cells with 43 and 45 chromosomes. As far as the ovariectomized animals were concerned, the χ^2-test confirmed this assumption as the resulting $p < 0.2$ is not significant. As the old hamsters showed a predominance of cells with 43 chromosomes over such with 45 the resulting $p < 0.001$ proved to be a highly significant deviation. This points to the fact that nondisjunction alone cannot be responsible for the hypoploidy described above.

One important explanation would be the lack of female sexual hormones. It has been mentioned that a sudden increase of aneuploid cells can also be observed in human females along with the ceasing of sexual hormones. Likewise the hamsters of group II showed a significant increase of aberrant cells compared to the control group, close to the group of senile animals. With these hamsters of group B, a condition comparable to menopause had been prematurely induced by tying off the ovaries (exploration at the time of chromosome-preparation showed complete atrophy). This appears to be strong evidence for the fact that sexual hormones, in some way yet unknown, keep cells from deviating into aneuploidy. Several different factors might be responsible for this restraining effect: it might be caused by a time regulator controlling divisional frequency genetically, and this preventing precipitous cell-divisions which are always accompanied with the risk of nondisjunction, as is known to be the case with tumors. Other possibilities might be hormonal components also acting as a regulative control in a fashion yet unknown. In any case, one should not accuse the X-chromosomes, because they were not lost.

Evidence for rapid speciation in African cichlid fishes

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Summary. Extremely rapid divergence among 7 species of African cichlid fishes is suggested by high estimates of allozymic similarity. Significant differences in gene frequencies among sympatric populations support reproductive isolation of these taxa.

Extreme examples of adaptive radiation and community complexity occur among African fishes of the family Cichlidae. In Lake Malawi, Africa, approximately 300 cichlids are endemic. It has been suggested that this level of taxonomic diversity may have been achieved by fairly rapid rates of speciation[2–4]. In turn, rapid speciation has suggested a variety of novel modes of divergence[5–7]. To examine relative rates of speciation in this fauna, genetic similarity estimates among 7 endemic Malawi cichlids were examined by electrophoresis. Extremely rapid speciation is supported by the low degree of genetic differentiation among these species.

The species examined (table 1) are the most common members of the Mbuna complex a presumably monophyletic group of approximately 30 species generally restricted to the rocky littoral zone. This particular complex is of interest to students of evolution because it occurs in an area which lacks obvious physical barriers usually associated with allopatric speciation[2]. A minimum of 16 allozyme loci encoded by 10 protein systems was examined by standard methods of starch gel electrophoresis from tissue extracts of fish collected sympatrically near Monkey Bay, Malawi[8]. Genetic similarities were computed from estimates of allele frequencies by Nei's Coefficient of Identity (I)[9]. This statistic can vary from 0 to 1, with 1 indicating complete genetic identity. Interspecific similarities in fishes vary widely, but are generally $I < 0.90$ (Sarich[10]). Similarities among the 7 endemic cichlids ranged from 0.85 to 0.99 (table 1; mean 0.934 ± 0.008). Genetic distance between species is apparently a simple function of elapsed time since divergence from a common ancestor[11,12]. Unfortunately, accurate rate constants de-

Table 1. Genetic similarities (I)[9] among 7 endemic Malawi cichlids

		A	B	C	D	E	F	G
Petrotilapia tridentiger	A	–	0.956	0.973	0.983	0.955	0.919	0.906
Labeotropheus fulleborni	B		–	0.903	0.932	0.919	0.864	0.856
Pseudotropheus tropheops	C			–	0.978	0.994	0.923	0.931
P. auratus	D				–	0.966	0.923	0.899
P. zebra	E					–	0.912	0.938
P. elegans	F						–	0.991
P. livingstoni	G							–

Horizontal starch gel electrophoresis was performed on tissue extracts in a standard manner[8]. At least 28 individuals were examined for each species. Genetic similarities were calculated from observed allele frequencies at loci encoded by the following proteins: aminopeptidase, esterase (EST), aldolase, general protein (GP), lactate dehydrogenase (LDH), malate dehydrogenase, phosphoglucose isomerase (PGI), phosphoglucomutase, sorbitol dehydrogenase, superoxide dismutase, and xanthine dehydrogenase.

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scribing the relationship between electrophoretic distance and time are currently unreliable[13]. Nevertheless, the relative degree of temporal isolation between species can be appreciated when compared to levels of differentiation between conspecific populations. For example, similarities among geographic samples of continuously distributed North American fishes typically have $I = 0.95–0.98$[10, 14, 15]. In Lake Malawi, similarities among 3 geographic samples of *Labeotropheus fulleborni* (table 1, B) ranged from $I = 0.940$ to 0.977. 8 separate comparisons between endemic cichlids exhibited $I > 0.95$, 3 of which had I in excess of 0.980 (table 1, A–D, C–E, F–G). Against the background of intraspecific divergence, most interspecific differences are trivial and suggest very recent genetic continuity. This idea is consistent both with electrophoretic estimates in other cichlid fishes (Kornfield, Ritte, Richler and Wahrman, in preparation) as well as with stratigraphical estimates of divergence (5000 years) for the endemic cichlids of Lake Nabagaboo, Uganda[3].

Table 2. Allele frequencies from endemic Malawi cichlids collected in sympatry at 2 localities*

		Locality 1					Locality 2	
Locus	Allele	A	B	C	D	E	F	G
PGI-1	1.00	1.0	0.89	1.0	1.0	0.99	0.83	0.99
	1.05		0.11			0.01	0.17	0.01
	n	80	97	90	102	111	48	100
GP-1	1.00	0.69	1.0	1.0	1.0	1.0	1.0	1.0
	1.10	0.31						
	n	26	44	74	80	96	62	96
GP-3	1.00	1.0	1.0	1.0	1.0	1.0	0.79	1.0
	1.05						0.04	
	0.95						0.17	
	n	52	46	74	102	96	56	100
EST-1	0.85	0.23						
	0.90	0.61	0.09	0.21	0.52			
	0.95	0.11	0.55	0.38	0.06	0.01		
	1.00		0.10	0.10	0.40	0.08		
	1.05			0.02		0.86		
	0.00	0.05	0.26	0.29	0.02	0.05		
	n	48	90	97	102	108		
LDH	1.00						0.44	0.64
	1.10						0.56	0.36
	n						64	98

*Locality 1 (14° 02′00″ S; 34° 54′ E); Locality 2 (14° 17′ S; 34° 56′ E). Species and loci abbreviations as in table 1.

The high degree of similarity among these fishes makes it imperative that specific status be critically established. Viable hybrids can be artifically produced between some Mbuna[16], but hybrids in the lake are unknown[2]. The 7 Malawi endemics differ in breeding coloration and morphology[17], and most species are ecologically distinguishable[2]. However, morphological and ecological distinctness may be misleading. In New World cichlids, discrete ecomorphotypes may exist sympatrically within a single species of *Cichlasoma*[18]. Though some evidence has cast doubt upon this interpretation[19, 20], recent ethological observations support conspecificity of trophic morphs (Taylor, personal communication).

Morphological polymorphism must be considered for the Lake Malawi cichlids. If any of these endemics were conspecific, allele frequencies at all loci would be the same for morphotypes collected simultaneously at any locality. That is, panmaxia would ensure allelic uniformity among morphs. Allele frequencies, however, differ significantly among species collected sympatrically in Lake Malawi (table 2). This genetic evidence further supports reproductive isolation among these species.

Several recent studies have also reported high similarities among reproductively isolated taxa[10, 14, 21]. The apparent discrepancy between such similarities and those presumably typical of most other species emphasizes that a general timetable for taxonomic differentiation may not be realistic. That is, rates of speciation may differ dramatically among taxonomic groups[22, 23]. Though structural genes provide convenient benchmarks to assess the rates of phyletic evolution, the structural loci are apparently not involved in speciation per se.

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Biological relationship of cucumis virus-3 and powdery mildew fungus in bottle gourd

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Summary. 2 kinds of interrelationship between cucumis virus-3 and powdery mildew fungus in bottle gourd were noted. The fungal conidia transmitted the mosaic virus infection from infected to healthy bottle gourd plants with ease. The transmission relation was found to be external. Powdery mildew symptoms were restricted on mosaic infected leaves and appeared late, while virus symptoms appeared precociously in mildew infected plants.

Viruses and fungi interact in many ways in their host plants. Fungal transmission of plant viruses has been established beyond doubt and fungus vector-virus relationship has been extensively studied[1]. Synergism or antagonism between viruses and non-vector fungal pathogens in plants has also been described by many workers[2–11]. However, the interaction between the vector fungus and the transmitted virus in respect of disease development has not been sufficiently explored. Moreover, the majority of the examples of transmitting fungi are found in soilborne group where the infection is brought through host roots. The present investigation reveals both the aspects of relationship between the 2 leaf pathogens, namely *Oidium* sp. (powdery mildew) and cucumis virus-3 (mosaic) of bottle gourd (*Lagenaria siceraria* Mol. Standl.).