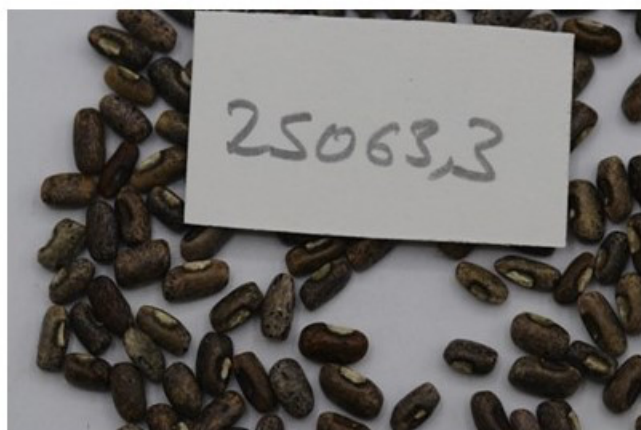
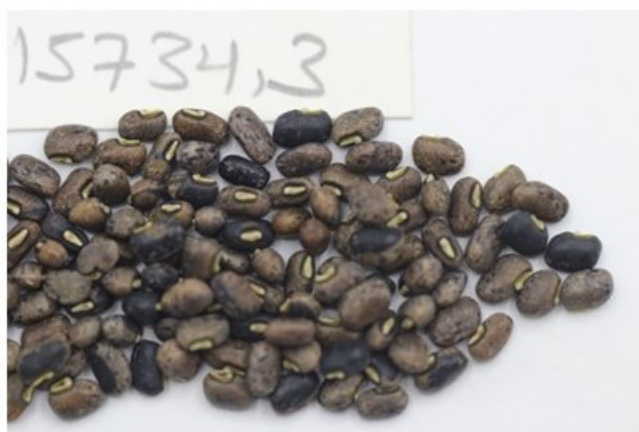
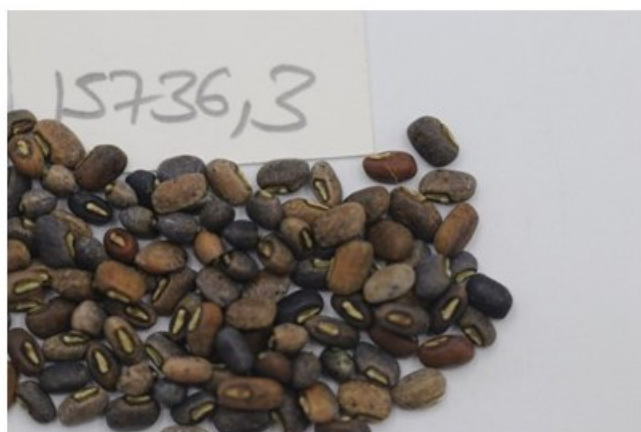


A subset of cowpea (*Vigna unguiculata*) wild subspecies in the ILRI Forage Genebank

July 2026

Report



Contents

BACKGROUND	3
-------------------	----------

SUMMARY	3
----------------	----------



Authors: Meki Shehabu Muktar, Alemayehu Teressa Negawo, and Chris S Jones

International Livestock Research Institute

Suggested citation: Muktar, M.S., Negawo, A.T. and Jones, C.S. 2026. A subset of cowpea (*Vigna unguiculata*) wild subspecies in the ILRI Forage Genebank. Nairobi, Kenya: International Livestock Research Institute (ILRI).

Cover photo: ILRI/Yayetiru Mulugeta and Arega Alemayehu.

Copyright: © 2026. ILRI. This publication is licensed for use under a Creative Commons Attribution 4.0 International License (CC BY 4.0). To view this license, visit <https://creativecommons.org/licenses/by/4.0>.

Disclaimers: This publication has been prepared as an output of the CGIAR Genebanks Accelerator. Any views and opinions expressed in this publication are those of the author(s) and are not necessarily representative of or endorsed by the CGIAR System Organization.

Acknowledgements: This work was conducted as part of the CGIAR Genebanks Accelerator with the aim to strengthen the global genebank system in conserving and making available a wide variety of plant genetic resources vital for the development of climate-adapted crops and resilient food systems. CGIAR research is supported by contributions to the [CGIAR Trust Fund](#). CGIAR is a global research partnership for a food-secure future dedicated to transforming food, land, and water systems in a climate crisis.

Background

Cowpea wild subspecies are a valuable genetic resource that play a critical role in cowpea improvement and long-term crop resilience. They harbor extensive genetic diversity that is often absent in cultivated varieties, including novel alleles for biotic and abiotic stress tolerance. Wild cowpea relatives possess resistance to major pests and diseases, including aphids, bruchids, root-knot nematodes, and various foliar pathogens. They also exhibit adaptive traits that support survival in harsh environments, such as drought and heat tolerance - traits that are increasingly important under current climate change conditions. In addition to stress-related traits, cowpea wild species contribute to enhancing seed quality, biomass production, and reproductive traits that can be used in both grain and forage cowpea breeding. Their genetic diversity is essential for broadening the narrow genetic base of cultivated cowpea, supporting the development of improved varieties suited to climate change and emerging production challenges.

Summary

The cowpea wild subspecies were genotyped using the DArTseq platform alongside the large collection of cultivated cowpea accessions maintained in the International Livestock Research Institute (ILRI) Forage Genebank. Based on passport data, the wild set included three major groups: 16 *Vigna unguiculata* ssp. *dekindtiana*, five *V. unguiculata* ssp. *pubescens*, and two *V. unguiculata* ssp. *unguiculata* var. *spontanea*. Additional accessions were assigned to the subspecies using hierarchical clustering with a subset of high-quality genome-wide SNP markers, resulting in the inference of additional nine subsp. *dekindtiana*, two subsp. *pubescens*, and six var. *spontanea*. These cowpea wild species can be distributed upon request through the genebank and represent a vital reservoir of genetic diversity for breeding programs, conservation initiatives, and sustainable agricultural production.

Figure 1. Hierarchical clustering shows the wild cowpea subspecies clustered together on the left and distinctly separated from the cultivated species.

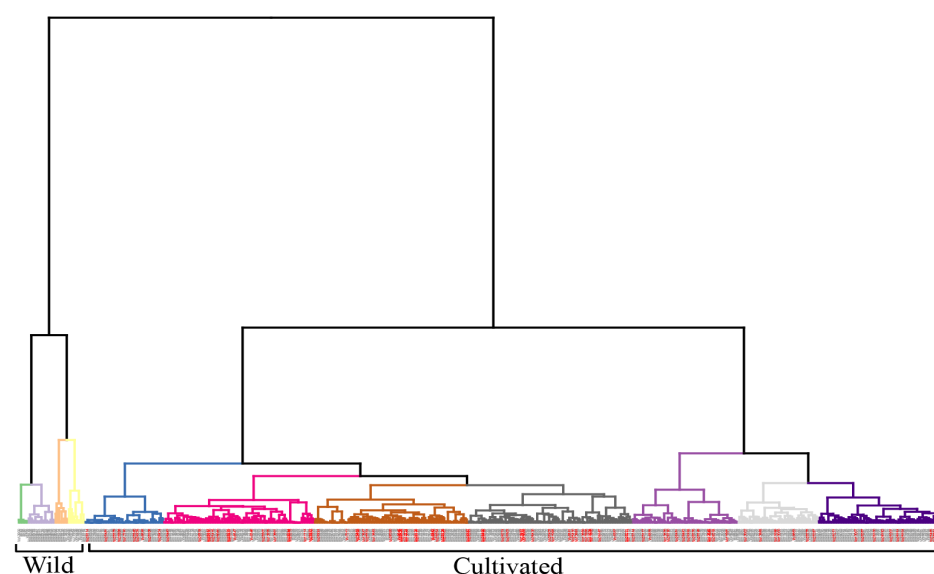


Table 1. The list and detailed information of the cowpea wild subspecies

No.	Accession	Taxon	DOI	Origin	Cluster
1	12900	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/FRRQ\$	Kenya	7
2	706	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/G6629	Tanzania	7
3	43	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/G4KTX	Tanzania	7
4	41	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/G4K9C	Tanzania	7
5	44	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/G4M42	Tanzania	7
6	40	<i>Vigna unguiculata</i> subsp. <i>pubescens</i>	10.18730/G4K03	Tanzania	7
7	25173	<i>Vigna unguiculata</i> subsp. <i>dekindtiana</i>	10.18730/G43JV		8

8	25176	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G43NY	Kenya	8
9	25174	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G43KW		8
10	25206	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G44MR	Botswana	8
11	25067	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G408*	Botswana	8
12	25068	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G409~	Botswana	8
13	25071	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40CU	Botswana	8
14	25077	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40J5	Botswana	8
15	25073	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40E1	Botswana	8
16	25063	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G404W	Botswana	8
17	25066	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G407Z	Botswana	8
18	24603	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G3HM8	Botswana	8
19	25070	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40B=	Botswana	8
20	25074	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40F2	Botswana	8
21	25076	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40H4	Botswana	8
22	25072	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G40D0	Botswana	8
23	12833	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/FRPK3	Kenya	9
24	7310	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G6BR6	Kenya	9
25	16265	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/FVEPA	Eritrea	9
26	25172	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G43HT	Kenya	9
27	25212	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G44TY	Papua New Guinea	9
28	25224	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G4565		9
29	25065	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G406Y	Botswana	9
30	25210	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G44RW		9
31	15409	<i>Vigna unguiculata var. spontanea</i>	10.18730/FTNZ~	Ethiopia	10
32	17792	<i>Vigna unguiculata var. spontanea</i>	10.18730/FWR77	Nigeria	10
33	2220	<i>Vigna unguiculata var. spontanea</i>	10.18730/G1403	Ethiopia	10
34	7823	<i>Vigna unguiculata var. spontanea</i>	10.18730/G6QTP	Ethiopia	10
35	1036	<i>Vigna unguiculata var. spontanea</i>	10.18730/FPE1C	Burundi	10
36	25220	<i>Vigna unguiculata var. spontanea</i>	10.18730/G4521	Zambia	10
37	24990	<i>Vigna unguiculata subsp. dekindtiana</i>	10.18730/G3XTW	Zambia	10
38	42	<i>Vigna unguiculata subsp. pubescens</i>	10.18730/G4KGK	Tanzania	10
39	15736	<i>Vigna unguiculata var. spontanea</i>	10.18730/FTZ8\$	Chad	10
40	15734	<i>Vigna unguiculata var. spontanea</i>	10.18730/FTZ6*	Chad	10

Subspecies inferred based on hierarchical clustering are shaded gray.



Contact: genebanks@cgiar.org

CGIAR is a global research partnership for a food-secure future. CGIAR science is dedicated to transforming food, land, and water systems in a climate crisis. Its research is carried out by 13 CGIAR Centers/Alliances in close collaboration with hundreds of partners, including national and regional research institutes, civil society organizations, academia, development organizations and the private sector. www.cgiar.org

We would like to thank all funders who support this research through their contributions to the CGIAR Trust Fund: www.cgiar.org/funders.

To learn more about the CGIAR Genebanks Accelerator, please visit [this webpage](#).

To learn more about this and other Science Programs and Accelerators in the CGIAR Research Portfolio 2025–2030, please visit www.cgiar.org/cgiar-research-portfolio-2025-2030/

Copyright: © 2026. International Livestock Research Institute (ILRI). This publication is licensed for use under a Creative Commons Attribution 4.0 International License (CC BY 4.0). To view this license, visit <https://creativecommons.org/licenses/by/4.0>.

