired by HTK and control cockerels*

Karyotype of sire	Number of eggs set	Number and (percentage ± S.E.) fertile	Number and (percentage ± S.E.) hatching[a]	Percentage ± S.E. embryonic mortality
+/+	259	238 (91·89 ± 1·70)	197 (82·77 ± 2·45)[1]	17·23 ± 2·45
t1/+	174	149 (85·63 ± 2·66)	64 (42·95 ± 4·06)[2]	57·05 ± 4·06
t2/+	173	155 (89·60 ± 2·32)	64 (41·29 ± 3·95)[2]	58·71 ± 3·95
t1/t2	216	184 (85·19 ± 2·42)	20 (10·87 ± 2·29)[3]	89·13 ± 2·29

[a] Percentages with a different superscript are significantly different ($P < 0·05$).

Table 2. *Chromosome complements of hatched chicks sired by HTK cockerels*

Karyotype of sire	Number of chicks	Chromosome complement						
		+/+	t1/+	t2/+	t1/W	t2/W	+/W	χ^2_a
t1/+	64	15	17	—	15	—	17	0·25
t2/+	64	19	—	15	—	16	14	0·87
t1/t2	20	—	8	6	2	4	—	0·24
Total	148			80 males	68 females	$\chi^2_b = 0·97$		

χ^2_a = test for a 1:1:1:1 ratio of progeny within each sire group.
χ^2_b = test for a 1:1 sex ratio.

during, hatching. Comparison between control and HTK groups revealed a significantly increased proportion of mortality on days 1, 2 and 3 and a significantly reduced mortality at 21 days in embryos sired by HTK cockerels ($P < 0·05$). Significant differences were also found in embryo mortality between the different HTK groups. A greater proportion of embryos sired by t1/+ cockerels developed to 3 days as compared to those sired by t2/+ or t1/t2 cockerels (Table 3, $P < 0·05$). Approximately 47 % and 68 % of dead embryos from t2/+ and t1/t2 cockerels, respectively, had developed no further than 2 days; the corresponding value is 28 % for embryos sired by t1/+ cockerels. The difference between t1/+- and t2/+-sired embryos vanishes by 3 days but the proportion of dead embryos sired by t1/t2 cockerels remains significantly higher owing to greater mortality during the first day of incubation. Little difference exists in the pattern of mortality after 3 days in embryos sired by different HTK cockerels. More than 75 % of all deaths occurring in embryos sired by HTK cockerels occur by 4 days of development.

Attempts to determine the chromosome complement of embryos dying during

incubation failed because of a lack of dividing cells. Embryos scored as dead by candling showed varying degrees of degeneration and may have died 12–24 h prior to detection. Only two embryos with gross deformities were observed: a double-bodied embryo sired by a +/+ cockerel and an embryo with severe head deformities sired by a t1/+ cockerel. Specific morphological defects associated with

Table 3. *Proportion of embryos sired by control and HTK cockerels dying by specific developmental stages*

Karyotype of sire	Number of fertile eggs	Latest developmental stage (in days of incubation) attained[a]							Total number and (percentage) of dead embryos
		1	2	3	4	10	20	21	
+/+	238	0·05	0·10	0·12	0·15	0·02	0·07	0·49	41 (17·2)
t1/+	149	0·12	0·16	0·39	0·19	0·01	0·05	0·08	85 (57·1)
t2/+	155	0·13	0·34	0·15	0·14	0·05	0·05	0·14	91 (58·7)
t1/t2	184	0·27	0·41	0·18	0·07	0·04	0·01	0·02	164 (89·1)

[a] Expressed as: No. embryos dying at specified stage/Total no. dead embryos.

Table 4. *Results of chromosome analysis of normal and abnormal embryos sired by +/+, t2/+ and t1/t2 cockerels*

Type of embryo	Number of embryos	Number and percentage karyotyped		Number and percentage balanced		Number and percentage unbalanced	
Morphologically normal	103	94	91·3	87	92·6	7	7·4
Morphologically abnormal	93	50	53·8*	6	12·0*	44	88·0*

* Denotes a significant difference ($P < 0·05$).

karyotypic group were not observed in the dead embryos. Gonads examined from embryos dying during days 10–21 presented no peculiarities. Chromosome analysis of live chicks which had broken the shell but failed to emerge (classified as embryo deaths on day 21) proved successful but only balanced chromosome complements were observed. The phenotypes of all of them were normal; gonadal sex and chromosomal sex were concordant.

Experiment B

The development of embryos sired by control and HTK cockerels during days 1–5 of incubation was similar to that described in experiment A. Approximately 54% of abnormal embryos recovered in experiment B yielded metaphase cells suitable for karyotype analysis (Table 4). Excluded from the data summarized in Table 4 are results from t1/+ cockerels since balanced and unbalanced chromosome complements, for the most part, are indistinguishable cytologically owing to microchromosomes involved in the translocation (Blazak & Fechheimer, 1980). A high percentage (93%) of embryos scored as developmentally normal had a balanced chromosome complement; the incidence of balanced complements in

abnormal embryos was low (12%). The developmental arrest observed in the abnormal embryos is primarily attributable to chromosome unbalance.

The types and frequencies of abnormal chromosome complements observed in the 44 karyotyped abnormal embryos are presented in Table 5. The majority of embryos (81·8%) bearing an unbalanced chromosome complement developed no further than 2 days; only embryos with partial monosomy or trisomy for chromo-

Table 5. *Developmental capacity of chick embryos bearing unbalanced chromosome complements*

Karyotype of embryos[a]	Number of embryos	Latest developmental stage (in days of incubation) attained					Normal at 5 days
		1	2	3	4	5	
Trisomy-1	2	2	—	—	—	—	—
Monosomy-1	1	1	—	—	—	—	—
Partial trisomy-1	13	1	5	4	2	0	1
Partial monosomy-1	18	14	3	1	—	—	—
Trisomy-*Z*	1	1	—	—	—	—	—
Monosomy-*Z*	2	2	—	—	—	—	—
ZZW	2	1	1	—	—	—	—
Partial trisomy-1–partial monosomy-*Z*	3	2	1	—	—	—	—
Partial monosomy-1–partial trisomy-*Z*	2	2	—	—	—	—	—
Total	44	26	10	5	2	0	1
Percentage	—	59·1	22·7	11·4	4·5	0·0	2·3

[a] Some karyotypes are confounded with unbalance for the microchromosomal elements of the t1 translocation.

some 1 developed further. A comparison between the latest developmental stages attained in embryos partially monosomic or trisomic for chromosome 1 revealed earlier death in the partial monosomic group ($P < 0{\cdot}001$). One embryo partially trisomic for chromosome 1 was found alive and developmentally normal when examined on the fifth day of incubation. Two triploid embryos (3*n*, *ZZW*), not listed in Table 5, were found among the abnormal embryos sired by t1/+ cockerels. Both triploids developed no further than 4 days.

4. DISCUSSION

(i) *Hatchability*

The observed hatchability of fertile eggs sired by t1/+ and t2/+ cockerels supports the cytogenetic evidence (Blazak & Fechheimer, 1979*b*) that cockerels bearing these translocations produce approximately 50% chromosomally unbalanced spermatozoa. These results conform to theoretical expectation in cases of reciprocal translocation (see Ford & Clegg, 1969) and have been experimentally demonstrated in mice heterozygous for an autosomal reciprocal translocation

(Oshimura & Takagi, 1975; Kaufman, 1976). Telloni *et al.* (1977) also found a 50% reduction in hatchability of embryos sired by t1/+ cockerels. This reduction must result from death of embryos unbalanced for the microchromosomal elements involved in the t1 translocation (i.e. chromosomes M and M^z, Fig. 1A).

The observed hatchability of fertile eggs sired by t1/t2 cockerels was significantly lower than the expected hatchability based on samples sired by the single heterozygotes. Approximately 13% excess embryonic mortality was observed in embryos sired by t1/t2 cockerels. These observations agree with the cytogenetic data compiled on 16–18 h embryos sired by t1/t2 cockerels (Blazak & Fechheimer, 1979*b*) and are compatible with the hypothesis of anaphase chromosome lagging during the first meiotic division in t1/t2 cockerels (Blazak & Fechheimer, 1979*b*).

(ii) *Developmental capacity of chromosomally unbalanced chick embryos*

Chromosome analysis of 16–18 h embryos (Blazak & Fechheimer, 1979*b*), day 1–5 embryos and hatched chicks sired by cockerels singly or doubly heterozygous for *Z*-autosome translocations revealed that all chromosomally unbalanced chick embryos died during incubation. Partial monosomy for chromosome one was found to be more deleterious to embryonic development than partial trisomy, and definite translocation sire-group differences were observed in embryonic developmental capacity. The latter differences reflect differences in the magnitude of embryonic chromosome unbalance expected among embryos of the different sire groups. Similar results have been observed in the development of chromosomally unbalanced mammalian embryos (see Ford, 1975). In contrast to mammals, however, the majority of chromosomally unbalanced chick embryos die very early in development. Some chromosomally unbalanced mammalian embryos are known to develop to term and, in some instances, enjoy a modest postnatal life (mouse: White *et al.* 1972; Ford, 1975; cattle: Herzog, Höhn & Rieck, 1977; human: Hamerton, 1971). The only published account of viable chromosome unbalance in the domestic fowl is trisomy for a microchromosome (Bloom, Shalit & Bacon, 1978). There are undoubtedly numerous factors contributing to the differences in developmental capacity of chromosomally unbalanced mammalian and avian embryos. The lack of dosage compensation for *Z*-linked genes (Cock, 1964) in the domestic fowl may explain the early death of embryos bearing *Z*-chromosome unbalance. The early lethal effects of unbalance for macrochromosomes or macrochromosomal segments may be due to the comparatively large amount of genetic unbalance imposed on the embryo. Chromosome one, for example, represents approximately 15% of the haploid chromosome complement of the male domestic fowl (Takagi & Sasaki, 1975). Unbalance for such a significant amount of the genome (or about half this amount in partial monosomics and trisomics) is not observed in newborn mammals, although similar large chromosome unbalances have been recovered in very early spontaneous human abortuses (Boué, Boué & Lazar, 1975). A dosage explanation, however, would not explain the early mortality of chick embryos bearing unbalance for microchromosomal elements.

The differential effects of chromosome unbalance on mammalian and avian

embryological development may also be a manifestation of the molecular organization of their respective genomes. In comparison to mammals, the avian genome contains significantly less satellite DNA (Comings & Mattoccia, 1972*a*; Edwards & Coleman, 1973), and a unique form of GC-rich, non-repetitious DNA believed to be confined mostly to the microchromosomes (heavy shoulder DNA, Comings, 1972; Comings & Mattoccia, 1972*b*). The avain genome also appears to be organized in a different manner than other eukaryotic organisms (Epplen *et al.* 1978). These differences in the basic organization of mammalian and avian genomes may be involved in the differential expression of embryonic chromosome unbalance.

We are grateful to Miss S. L. Woolard for skilful technical assistance with various aspects of this work. Approved as Journal Article no. 166-79 from the Ohio Agricultural Research and Development Center.

REFERENCES

Blazak, W. F. & Fechheimer, N. S. (1979*a*). Gonosome–autosome translocations in the domestic fowl: their effect upon male fertility and semen characteristics. *Biology of Reproduction* **21**, 575–582.

Blazak, W. F. & Fechheimer, N. S. (1979*b*). Gonosome–autosome translocations in fowl: chromosome complements of gametes and viability of embryos derived from singly and doubly heterozygous cockerels. *Journal of Heredity* **70**, 407–412.

Bloom, S. E., Shalit, P. & Bacon, L. D. (1978). Chromosomal localization of nucleolus organizers in the chicken. *Genetics* **88** (Suppl.), s13.

Bloom, S. E. & Buss, E. G. (1968). Effect of age and kind of tissue on mitotic activity in chicken embryos. *Poultry Science* **47**, 837–839.

Boué, J., Boué, A. & Lazar, P. (1975). The epidemiology of human spontaneous abortions with chromosomal anomalies. In *Aging Gametes* (ed. R. J. Blandau), pp. 330–348. Basel: S. Karger.

Cock, A. G. (1964). Dosage compensation and sex chromatin in non-mammals. *Genetical Research* **5**, 354–365.

Comings, D. E. (1972). Heavy shoulder DNA. *Experimental Cell Research* **70**, 259–263.

Comings, D. E. & Mattoccia, E. (1972*a*). DNA of mammalian and avian heterochromatin. *Experimental Cell Research* **71**, 113–131.

Comings, D. E. & Mattoccia, E. (1972*b*). Evidence that heavy shoulder DNA may be localized to the microchromosomes of birds. *Experimental Cell Research* **70**, 256–259.

Dinkel, B. J., O'Laughlin-Phillips, E. A., Fechheimer, N. S. & Jaap, R. G. (1979). Gametic products transmitted by chickens heterozygous for chromosomal rearrangements. *Cytogenetics and Cell Genetics* **23**, 124–136.

Edwards, K. & Coleman, J. R. (1973). Isolation of chicken satellite DNAs. *Journal of Cell Biology* **59**, 88*a*.

Epplen, J. T., Leipoldt, M., Engel, W. & Schmidtke, J. (1978). DNA sequence organisation in avian genomes. *Chromosoma* **69**, 307–321.

Fechheimer, N. S., Lodge, J. R. & Miller, R. C. (1970). Sex proportion of domestic chicken at 16 hours of incubation. *Journal of Reproduction and Fertility* **23**, 365–367.

Ford, C. E. (1975). The time in development at which gross genome unbalance is expressed. In *The Early Development of Mammals* (ed. M. Balls and A. E. Wild), pp. 285–304. Cambridge University Press.

Ford, C. E. & Clegg, H. M. (1969). Reciprocal translocations. *British Medical Bulletin* **25**, 110–114.

Gropp, A., Giers, D. & Kolbus, U. (1974). Trisomy in the fetal backcross progeny of male and female metacentric heterozygotes of the mouse. I. *Cytogenetics and Cell Genetics* **13**, 511–535.

Gropp, A., Kolbus, U. & Giers, D. (1975). Systematic approach to the study of trisomy in the mouse. II. *Cytogenetics and Cell Genetics* **14**, 42–62.

HAMBURGER, V. & HAMILTON, H. L. (1951). A series of normal stages in the development of the chick embryo. *Journal of Morphology* **88**, 49–92.

HAMERTON, J. L. (1971). *Human Cytogenetics*, vol. II, *Clinical Cytogenetics*. New York: Academic Press.

HERZOG, A. H., HÖHN, H. & RIECK, G. W. (1977). Survey of recent situation of chromosome pathology in different breeds of German cattle. *Annales de Génétique et de Sélection Animale* **9**, 471–492.

KAUFMAN, M. H. (1976). The incidence of chromosomally unbalanced gametes in T(14; 15)Ca heterozygote mice. *Genetical Research* **27**, 77–84.

OSHIMURA, M. & TAKAGI, N. (1975). Meiotic disjunction in T(14; 15)6 Ca heterozygotes and the fate of chromosomally unbalanced gametes in embryonic development. *Cytogenetics and Cell Genetics* **15**, 1–16.

TAKAGI, N. & SASAKI, M. (1974). A phylogenetic study of bird karyotypes. *Chromosoma* **46**, 91–120.

TELLONI, R. V., JAAP, R. G. & FECHHEIMER, N. S. (1977). Fertility, embryo viability and hatchability of chickens having 23% of the *Z* translocated to a micro-chromosome *Poultry Science* **56**, 193–201.

WHITE, B. J., TJIO, J.-H., VAN DE WATER, L. C. & CRANDALL, C. (1972). Trisomy for the smallest autosome of the mouse and identification of the T1Wh translocation chromosome. *Cytogenetics* **11**, 363–378.

WHITE, B. J., TJIO, J.-H., VAN DE WATER, L. C. & CRANDALL, C. (1974*a*). Trisomy 19 in the laboratory mouse. I. Frequency in different crosses at specific developmental stages and relationship of trisomy to cleft palate. *Cytogenetics and Cell Genetics* **13**, 217–231.

WHITE, B. J., TJIO, J.-H., VAN DE WATER, L. C. & CRANDALL, C. (1974*b*). Trisomy 19 in the laboratory mouse. II. Intrauterine growth and histological studies of trisomics and their normal littermates. *Cytogenetics and Cell Genetics* **13**, 232–245.

WOOSTER, W. E., FECHHEIMER, N. S. & JAAP, R. G. (1977). Structural rearrangements of chromosomes in the domestic chicken: experimental production by X-irradiation of spermatozoa. *Canadian Journal of Genetics and Cytology* **19**, 437–446.