

Collaborative Oat Research Enterprise (CORE): Outcome, Progress, and Beyond

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Origin and Goal of CORE

Oat has been widely recognised as a healthy food since the start of the “oats craze” in the late 1980s. However, oat production in North America has continued to decrease, and any increased future demand for oats will likely come through innovation at different stages of the oat value-chain. The belief that superior oat varieties are a key innovation of the whole value-chain was the primary motivator for CORE. In 2009, the idea to develop newly available tools to support molecular breeding was presented to oat workers from across North America by Eric Jackson, then research scientist at USDA-ARS, Aberdeen, Idaho. People were filled of enthusiasm and the CORE, a combined effort of oat breeders and researchers, was born.

CORE aimed to develop a high-throughput genotyping array and to collect extensive phenotypic data of key oat traits. As a first step, CORE members have selected a suite of diverse genetic material (*cf.* **Germplasm** box). The CORE material were then phenotyped across multiple locations over two years (*cf.* **Phenotyping** box) and used for high-throughput genotyping array design and application (*cf.* **Outcome and Progress** boxes).

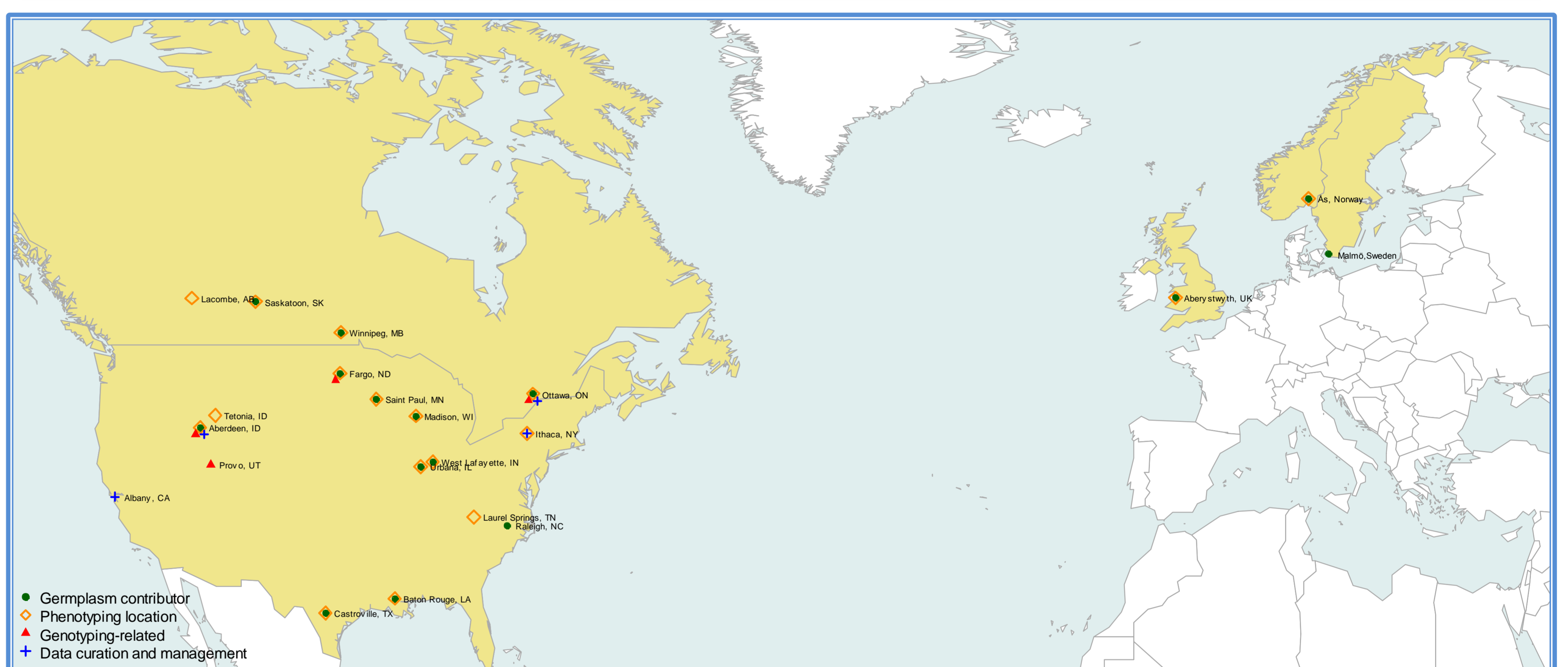


Figure 1. CORE map. Geographical distribution of the origin of CORE germplasm is not shown.

Phenotyping

In 2010 and 2011, phenotypes were assessed across fifteen locations in North America and two locations in Europe. Four categories of traits can be distinguished: agronomic traits (yield, test-weight, days to heading, etc.), disease (crown rust, stem rust, smut), milling-related (groat percentage), and nutrition-related (beta-glucan, avenanthramides).

Figure 2. CORE phenotypic data map. Available data are shown in green.

Location	Panel	Year	Agronomic	Disease	Milling-related	Nutrition-related
Aberdeen, ID	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Aberystwyth, UK	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Baton-Rouge, LA	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Castroville, TX	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Fargo, ND	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Urbana, IL	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
West Lafayette, IN	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Ithaca, NY	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Lacombe, AB	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Laurel Springs, TN	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Ås, Norway	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Ottawa, ON	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Saint Paul, MN	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Saskatoon, SK	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Tetonia, ID	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Winnipeg, MB	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y
Madison, WI	AFRI109	2010	Y	Y	Y	Y
	Spring	2011	Y	Y	Y	Y
	Winter	2011	Y	Y	Y	Y

Germplasm

Germplasm is the foundation of all breeding-related research. Thirteen oat breeding programs from twelve locations in North America have contributed from six to 60 lines. Three breeding programs in Europe (Norway, Sweden and the United Kingdom) contributed their germplasm shortly afterwards. Breeding materials were distinguished as belonging to the “Spring” or “Winter” panel according to the source breeding programs. In addition to the breeding material, a panel of 109 oat lines, representing the worldwide diversity of cultivated oat (AFRI109), was selected from a larger panel put together previously through the leadership of Nick Tinker at Agriculture and Agri-Food Canada, Ottawa. Six bi-parental mapping populations were also part of the CORE plant material, including the two well-known populations, Kanota x Ogle and Ogle x TAMO-301.

Table 1. CORE germplasm.

* Including five spring lines and one winter line.
** including spring and winter lines.

Source	No. of lines
"Spring" panel (total 431 lines)	
NULS, Ås, Norway	15
IBERS, Aberystwyth, Ceredigion, UK	6*
Lantmännen, Sweden	11
AAFC, Ottawa, Canada	45
AAFC, Winnipeg, Canada	41
CDC/U. Saskatchewan, SK, Canada	46
NDSU, ND, USA	48
Purdue U., IN, USA	35
U. Minnesota, St. Paul, MN, USA	39
U. Wisconsin, WI, USA	47
U. Illinois, IL, USA	46
USDA-ARS, Aberdeen, ID, USA	47
USDA-ARS, St. Paul, MN, USA	6
"Winter" panel (total 139 lines)	
LSU, LA, USA	60
NCSU, NC, USA	32
Texas A&M, TX, USA	46
World diversity panel **	
AFRI109	109
Bi-parental Mapping Populations (total 406 lines)	
CDC SolFi x HiFi (F7)	52
Hurdal x Z-597 (F6)	53
Kanota x Ogle (F10)	52
Ogle x TAMO-301 (F6:7)	53
Otana x PI269616 (F6)	98
Provena x GS7 (F8)	98

Project Organisation

The Small Grains and Potato Germplasm Research Unit of USDA-ARS in Aberdeen, Idaho was in charge of the seed increase and distribution of the plant material for genotyping and phenotyping.

Outcome and Progress: Markers and Consensus Map

The foundational tool for applying new-generation molecular breeding to oat is a set of reliable markers and a saturated genetic map. After the development of a pilot Illumina OPA SNP assay, CORE provided the whole oat community with the **first chromosome-anchored oat consensus map** (Oliver *et al.*, 2013, Figure 3). This map contains 1054 markers and covers 21 linkage groups with a total length of 1838.8 cM. In addition, a new **Illumina Infinium BeadChip SNP assay** was recently made available (Tinker *et al.*, 2014). This release provides approximately 3500 high-quality SNPs. A genotyping technology based on next-generation sequencing, **genotyping-by-sequencing (GBS)**, has been successfully applied to the CORE germplasm as well (Huang *et al.*, 2014). We are currently developing a new version of the oat consensus map based on approx. 3500 Infinium SNP markers, 10,320 GBS markers, 2000 historical RFLP loci, and 500 wheat SNPs (*cf.* Schlueter *et al.* at this conference). This new map will be the foundation of oat molecular breeding and genetic dissection of key oat traits.

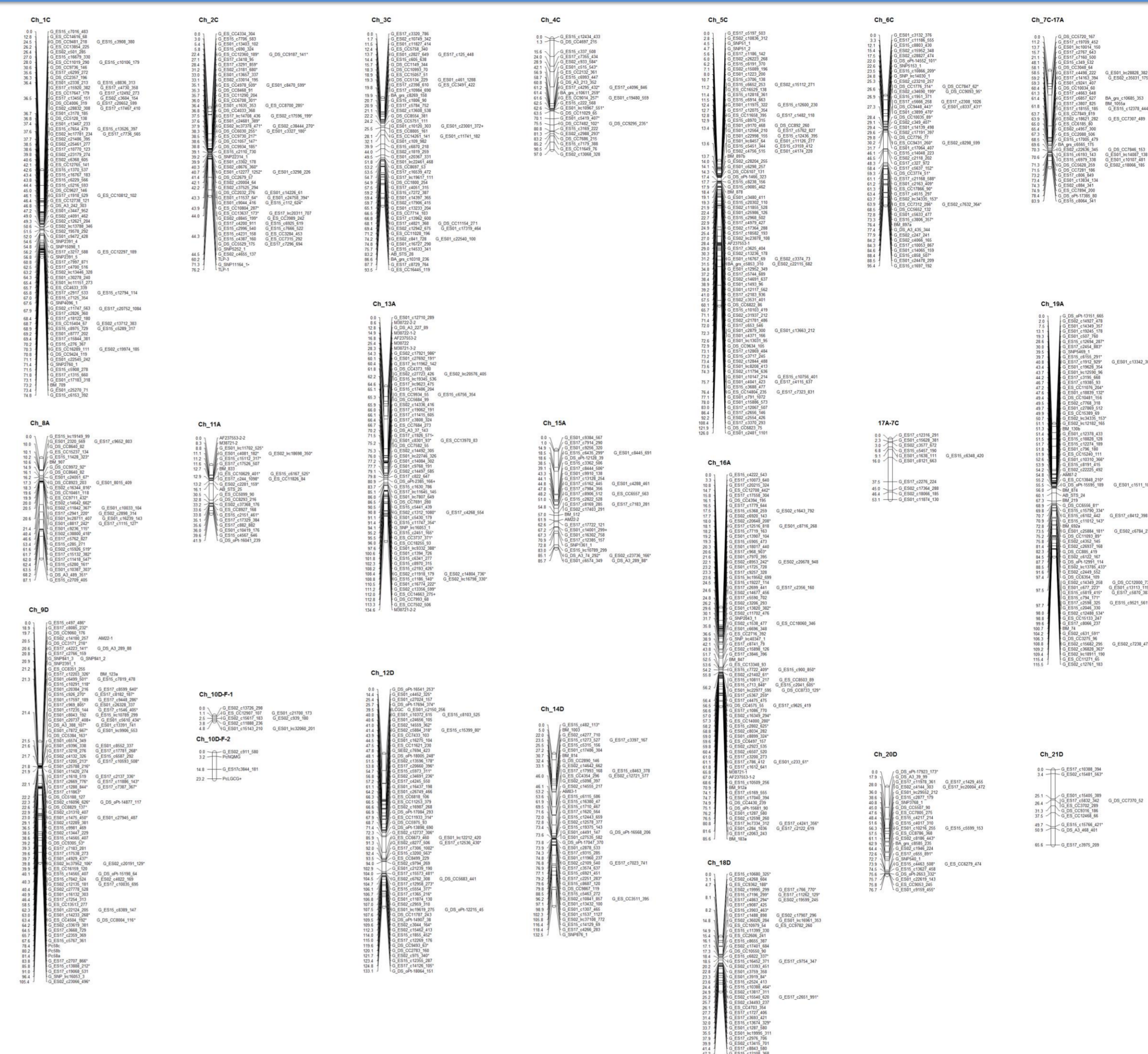


Figure 3. First chromosome-anchored oat consensus map. From Oliver *et al.*, 2013, Figure S1.

Outcome and Progress: Knowledge of Oat Diversity and Genetic Dissection of Key Traits

The “Spring”, “Winter”, and “AFRI109” panels were both genotyped and phenotyped (*cf.* Figure 2). They are, therefore, excellent material for use in the genetic dissection of key oat traits, which is the basis for rational employment of molecular tools in oat breeding. We have recently finalised data curation of both genotypic and phenotypic data. Currently, we are in the process of analysing the genetic organisation of CORE material; in other words, how the lines are related (or not) (*cf.* Klos *et al.* at this conference). The principal component analysis (PCA) of genotypic data showed that the full CORE panel (Spring, Winter, AFRI109) can, for the most part, be distinguished through growth habit (Figure 4). The genotypic data also revealed features of the material coming from different breeding programs: some are highly related and others represent a broader genetic background. Soon, we expect to release standard datasets for genome-wide association mapping to the community.

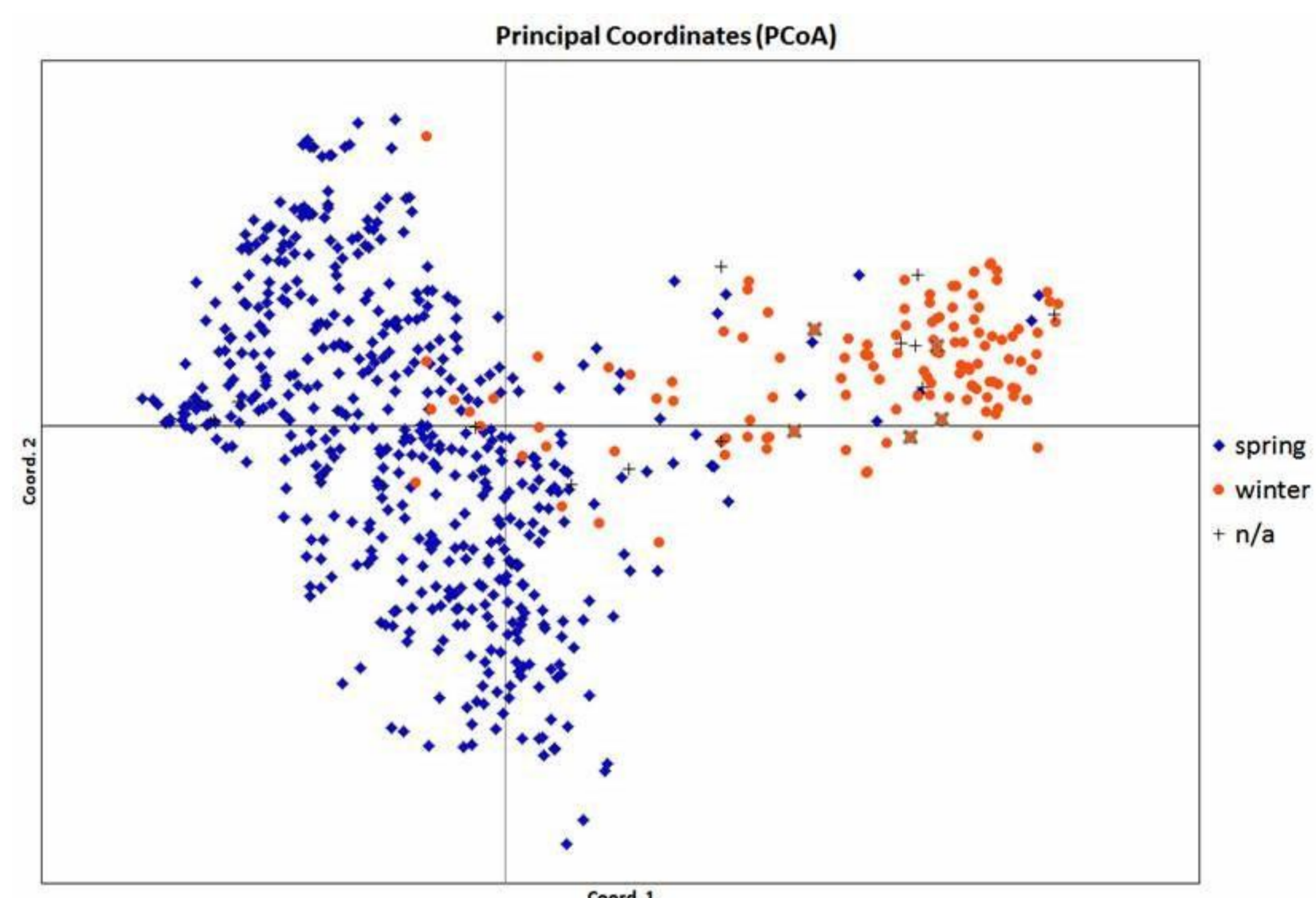
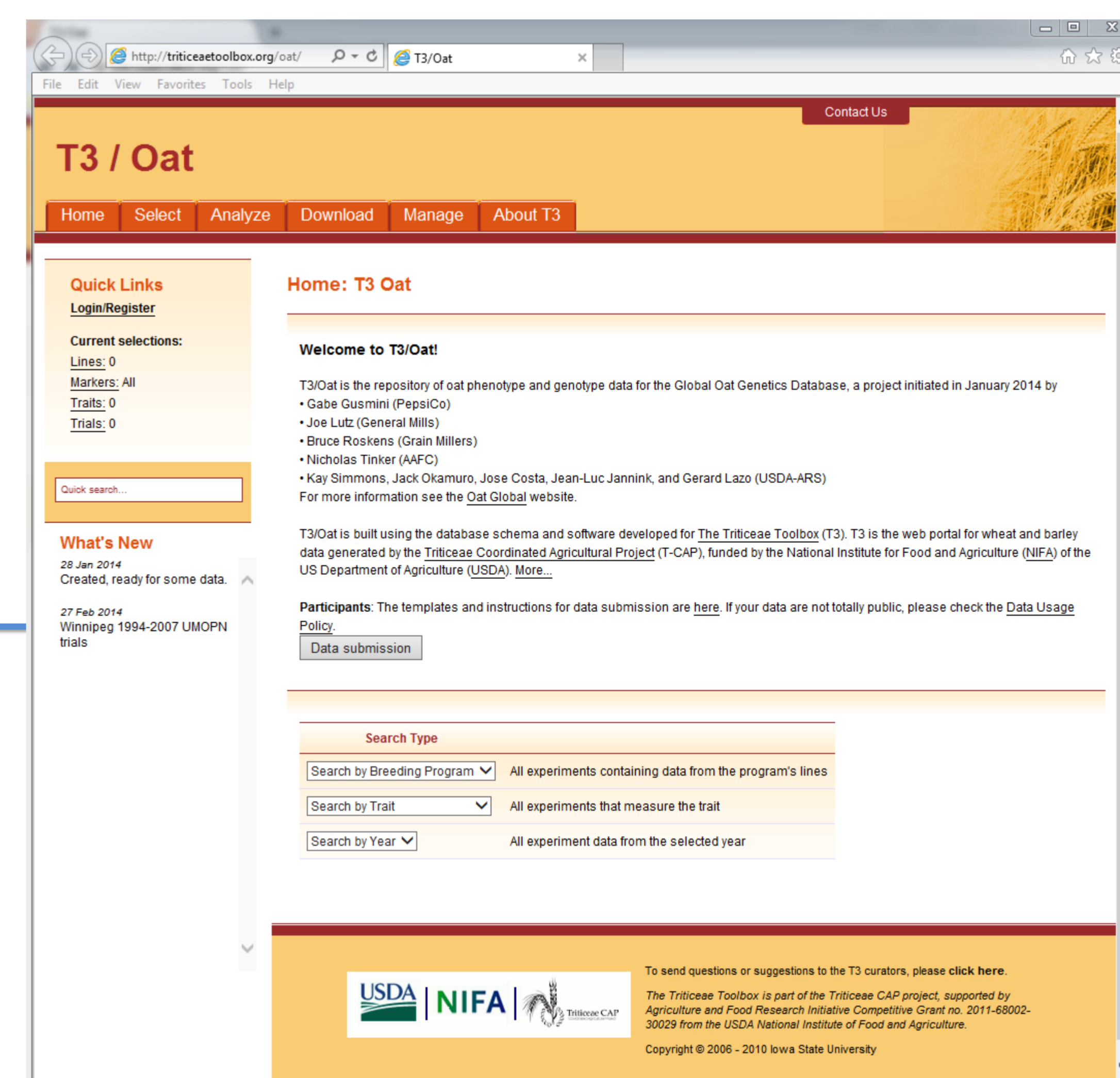


Figure 4. PCA of molecular marker data from all CORE material. The first two PC are shown. Oat lines are coloured according to growth habit. *Cf.* Klos *et al.* at this conference.

Moving Forward: Oat Data Management

Once the major outcomes of the CORE project have been communicated, there will be many opportunities to mine the data further. The spirit of the CORE project has been that the data should remain in the public domain as long as the publication intentions of the original CORE members are respected. With this in mind, the CORE community has curated and is preparing a relational database containing the genotypic and phenotypic data collected on CORE germplasm. This database will be presented and described at this conference (Jannink *et al.*, session 1).



Acknowledgement

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Reference

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