already weakened by overfishing (18). Possible mechanisms by which such changes may be manifest are reviewed by Sundby (19). Because changes in community structure reflect the adjustment of pelagic ecosytems to modifications in water masses, currents, and/or atmospheric forcing, it is clearly important to continue to monitor plankton associations, which provide us with a valuable means of checking the well-being of marine ecosystems in the North Atlantic Ocean and possibly in other oceanic regions.

References and Notes
8. Supporting material is available on Science Online.
the 21-year “DOK” system comparison trial (bio-Dynamic, bio-Organic, and “Konventionell”), which is based on a ley rotation. The field experiment was set up in 1978 on a loess soil at Therwil, Switzerland [(7) and supporting online material]. Two organic farming systems (biodynamic, BIODYN; bioorganic, BIOORG) and two conventional systems (using mineral fertilizer plus farmyard manure: CONFYM; using mineral fertilizer exclusively: CONMIN) are emulated in a replicated field plot experiment (table S1 and fig. S1). Both conventional systems were modified to integrated farming in 1985. Crop rotation, varieties, and tillage were identical in all systems (table S2).

We found nutrient input (N, P, K) in the organic systems to be 34 to 51% lower than in the conventional systems, whereas mean crop yield was only 20% lower over a period of 21 years (Fig. 1, Table 1), indicating an efficient production. In the organic systems, the energy to produce a crop dry matter unit was 20 to 56% lower than in conventional and correspondingly 36 to 53% lower per unit of land area (tables S4 and S5).

Potato yields in the organic systems were 58 to 66% of those in the conventional plots (Fig. 1), mainly due to low potassium supply and the incidence of Phytophthora infestans. Winter wheat yields in the third crop rotation period reached an average of 4.1 metric tons per hectare in the organic systems. This corresponds to 90% of the grain harvest of the conventional systems, which is similar to yields of conventional farms in the region (8). Differences in grass-clover yields were small.

Cereal crop yields under organic management in Europe typically are 60 to 70% of those under conventional management, whereas grassland yields are in the range of 70 to 100%. Profits of organic farms in Europe are similar to those of comparable conventional farms (9). Appropriate plant breeding may further improve cereal yields in organic farming. There were minor differences between the farming systems in food quality (10).

The maintenance of soil fertility is important for sustainable land use. In our experimental plots, organically managed soils exhibit greater biological activity than the conventionally managed soils. In contrast, soil chemical and physical parameters show fewer differences (Fig. 2).

Soil aggregate stability as assessed by the percolation method (11) and the wet sieving method (12) was 10 to 60% higher in the organic plots than in the conventional plots (Fig. 2A). These differences reflect the situation as observed in the field (Fig. 3, A and B), where organic plots had a greater soil stability. We found a positive correlation between aggregate stability and microbial biomass \((r = 0.68, P < 0.05)\), and between aggregate stability and earthworm biomass \((r = 0.45, P < 0.05)\).

Soil pH was slightly higher in the organic systems (Fig. 2B). Soluble fractions of phosphorus and potassium were lower in the organic soils than in the conventional soils, whereas calcium and magnesium were higher. However, the flux of phosphorus between the matrix and the soil solution was highest in the BIODYN system (13). Soil microorganisms govern the numerous nutrient cycling reactions in soils. Soil microbial biomass increased in the order CONMIN < CONFYM < BIOORG < BIODYN (Fig. 2C). In soils of the organic systems, dehydrogenase, protease, and phosphatase activities were higher than in the conventional systems, indicating a higher overall microbial activity and a higher capacity to cleave protein and organic phosphorus (12). Phosphorus flux through the microbial biomass was faster in organic soils, and more phosphorus was bound in the microbial biomass (14, 15). Evidently, nutrients in the organic systems are less dissolved in the soil solution, and microbial transformation processes may contribute to the plants’ phosphorus supply.

### Table 1. Input of nutrients, pesticides, and fossil energy to the DOK trial systems.

<table>
<thead>
<tr>
<th>Farming system</th>
<th>Total nitrogen (kg N ha(^{-1}) year(^{-1}))</th>
<th>Soluble nitrogen (kg N ha(^{-1}) year(^{-1}))</th>
<th>Phosphorus (kg P ha(^{-1}) year(^{-1}))</th>
<th>Potassium (kg K ha(^{-1}) year(^{-1}))</th>
<th>Pesticides (kg active ingredients ha(^{-1}) year(^{-1}))</th>
<th>Energy (GJ ha(^{-1}) year(^{-1}))</th>
</tr>
</thead>
<tbody>
<tr>
<td>BIODYN</td>
<td>99</td>
<td>34</td>
<td>24</td>
<td>158</td>
<td>0</td>
<td>12.8</td>
</tr>
<tr>
<td>BIOORG</td>
<td>93</td>
<td>31</td>
<td>28</td>
<td>131</td>
<td>0.21</td>
<td>13.3</td>
</tr>
<tr>
<td>CONFYM</td>
<td>149</td>
<td>96</td>
<td>43</td>
<td>268</td>
<td>6</td>
<td>20.9</td>
</tr>
<tr>
<td>CONMIN</td>
<td>125</td>
<td>125</td>
<td>42</td>
<td>253</td>
<td>6</td>
<td>24.1</td>
</tr>
</tbody>
</table>

Mycorrhizae as members of the soil community ameliorate plant mineral nutrition and contribute to soil aggregate formation (16). Root length colonized by mycorrhizae in organic farming systems was 40% higher than in conventional systems (7) (Fig. 2C).

Biomass and abundance of earthworms were higher by a factor of 1.3 to 3.2 in the organic plots as compared with conventional (17) (Fig. 2D). We also investigated epigaeic arthropods that live above ground, because they are important predators and considered sensitive indicators of soil fertility. Average activity density of carabids, staphylinids, and spiders in the organic plots was almost twice that of the conventional plots (18) (Fig. 2D).

Healthy ecosystems are characterized by high species diversity. The DOK trial shows that organic farming allows the development of a relatively diverse weed flora. Nine to 11 weed species were found in organically managed wheat plots and one species in conventional plots. Between 28 and 34 carabid species were found in the BIODYN system, 26 to 29 species in the BIOORG system, and 22 to 26 species in the CONFYM system (18). Some specialized and endangered species were present only in the two organic systems. Apart from the presence and diversity of weeds, direct effects of pesticides and the density of the wheat crop stand are most likely influencing arthropod activity and diversity.

One of the particularly remarkable findings, presented in Fig. 4, was a strong and significant increase in microbial diversity (BILOG Inc., Hayward, CA) in the order CONMIN, CONFYM < BIOORG < BIODYN, and an associated decrease in the metabolic quotient ($q_{CO_2}$) (19). According to Odum’s theory on the strategy of ecosystem development, the ratio of total respiration to total biomass decreases during succession in an ecosystem (20). This quotient has been adapted to soil organisms (21), where CO$_2$ evolution is a biological process mainly governed by microorganisms. The lower $q_{CO_2}$ in the organic systems, especially in the BIODYN system, indicates that these communities are able to use organic substances more for growth than for maintenance.

Under controlled conditions, the diverse microbial community of the BIODYN soil decomposed more 14C-labeled plant material than the ones of the conventional soils (22). In the field, light fraction particulate organic matter, indicating undecomposed plant material, decayed more completely in organic systems (23). Hence, microbial communities...
Control of Stomatal Distribution on the Arabidopsis Leaf Surface

Jeanette A. Nadeau and Fred D. Sack*

Stomata regulate gas exchange and are distributed across the leaf epidermis with characteristic spacing. Arabidopsis stomata are produced by asymmetric cell divisions. Mutations in the gene TOO MANY MOUTHS (TMM) disrupt patterning by randomizing the plane of formative asymmetric divisions and by permitting ectopic divisions. TMM encodes a leucine-rich repeat–containing receptor-like protein expressed in proliferative postprotodermal cells. TMM appears to function in a position-dependent signaling pathway that controls the plane of patterning divisions as well as the balance between stem cell renewal and differentiation in stomatal and epidermal development.

Stomata allow gas exchange and thus are key to the survival of land plants, yet the genes controlling stomatal development are poorly understood (1, 2). Both the number and distribution of stomata are regulated during leaf development. Stomata are formed after a series of asymmetric divisions of transiently self-renewing precursors termed meristemoids (Fig. S1 (3)). Stomata are continually produced during the mosaic of the leaf, and many form by division of cells next to preexisting stomata (Fig. 1A). Correct spacing results when the plane of formative asymmetric divisions is oriented such that the new precursor, the satellite meristemoid, does not contact the preexisting stoma or precursor (1, 4). Intercellular signaling provides spatial cues that regulate division orientation and may also block asymmetric division in cells adjacent to two stomata or precursors (4). The recessive too many mouths (tmm) mutation randomizes the plane of asymmetric division in cells next to a single stoma or precursor and permits asymmetric divisions in cells next to two stomata or precursors, thus producing clusters of stomata (Fig. 1, A and C). Also, tmm meristemoids divide fewer times before assuming the determinate guard mother cell fate. These phenotypes suggest that TMM is required for cells to respond appropriately to their position during stomatal development and that TMM participates in intercellular signaling.

With the use of positional cloning (3), TMM was found to encode a leucine-rich repeat (LRR)–containing receptor-like protein of 496 amino acids with a molecular weight of ~54 kD (Fig. 2A). The predicted protein product contains 10 uninterrupted plant-type LRRs (5) and a putative COOH-terminal transmembrane domain. TMM en-

References and Notes
4. www.organic.aber.ac.uk/stats.shtml
10. T. Allföldi et al., unpublished observations.
26. We sincerely thank all co-workers in the DOK trial, especially W. Stauffer and R. Frei and the farmer groups. We also thank T. Boller and A. Wiemken and two unknown referees for their helpful comments.

Supporting Online Material
www.sciencemag.org/cgi/content/full/296/5573/1694/DC1
Materials and Methods
Fig. S1
Tables S1 to S5
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