Differential selection of yield and quality traits has shaped genomic signatures of cowpea domestication and improvement

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Cowpeas are important tropical legumes in ensuring food and nutritional security in developing countries especially in sub-Saharan Africa. Herein, we reported two high-quality genome assemblies of grain and vegetable cowpeas and resequenced 344 accessions to characterize the genomic variations landscape. We identified thirty-nine loci for ten important agronomic traits and more than 541 potential loci underwent selection during cowpea domestication and improvement. Particularly, the synchronous selections on the pod-shattering loci and their neighboring stresses relevant loci likely led to the enhancement of pod-shattering resistance and the compromise of stresses-resistance during the domestication from grain to vegetable cowpeas. Moreover, differential selections on multiple loci associated with pod length, grain number per pod, seed weight, pod / seed soluble sugars and seed crude proteins shaped the yield and quality diversity in cowpeas. Our findings provide genomic insights into cowpea domestication and improvement footprints, enabling further genome-informed cultivar improvement of cowpeas.