Digging into the adaptive response to drought in Asian rice (*Oryza sativa* L.)

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Background

- Asian rice (Oryza sativa) is the primary calorie source for > 50% of the global population.

- Water scarcity is a major challenge for current and future rice production (**Fig. 1**).

- We will use key trait genetic architectures and existing genetic and varietal resources of rice to predict high-yielding genotypes under drought stress.
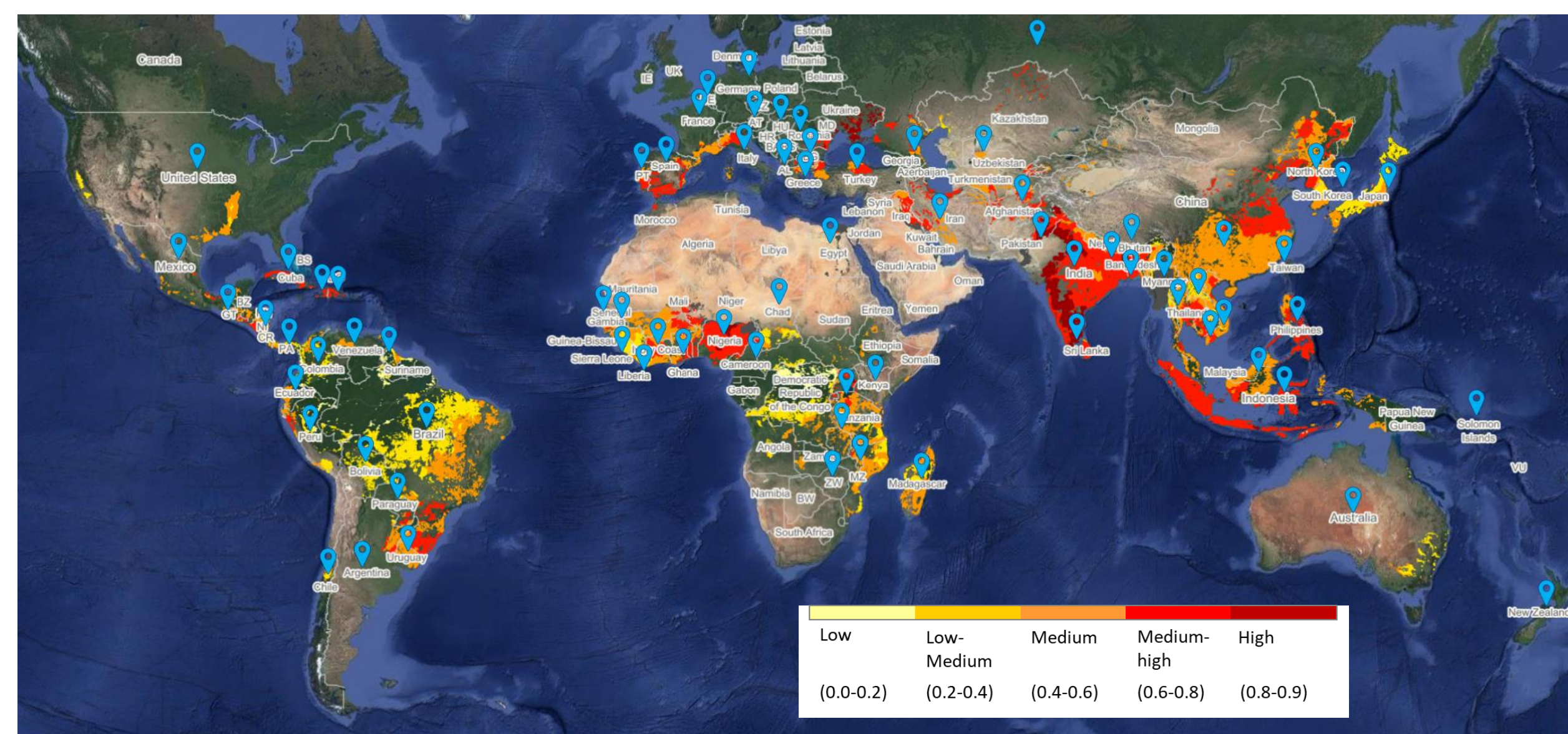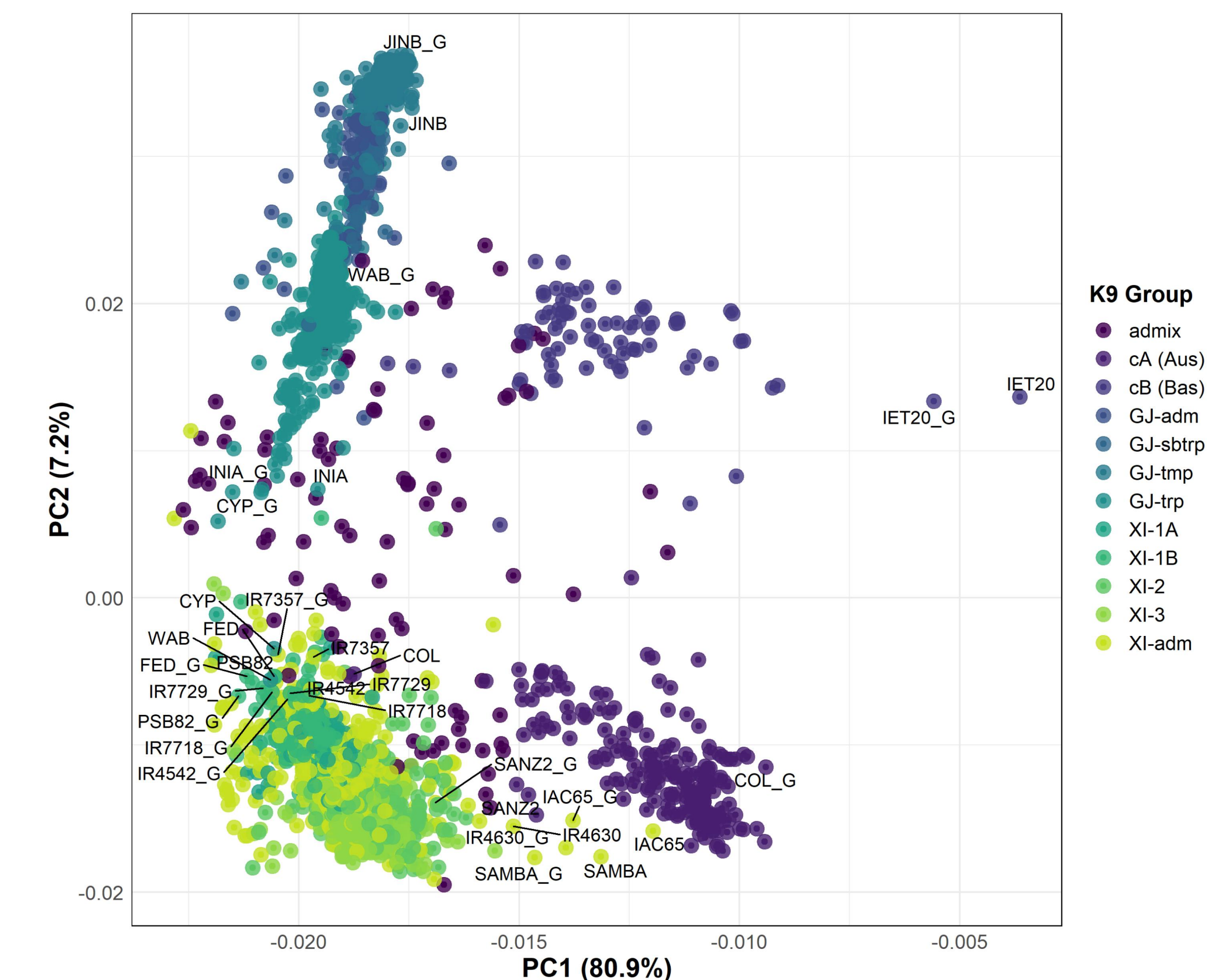

Figure 1. Drought risk in irrigated and rainfed rice production areas worldwide. Blue pointers indicate country of origin for the 3,024 rice accessions sequenced by [2]. Created with the Aqueduct Food tool from the Water Resource Institute (USA).

Low (0.0-0.2)	Low-Medium (0.2-0.4)	Medium (0.4-0.6)	Medium-high (0.6-0.8)	High (0.8-0.9)

The Plan

- We evaluated growth, phenology, and yield component traits under drought and well-watered conditions across multiple growing seasons in the 16-parent diverse Global Multi-parent Advanced Generation Inter-Cross (**MAGIC**) population developed by inter-crossing elite varieties from *indica* and *japonica* subspecies [1].

- We identified significant marker-trait associations for these traits across treatments and seasons, finding that **many loci exhibit dynamic reaction norms of effect size with respect to environment** (**Fig. 2**) **and developmental time.**

- We will use these GWAs to predict trait **polygenic scores** [2] in a diverse re-sequenced collection of **3,024 rice accessions** [3] originating from **89 countries** (**Fig. 1**).

- Shifts in allele frequencies at candidate loci reflect historical and geographic patterns of selection for key traits. **Our aim is to identify both patterns of adaptation in drought response and potential donors of drought tolerance alleles in rice.**

- We aligned genotyping-by-sequencing (GBS) derived variants from the Global MAGIC population against the two best subspecies genomes: (*i*) *japonica* Nipponbare (**7,793 loci**); (*ii*) *indica* 93-11 (**7,607 loci**).

- We retrieved whole-genome resequencing data from the 3K rice panel [2] and filtered for these variants.

- **The population structure of these variants is similar to that from the whole genome data [2]**, although they primarily differentiate the aus/basmati subpopulations from *indica/japonica*, and only secondarily the two major subspecies (**Fig. 3**).

- We observe genotypic discordance between the GBS and 3K data for three of 16 MAGIC parents in both datasets (**Fig. 3**), likely from low quality 3K data or different DNA source.

- **After filtering for high-quality genotypes and imputing missing data, we will estimate trait polygenic scores following the approach of Josephs et al. [4] and examine how these vary with geography.**

Figure 3. Genetic variation among the 3K rice accessions and the 16 Global MAGIC parents along the first two Principal Component axes of GBS-derived Global MAGIC variants. Labels indicate the parental lines both from the MAGIC data and the 3K WGS data (labels with the suffix "_G"). Samples are colored based on population structure as in [2]. *cA = Aus type accessions; cB = Basmati; GJ = japonica; XI = indica, with various subpopulations; adm = admixed; sbtrp = subtropical; tmp = temperate; trp = tropical.*

Figure 2. Effect sizes from genome-wide associations for: (top; left-to-right) plant height, grain yield, harvest index; (bottom; left-to-right) mesocotyl length, straw biomass, and axial root number. Lines connect the same genetic variant across environments. Only genetic variants with a significant association to trait variance in at least one environment are shown. DS14s = dry season 2014 – seedling stage drought stress; DS15s = dry season 2015 – seedling stage drought stress; DS15w = dry season 2015 – well-watered conditions.

References. [1] Bandillo *et al.* "Multi-parent advanced generation inter-cross (MAGIC) populations in rice: progress and potential for genetics research and breeding." *Rice* 2013 6:11. [2] Wang *et al.* "Genomic variation in 3,010 diverse accessions of Asian cultivated rice." *Nature* 2018 557: 43-49. [3] Berg and Coop "A Population Genetic Signal of Polygenic Adaptation." *PLoS Genetics* 2014 10(8): e1004412. [4] Josephs *et al.* "Detecting Adaptive Differentiation in Structured Populations with Genomic Data and Common Gardens." *Genetics* 2019 211: 989-1004.