a *b*

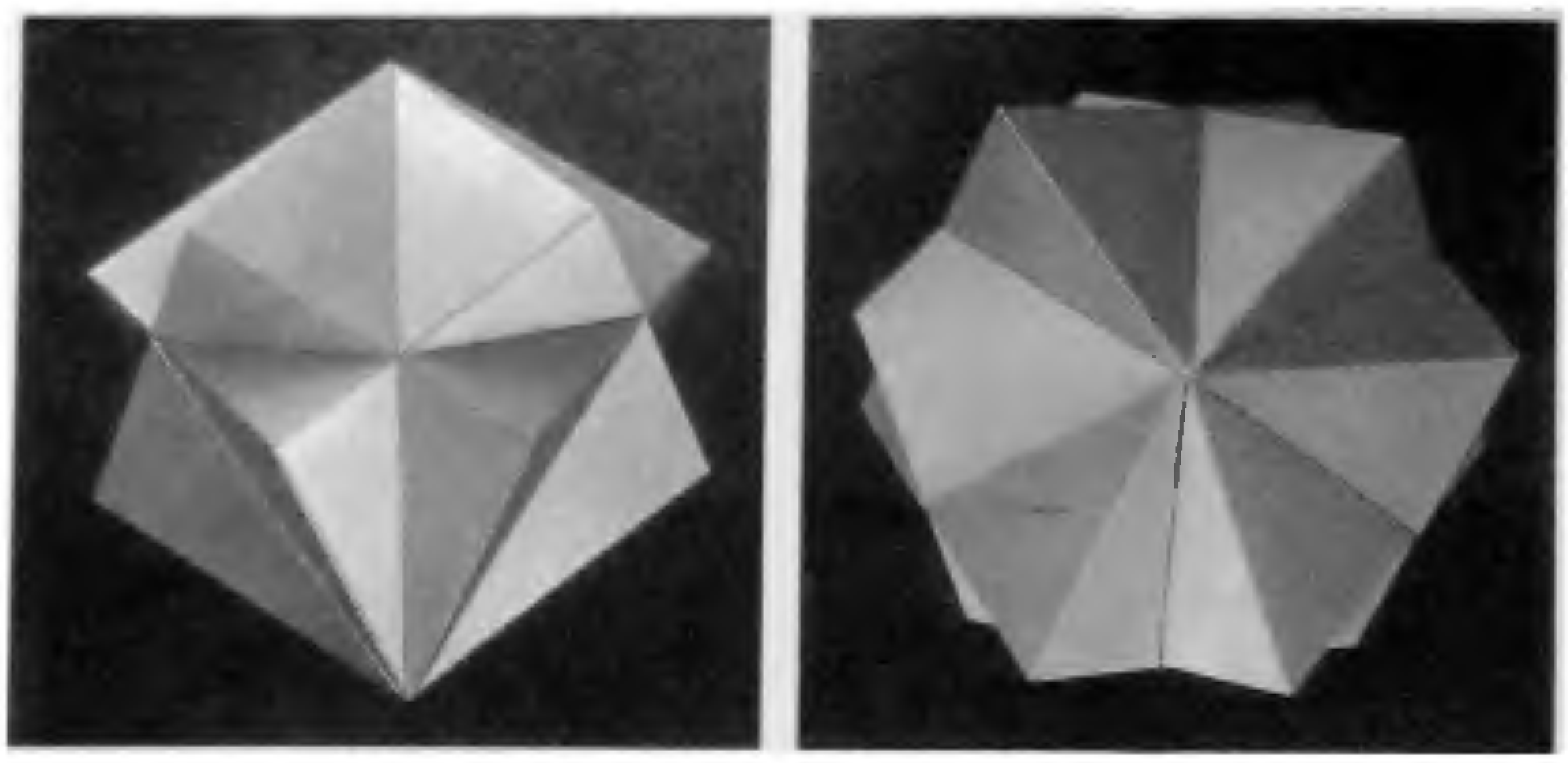

Figure 2 *a*, *b*. Two positions of a $D_3 \times I$ group in its $C_3 \times I$ orientation, shown together as images of one another rotated through an angle of 22°14'19".52. ***a***, general view; ***b***, along a threefold axis. A large number of such compounds (regular polyhedra with common centre) are introduced in the book for the first time.

Another perspective can come from artists or people who love activities like origami. In other words, the group theoretic insight can also mean for those gifted in art, a rational outlook towards structured or not so sttuctured design. To put it lightly, it could be interesting material for adults, who take toys seriously. In chapter 7, titled 'Assembling Models', instructions are given on how to design 3-D models from cardboard pieces like a jigsaw puzzle. This is similar to constructing the Brillouin zones of a crystalline structure with the Miller planes clearly marked. This can indeed be a lot of fun.

There are a few things that should excite lovers of geometry. For instance, the photograph of a 2.3 metres high ball and stick model of platonic solids, that the author had made inspired by an old Dutch book written by H. Naber. The author's cat eventually brought this piece of art and mastery to extinction. A personal memoir of history leading to the publication of the book, in the appendix, is an interesting reading.

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Genetics and Evolution of Aquatic Organisms. A. R. Beanmont ed. Chapman and Hall, Cheriton House, North Way, Andover, Hampshire SP10 5BE, UK. 1994. 539 pp. Price: not known.

Genetics – survey, inventories and experimentation – of aquatic organisms is rather a slow starter. Emphasis in the early 70s used to be on the measurement of genetic variations; its relationship to environmental variability; its maintenance by selection and its use in taxonomy. However with the emerging field of biotechnology, the technical advances in the study of genetics and the increasing dominance of neutral theory as the explanation for genetic variation at both the protein and DNA level, a major shift is discernible.

Out of 44 contributions under segregated titles, 24 relate to marine species, 10 to limnetic domain and the remaining 8 to aquatic environment in general. Large abundance with patchy distribution is a hallmark of aquatic organisms, more specifically the marine species. However, the paradox is that most species do not have enough genetic variations. Consequently, the intraspecific genetic diversities having discrepancies of very high magnitude, between abundance and population size still remain unexplained.

Another unanswered question relates to large temporal variations, particularly in marine biota. In spite of high gene flow, genetic differentiation on spatial scale requires differential survival of genotype after recruitment from planktonic larval stock. Of course, the large variance in reproductive process is mediated by hydrographic regimes. Thus there is a strong and direct linkage between population genetics and environment. Further, the large variance in reproductive process also affects population structure because of temporal and spatial variations in the genetic composition of the recruiting larvae. So far, the impact of DNA technology in population genetics is less than projected.

Talking about the evolution, several sets of biochemical databases (allozyme, immunological and DNA – RNA hybridization) have been applied to collate phylogenetic relationship among aquatic species. In terms of tools, the advent of polymerase chain reaction (PCR) technique has generated large amount of information on DNA, especially in finfishes. The population genetics studies on a wide range of agametic clones provide information on the evolutionary consequences of the basic differences between agametic clones in terms of genetic variability and extent of ecological differentiation. In this context, an unanswered question in chromosome genetics is 'do marine species frequently exhibit greater number of chromosomes than freshwater species?'

Genetic research complimentary to pollution monitoring programmes is becoming indispensable. Pollution-mediated mutations directly cause damage to the DNA molecule within the individual cell nucleus, resulting in gene mutation or chromosomal aberrations, though not much is on record about chromosomal aberrations. Another discernible influence of pollution is through selective pressure on the genetic structure of the population by modifying the environment. Heterozygote genotypes, because of their less energy demanding maintenance have better chances of survival in stressful environment.

Aquaculture has tremendous scope for genetic research, especially the quantitative genetics; chromosome ploidy manipulation; allozyme genetic and transgenic organisms. An important observation is 'standard errors on heritability estimates are uncomfortably larger unless..... based on very large numbers'. Hybrids which are heterotic for growth and resistant to disease have to be the goal as evidence from the success of different strains of crabs and catfishes indicates. In spite of the inherent sterility of triploids, a promising approach is to induce tetraploidy by cell fusion. Rather a disheartening finding for fish farmers is the repeatedly significant loss of genetic diversity following hatchery culture. Studies on effects of cultured fish on wild populations have demonstrated that in many cases, coadapted gene complexes may be broken down and unique alleles lost in wild population, following extensive hybridization and introgression of genes from cultured organisms. Transgenic involving DNA techniques is currently centered around transfection, i.e., the introduction of novel genes in aquaculture species. The number of genes which might be appropriate for genetic engineering in finfishes and several growth genes have now been identified and cloned.

The contents are mainly confined to reports from Europe. It warrants an early compilation of results from the rest of the world, so as to have a global perspective.

Indeed a good read.

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