

## **The Pricopian «gene theory of sexuality» is just a hypothesis, but good enough to explain the sex determination in fish**

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**Abstract.** The present paper summarizes the Pricopian theory of sexuality, discussed in the context of fishes' sex determination. On a logical approach and considering the most recent genetic evidences reported from studies on bacteria, invertebrates, fish, frogs, reptiles, birds, mammals and even humans, one may already abandon the chromosomal concept of the sex determination (such as the dosage of Z chromosomes). The sex-determining locus is not a true locus, but an agglomeration of loci very seldom separated by genetic recombination. Moreover, the W chromosome in ZZ-ZW systems and the Y in XX-XY systems are not empty at all, but still carry information.

**Key Words:** theories, hypotheses, sex determination, sex chromosomes.

**Résumé.** Le présent article résume la théorie de la sexualité Pricopienne, discutée dans le contexte de la détermination du sexe des poissons. Sur une approche logique et compte tenu des preuves génétiques les plus récentes rapportées dans les études sur les bactéries, les invertébrés, les poissons, les grenouilles, reptiles, oiseaux, mammifères et même les hommes, on peut déjà abandonner le concept de la détermination chromosomique du sexe (comme la dose de A à Z chromosome). La détermination du sexe locus n'est pas un lieu vrai, mais une agglomération de loci très rarement séparés par recombinaison génétique. En outre, le chromosome W dans les systèmes de ZZ-ZW et Y dans les systèmes de XX-XY ne sont pas vides à tous, mais ils présentent néanmoins d'information.

**Mots clés:** théories, hypothèses, la détermination du sexe, les chromosomes sexuels.

**Rezumat.** Lucrarea noastră prezintă teoria pricopiană a sexualității în contextul determinismului sexelor la pești. Gândind logic și ținând cont de cele mai recente evidențe genetice relatate în urma unor studii la bacterii, animale nevertebrate, pești, broaște, reptile, păsări, mamifere și chiar la om, conchidem că vechiul concept cromosomal al determinismului sexelor (ca și - spre exemplu - dozajul cromosomilor Z) este caduc. Locusul determinant al sexelor este, de fapt, nu un singur locus ci o aglomerare de loci foarte rar separați de recombinarea genetică. Mai mult, cromosomul W în sistemele ZZ-ZW și cromosomul Y în sistemele XX-XY nu sunt "complet goi", ei sunt totuși purtători de informație.

**Cuvinte cheie:** teorii, ipoteze, determinismul sexelor, cromosomi sexuali.

**Introduction.** Today, scientific research is a constant debate between scientists worldwide and the resulting ideas are the key to scientific and technological progress (see for example Tlusty 2010 vs Appelbaum & Arockiaraj 2009, Arockiaraj & Appelbaum 2010; Shaddock 2008 vs Petrescu-Mag et al 2007 and so on).

Many fish species are very good models for studies of genetic research, ethology and sex-chromosomes evolution (see Bourne & Sammons 2008; Bourne & Watson 2009; Gorgan 2009; Petrescu-Mag 2007, 2008; Petrescu-Mag et al 2007bcd, 2008; Petrescu-Mag & Petrescu-Mag 2010). The present paper summarizes the Pricopian theory of sexuality, discussed in the context of fishes' sex determination.

**Pricopian Theory of the Sexuality.** Recently, Pricop (2003, 2005, 2009 presented in Pricop 2009) emitted a new theory which, after our opinion, is rather hypothesis than theory due to the fact that molecular evidences are still poor. It refers to sexuality and genetic basis of sex determination (in animals generally, and Galinaceae specially). Most of his results were obtained in a classical breeding programme similar to that of Morgan

(1919). However, the results and interpretation of Pricop (2009) were obviously different from those of Morgan (1919) (see Plates 1-6, taken from Pricop 2009).

Using the color of the plumage as a phenotype marker, Pricop suggests that the existence of unexpected categories in generation F2 both in the direct and reciprocal cross might be explained by the presence of a pseudoautosomal region in chicken (see also Berlin & Ellegren 2004; Wahlberg et al 2007), similar with those observed in mammalian (Petit et al 1988; Henke et al 1993; Rappold 1993; Chandra 1994; Blaschke & Rappold 2006) and fish sex chromosomes (Traut & Winking 2001; Petrescu-Mag & Bourne 2008; Petrescu-Mag 2009), where the genes determining the plumage color inheritance are located. In that pseudoautosomal region the genes are recombining by crossing-over just like in the autosomal regions, although this area is located in the heterosomes.

Moreover, identification of the gene that determines the down color linked to the dominant sex gene within the chromosome W (SDW) and of the recessive sex allele within the chromosome Z (sdw) allowed, for the first time, a gene approach of sex inheritance in birds. The experimental results obtained by Pricop require the revision and amendment of Morgan's chromosomal theory of sex inheritance through heterosomes.

Pricop also proposed some amendments of the heterosome map modified by Hutt (1936). However, the suggested amendments of Pricop are rather simplistic, and the heterosomal map of Hutt (1936) is not the latest (at least not the most accepted) one in poultry science or animal genetics. Most of the recent published genetic maps are plenty of molecular evidences (see for example the map of Groenen et al 2000), and the amendments should be presented in the context of such complete genetic maps.

The hypothetical SDW gene of Pricop (2009) could be the HINTW gene, described by Smith (2007) and Smith et al (2007) as an intriguing candidate for a dominant female-determining gene on W chromosome. HINTW gene encodes an aberrant form of a hydrolase enzyme. In chicken embryos, HINTW is strongly expressed in the gonads and other tissues of ZW embryos (Smith 2007; Smith et al 2007). The same authors indicated that in vitro biochemical data show the fact HINTW gene can interfere with the action of a Z-linked orthologue: HINTZ, which could be the hypothetical sdw gene of Pricop. Smith (2007) underlines that HINTW is conserved among flying birds, and recent molecular analysis indicates that it has undergone positive selection over evolution.

Bacteria can transfer genes from one strain to another by three different mechanisms: transformation, conjugation and transduction, these events showing the universality of sexuality in the living world. Once more, the sex determination of a group of organisms is "genetic" and not "chromosomal" (Carpa 2010).

**The Basic Steps of Sex Chromosomes Evolution in Fish.** According to Traut & Winking (2001), three fish species are representative of the basic steps in sex chromosome evolution: (I) the zebrafish, *Danio rerio* (Hamilton), has environmental or polygenic sex determination without heterosomes; (II) the southern platyfish, *Xiphophorus maculatus* (Gunther), which has genetically defined sex chromosomes; and (III) the guppy, in which the acrocentric Y chromosome can be identified cytogenetically. Comparative genomic hybridization (CGH) indicated that a large part of the nonpairing region of the guppy Y chromosome comprises male-specific repetitive DNA. Only one-half of the Y chromosome pairs with homologous regions of the X in synaptonemal complexes. Orientation of guppy heterosomes allowed the recombination in only two of 49 observed synaptonemal complexes, suggesting that crossover is greatly reduced even in the homologous region.

However, even in the most evolved sex chromosomal systems of fish (such as guppy), all the possible kinds of recombination between sex chromosomes were reported: from X to X, from X to Y, from Y to X, and from Y to Y (see Lindholm & Breden 2002 and citations therein, but see also the results of Petrescu-Mag & Bourne 2008).

**Sex-linked Color Patterns and Sex Determining Locus in the Guppy: Genes or Gene Complexes?** Different phenotypes appear in the guppy due to dominance, codominance, poligeny, or some demonstrated interallelic interactions. Recent (both

molecular and classical) investigations suggest a mechanism of expression of several different loci in a single color pattern, resulting in high numbers of possible color pattern phenotypes. These genetic mechanisms that enhance natural variation, are additive effects of codominant alleles, suppressive actions of dominant alleles, and complex interplay between sex-linked and autosomal cofactors. In *Poecilia reticulata*, but also in many other vertebrates, the color pattern seems to be determined by complex interactions of many genes (at the same locus or not, located in the same chromosome or not), under variable environmental conditions. For example, the *Maculatus* color pattern is due to the presence of both *Maculatus* red and *Maculatus* black elements. On their turn both *Maculatus* red and *Maculatus* black could be composite in nature (see also details in review Petrescu-Mag 2009).

The deepest mechanism of sex determination is not clear yet, but even with respect to the major male sex determining locus on the Y chromosome we cannot tell whether it acts as a single locus or as a multifactorial complex that is almost never separated by genetic recombination – as long as we don't know the molecular mechanism (Dreyer cited by Petrescu-Mag 2009). However, the earlier studies of Winge (1922-1934) and recent molecular studies (Tripathy et al 2008) revealed a possible composite nature of the so called master sex determining gene located at the sex determining locus of the Y chromosome (Petrescu-Mag 2009).

**Conclusion.** Thinking well and looking to the most recent genetic evidences reported from studies on bacteria, invertebrates, fish, frogs, reptiles, birds, mammals and even humans, we can already drop the chromosomal concept of the sex determination (such as dosage of Z). The sex determining locus is not a true locus, but an agglomeration of loci very seldom separated by genetic recombination. Moreover, the W in ZZ-ZW systems and the Y in XX-XY systems are not empty at all, they still carry information.

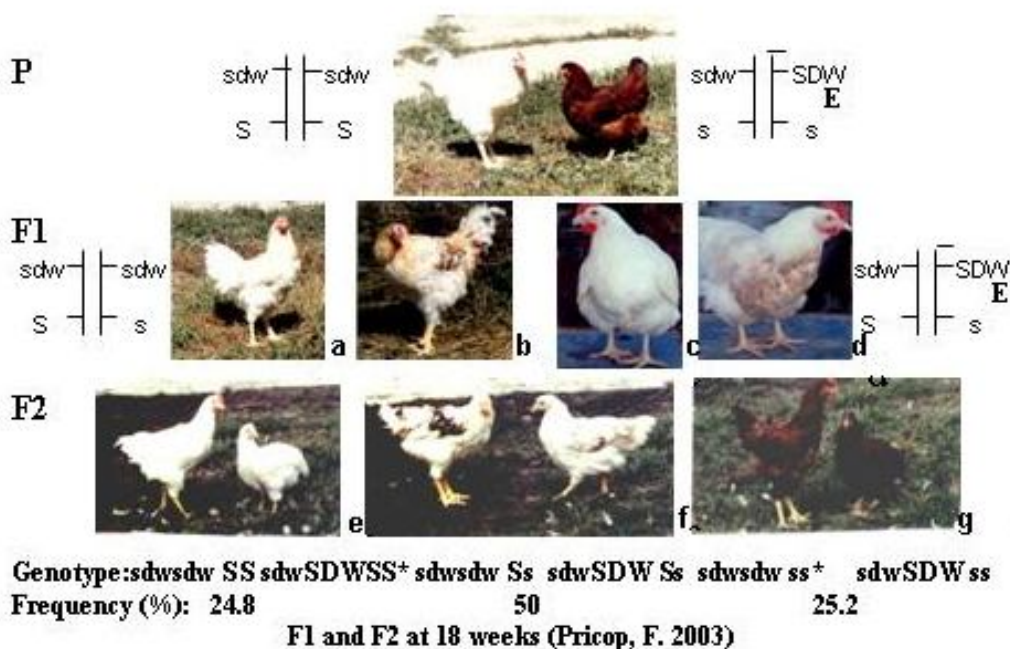
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**Cross between white *Rhode-Island* (SS) cocks and red *Rhode-Island* hens (ss)**



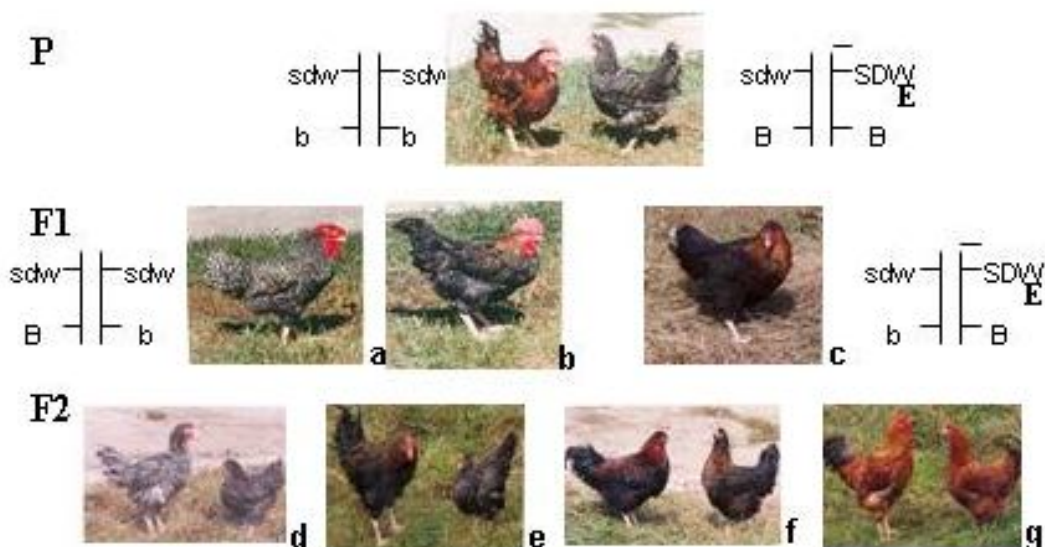
**Legend:**

**P**- parents, **F1** - first generation, **F2** - second generation, **SDW** - dominant sex gene, **sdw** - recessive sex allele, **S** - silver gene, **s** - gold gene, **E** – epistasis, **a** and **b** - silver heterozygous males, **c** and **d** - silver heterozygous females, **e** - silver homozygous males and female, **f** - silver heterozygous males and female, **g** - gold homozygous males and female,

\* Unexpected subjects in F2



**Cross between red *Rhode-Island* cocks (bb) and barred *Marans* hens (BB)**



**Genotype/Frequency (%):**

$sdwsdw BB$	$sdwSDWBB^*$	$sdwsdw Bb$	$sdwSDW Bb$	$sdwsdw bB^*$	$sdwSDW bB$	$sdwsdw bb^*$	$sdwSDW bb$
24.7		24.7		25.1		25.5	

**F1 and F2 at 18 weeks (Pricop, F. 2003)**

**Legend:**

**P**- parents, **F1** - first generation, **F2** - second generation, **SDW** - dominant sex gene, **sdw** - recessive sex allele, **B** - barred gene, **b** - gold gene, **E** – epistasis, **a** and **b** - barred heterozygous males, **c** – redish black heterozygous females, **d** - barred homozygous males and female, **e** – barred heterozygous male and female, **f** - redish black heterozygous males and female, **g** - gold homozygous males and female,  
 \* Unexpected subjects in F2





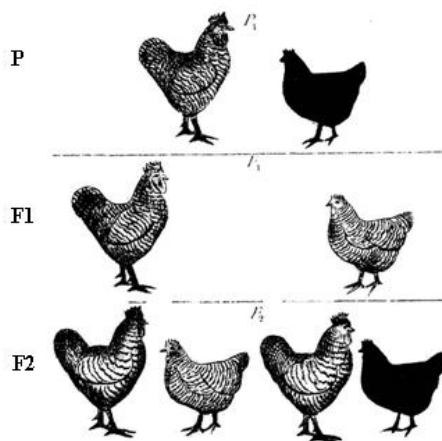
Experimental data I: Pricop (2003) vs. Morgan (1919)



Cross between barred *Marans* cocks (BB) and red *Rhode-Island* hens (bb)



Cross between white *Rhode-Island* cocks (SS) and red *Rhode-Island* hens (ss)



Cross between barred *Plymouth Rock* cocks (BB) and *Langshan* hens (b-)

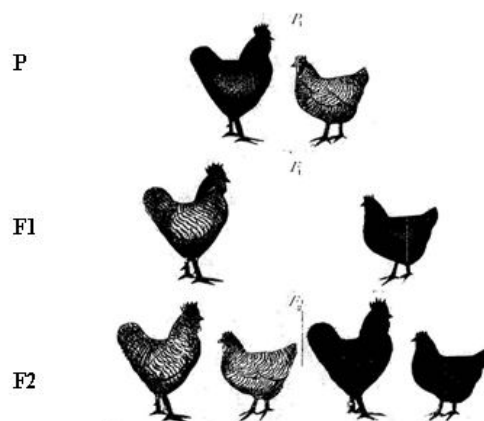
Experimental data II: Pricop (2003) vs. Morgan (1919)



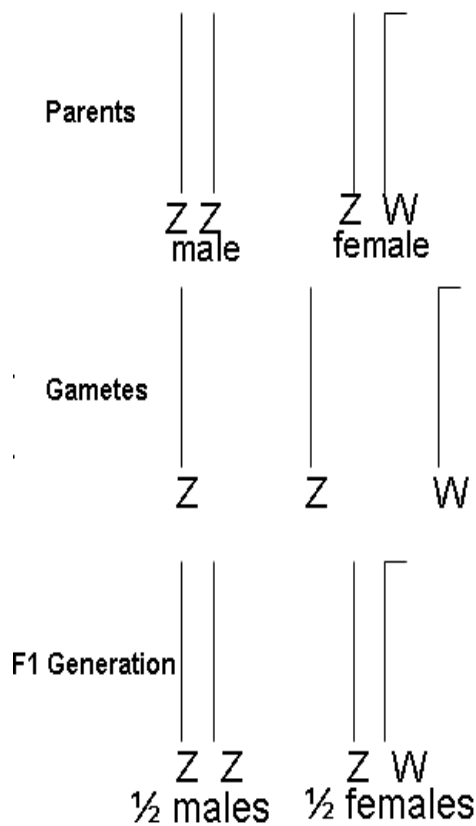
Cross between red *Rhode-Island* cocks (bb) and *Marans* barred hens (BB)



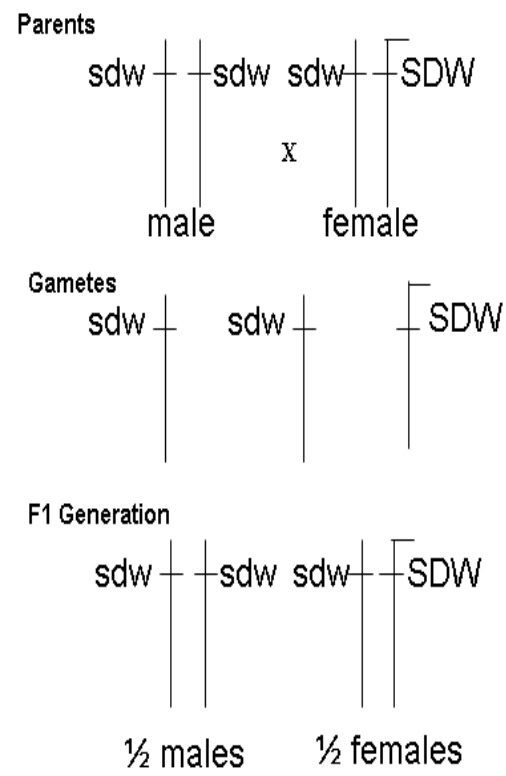
Cross between red *Rhode-Island* cocks (ss) and white *Rhode-Island* hens (SS)



Cross between *Langshan* cocks (bb) and barred *Plymouth Rock* hens (B-)



**The chromosomal theory of sex determination – Morgan (1919)**



**The gene theory of sex determination – Pricop (2005)**

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