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**Evaluation of hooded (*Kap1*), awnless (*Lks1*) and orange lemma (*rob1*) mutants of barley (*Hordeum vulgare* L.) for their use as forage crop**

Barley (*Hordeum vulgare* L.) is grown on around 50 million hectares and is the fifth important crop in the world. Its grain is mostly used as fodder for livestock or as malt for beer and whisky. Within this study, mutant stocks of barley were investigated for their suitability as forage crop. The mutant stocks included spontaneous occurring mutants and isolines created with spontaneous mutants in different genetic backgrounds by back-crossing. Forage barley can either be grazed at early growth stage or produced into silage or hay at heading, milk or early dough stage. Awns can cause injury in the mouth of animals which can lead to infections and less acceptability of the fodder. The *Lks1* mutants have spikes without awns, in the *Kap1* mutants the awns are replaced by ‘hoods’, i.e. reversed sterile florets on the end of the lemma. The *rob1* mutant is supposed to produce less lignin and, therefore, a better digestibility is assumed. The barley mutants were investigated in three years field trials in the Pannonian region of Austria for early vigour and growth, resistance to fungal leaf diseases, biomass and grain yield, thousand grain weight and seed plumpness. Moreover, check variety ‘Optic’ and its EMS induced orange lemma mutant (*rob1*) were cut at two growth stages (i.e. booting, milk dough), dried to hay and submitted to a fermentation study using the rumen simulation technique (Rusitec). Some hooded and awnless mutant genotypes were identified with good to medium disease resistance, and biomass and grain yield similar to the check varieties ‘Optic’ and ‘Eunova’. The Rusitec experiment showed significant differences between wild-type ‘Optic’ and its *rob1* mutant with respect to chemical composition, fermentation characteristics and diversity of *in vitro* rumen bacterial community. A breeding program was started to combine awnless and/or hooded genotypes with orange lemma genotypes to combine the favourable mutant genes in one genotype.