Downy mildew caused by the oomycete Hyaloperonos- pora parasitica (syn.The objective of this study was to complete the assessment of the downy mildew resistance sources selected in previous work in order to determine if they could provide potentially durable control of downy mildew for UK vegetable production.The development and deployment of cultivars with sin- gle major disease resistance genes has frequently failed toprovide durable disease control due to the quick evolu- tion of pathotypes virulent on resistant cultivars, so in cases such as downy mildew (Bremia lactucae) of lettuce, blackleg (Leptosphaeria maculans) of oilseed rape, northern leaf blight (Setosphaeria turcica) of maize, leaf and stripe rust (Puccinia triticina and P. striiformis) of wheat and potato late blight (Phytophthora infestans) there has been a continuous effort to find sources of broad-spectrum resistance and to devise strategies to deploy the resistant cultivars (Crute & Norwood, 1981; Sivasithamparam et al., 2005; Stuthman et al., 2007; Zhang et al., 2009).Several sources of seedling resis- tance to H. parasitica in B. oleracea have been reported previously, and heritability of the resistance has been characterized in many cases including: single dominant genes in broccoli and cauliflower (Natti et al., 1967; Jen- sen et al., 1999a; Farnham et al., 2002), a single recessive gene in cauliflower (Hoser-Krauze et al., 1984), recessive gene(s) in kale, Savoy cabbage and Brussels sprouts (Carlsson et al., 2004) and multiple (additive) genes in cauliflower, broccoli and cabbage (Moss et al., 1988; Hoser-Krauze et al., 1995; Jensen et al., 1999b).The same approach was subsequently applied to B. oleracea in a coordinated effort to identify sources of resistance to black rot (Xanthomonas campestris pv. campestris), downy mildew (H. parasitica), white blister rust (Albugo candida) and cabbage aphid (Brevicoryne brassicae) in a core diversity collection of more than 400 B. oleracea accessions (Leckie et al., 1996; Ellis et al., 1998; Taylor et al., 2002).In the current study, a systematic approach pioneered more than four decades ago at the National Vegetable Research Station (NVRS), Wellesbourne, UK, for predic- tive breeding of durable resistance to downy mildew in lettuce, and subsequently applied to other major vegeta- ble diseases (Crute, 1992; Taylor et al., 1996, 2002) has been followed.Repeated application of fungicides is generally used for control, but the effective- ness of this approach has been limited because there is a restricted range of active ingredients effective against oomycete pathogens, and frequent prophylactic applica- tion of fungicides has led to the selection and widespread distribution of fungicide-insensitive variants of the path- ogen (Brophy & Laing, 1992).To achieve this, the resistance of selected lines was assessed against a spectrum of UK isolates of H. par- asitica, the inheritance of resistance in some of the resistant lines was studied and breeding for the development of broccoli and cauliflower lines pos- sessing the resistance identified in selected lines was initiatedInbreeding and selection of true-breeding resistant lines may often be required at this stage, because plant genetic resources (e.g. older open pollinated culti- vars and land races or wild crop relatives) can comprise heterogeneous mixtures of resistant and susceptible geno- types. Peronospora parasitica) is an eco- nomically important foliar disease of Brassica oleracea crops (cabbage, broccoli, cauliflower, kale and Brussels sprouts).Downy mildew can affect plants at all growth stages, but the most damaging effects are generally restricted to young seedlings, causing heavy losses in plant nurseries, and to particular organs such as cauli- flower curds (Channon, 1981).The NVRS approach was used successfully to identify race non-specific resistance to lettuce downy mildew and bac- terial diseases of common bean and pea (Crute & Norwood, 1981; Schmit et al., 1993; Taylor et al., 1996).Genetically uniform resistant lines can then be screened against a more extensive sample of pathogen isolates, collected widely from vegetable production regions, to identify examples of broad-spectrum disease resistance against the entire pathogen collection. A broadly virulent isolate (one which could cause typical disease symptoms in the initial subset of cultivars) was then chosen to screen a much lar- ger host diversity collection to identify new sources of dis- ease resistance.The approach began in each case with an initial characterization of differential reactions amongst standard vegetable cultivars for resistance to a small sam- ple of pathogen isolates.Downy mildew resistant cultivars would offer a prac- tical, environmentally acceptable alternative method to control downy mildew.The breadth of resistance provided against a collection of H. parasitica isolates was not investigated in these previ- ous reports, so the potential durability of each resistance is unknown.The disease is distributed worldwide wherever brassica crops are grown and is .(favoured by cool humid weather that is frequent in spring or autumn (Channon, 1981